

(19)



Europäisches Patentamt

European Patent Office

Office européen des brevets



(11)

**EP 0 756 006 A2**

(12)

**EUROPEAN PATENT APPLICATION**

(43) Date of publication:

29.01.1997 Bulletin 1997/05

(21) Application number: 96109204.6

(22) Date of filing: 07.06.1996

(51) Int. Cl.<sup>6</sup>: **C12N 15/31**, C12N 15/10,  
C12N 5/10, C12N 15/85,  
C12P 21/08, C07K 14/30,  
C07K 16/12, C12Q 1/68,  
A61K 39/395

(84) Designated Contracting States:

AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC  
NL PT SE

(30) Priority: 07.06.1995 US 488018

07.06.1995 US 473545

19.10.1995 US 545528

(71) Applicants:

- THE INSTITUTE FOR GENOMIC RESEARCH  
Rockville, Maryland 20850 (US)
- THE JOHNS HOPKINS UNIVERSITY  
Baltimore, MD 21205 (US)
- THE UNIVERSITY OF NORTH CAROLINA AT  
CHAPEL HILL  
Chapel Hill, North Carolina 27599-4105 (US)

(72) Inventors:

- Fraser, Claire M.  
Rockville, Maryland 20850 (US)
- Adams, Mark D.  
N. Potomac, Maryland (US)
- Gocayne, Jeannine D.  
Silver Springs, Maryland 20902 (US)
- Hutchison, Clyde A., III  
Chapel Hill, North Carolina 27514 (US)
- Smith, Hamilton O.  
Towson, Maryland 21204 (US)
- Venter, J. Craig  
Rockville, Maryland 20850 (US)
- White, Owen  
Gaithersburg, Maryland 20878 (US)

(74) Representative: VOSSIUS & PARTNER

Siebertstrasse 4  
81675 München (DE)

(54) **Nucleotide sequence of the mycoplasma genitalium genome, fragments thereof, and uses thereof**

(57) The present invention provides the nucleotide sequence of the entire genome of *Mycoplasma genitalium*, SEQ ID NO:1. The present invention further provides the sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use. In addition to the entire genomic sequence, the present invention identifies protein encoding fragments of the genome, and identifies, by position relative to two (2) genes known to flank the origin of replication, any regulatory elements which modulate the expression of the protein encoding fragments of the *Mycoplasma genitalium* genome.

**Description****Cross-Reference to Related Applications**

- 5 This application is a continuation-in-part of application nos. 08/488,018 and 08/473,545, both filed June 7, 1995, and both of which are hereby incorporated by reference.

**Background of the Invention**

10 **Statement as to Rights to Inventions Made Under Federally-Sponsored Research and Development**

Part of the work performed during development of this invention utilized U.S. Government funds. The U.S. Government may have certain rights in the invention -DE-FC02-95ER61962.A000; NP-838C; NIH-AI08998, AI33161, and HL19171.

15

**Field of the Invention**

- 20 The present invention relates to the field of molecular biology. The invention discloses compositions comprising the nucleotide sequence of *Mycoplasma genitalium*, fragments thereof, and its use in medical diagnostics, therapies and pharmaceutical development.

**Related Background Art**

- 25 Mycoplasmas are the smallest free-living bacterial organisms known (Colman, S.D. *et al.*, *Mol. Microbiol.* 4:683-687 (1990)). Mycoplasmas are thought to have evolved from higher gram-positive bacteria through the loss of genetic material (Bailey, C.C. *et al.*, *J. Bacteriol.* 176:5814-5819 (1994)). *Mycoplasma genitalium* (*M. genitalium*) is widely considered to be the smallest self-replicating biological system, as the molecular size of its genome has been shown to be only 570-600kp (Pyle, L.E. *et al.*, *Nucleic Acids Res.* 16(13):6015-6025 (1988); Peterson, S.N. *et al.*, *J. Bacteriol.* 175:7918-7930(1993)). All mycoplasmas lack a cell wall and have small genomes and a characteristically low G+C content (Razin, S., *Microbiol. Rev.* 49(4):419-455 (1985); Peterson, S.N. *et al.*, *J. Bacteriol.* 175:7918-7930(1993)). Some mycoplasmas, including *M. genitalium*, have a specialized codon usage, whereby UGA encodes tryptophan rather than serving as a stop codon (Inamine, J.M. *et al.*, *J. Bacteriol.* 172:504-506 (1990); Tanaka, J.G. *et al.*, *Nucleic Acids Res.* 19:6787-6792 (1991); Yamao, F.A. *et al.*, *Proc. Natl. Acad. Sci. USA* 82:2306-2309 (1985)).

- 30 Mycoplasmas are widely known to be significant pathogens of humans, animals, and plants (Bailey, C.C. *et al.*, *J. Bacteriol.* 176:5814-5819 (1994)). The metabolic systems of mycoplasmas indicate that they are generally biosynthetically deficient, and thus depend on the microenvironment of the host by characteristically adhering to host cells in order to obtain essential precursor molecules, *i.e.*, amino acids, fatty acids and sterols etc. (Baseman, J.B., 1987. *Mycoplasma Cell Membranes*, Vol. 20. The Plenum Press, New York, NY).

- 35 In particular, *M. genitalium*, a newly discovered species, is a pathogenic etiological agent first isolated in 1980 from the urethras of human males infected with non-gonococcal urethritis (Tully, J. G. *et al.*, *Lancet* 1:1288-1291 (1981); Tully, J.G., *et al.*, *Int. J. Syst. Bacteriol.* 33:387-396 (1983)). *M. genitalium* has also been identified in specimens of pneumonia patients as a co-isolate of *Mycoplasma pneumoniae* (Baseman, J.B. *et al.*, *J. Clin. Microbiol.* 26:2266-2269 (1988)). *M. genitalium* opportunistic infection has often been observed in individuals infected with human immunodeficiency virus type 1 (HIV-1) (Lo, S.-C. *et al.*, *Amer. J. Trop. Med. Hyg.* 41:601-616 (1989); Lo, S.-C. *et al.*, *Amer. J. Trop. Med. Hyg.* 41:601-616 (1989); Sasaki, Y. *et al.*, *AIDS Res. Hum. Retrov.* 9(8):775-780 (1993)). Mycoplasmas can also induce various cytokines, including tumor necrosis factor, which may enhance HIV replication (Chowdhury, I.H. *et al.*, *Biochem. Biophys. Res. Commun.* 170:1365-1370 (1990)).

- 40 A high amino acid homology exists between the attachment protein of *M. genitalium* and the aligned proteins of several human Class II major histocompatibility complex proteins (HLA), suggesting that *M. genitalium* infection may play an important role in triggering autoimmune mechanisms, thereby aggravating the immunodeficiency characteristics of acquired immune deficiency syndrome (AIDS) (Montagnier, L. *et al.*, *C.R. Acad. Sci. Paris* 311(3):425-430 (1990); Root-Bernstein, R.S. *et al.*, *Res. Immunol.* 142:519-523 (1991); Bisset, L.R. *Autoimmunity* 14:167-168 (1992)). A diagnostic immunoassay for detecting *M. genitalium* infection using monoclonal antibodies specific for some *M. genitalium* antigens has been developed. Baseman, J.B. *et al.*, U.S. Pat. No. 5,158,870.

- 45 Due to its diminutive genomic size, *M. genitalium* provides a useful model for determining the minimum number of genes and protein products necessary for a host-independent existence. *M. genitalium* expresses a characteristically low number of base-pairs and low G+C content, which along with its UGA tryptophan codon, has hampered sequencing efforts by conventional techniques (Razin, A., *Microbiol. Rev.* 49(4):419-455 (1985); Colman, S.D. *et al.*, *Gene* 87:91-96 (1990); Dybvig, K. 1992. *Gene Transfer In: Maniloff, J. (ed.) Mycoplasmas: Molecular Biology and Pathogenesis.*



Am. Soc. Microbiol. Washington, D.C., pp.355-362)). *M. genitalium* possesses a single circular chromosome (Colman, S.D. et al., *Gene* 87:91-96 (1990); Peterson, S.N. et al., *J. Bacteriol.* 175:7918-7930 (1993)). The characterization of the genome of *M. genitalium* has also been hampered by the lack of auxotrophic mutants and by the lack of a system for genetic exchange, precluding reverse genetic approaches. Thus, the sequencing of the *M. genitalium* genome would enhance the understanding of how *M. genitalium* causes or promotes various invasive or immunodeficiency diseases and to how best to medically combat mycoplasma infection.

Prior attempts at characterizing the structure and gene arrangement of the chromosomes of mycoplasmas using pulsed-field gel electrophoretic methods (Pyle, L.E. et al., *Nucleic Acids Res.* 16(13):6015-6025 (1988); Neimark, H.C. et al., *Nucleic Acids Res.* 18(18):5443-5448 (1990)), indicated that mycoplasmas have genomes ranging widely in size. Southern blot hybridization of digested DNAs of *M. genitalium* compared to the well-known human pathogen, *M. pneumoniae*, indicated overall low homology values of approximately 6-8% (Yogev, D. et al., *Int. J. Syst. Bacteriol.* 36(3):426-430 (1986)). However, high homologies have been reported between the adhesin genes of *M. genitalium* and *M. pneumoniae* (Dallo, S.F. et al., *Microbial Path.* 6:69-73 (1989)). Initial studies at characterizing the genome of *M. genitalium* by comparison to the well-known *M. pneumoniae* species, indicated that both species have three (3) rRNA genes clustered together in a chromosomal segment of about 5kb and form a single operon organized in classical procaryotic fashion, but differences exist between their respective restriction sites (Yogev, D. et al., *Int. J. Syst. Bacteriol.* 36(3):426-430 (1986)).

Restriction enzyme mapping of *M. genitalium* indicates that the genome is approximately 600kb. Several genes have also been mapped, including the single ribosomal operon, and the gene encoding the MgPa cytoadhesion protein (Su, C.J. et al., *J. Bacteriol.* 172:4705-4707 (1990); Colman, S.D. et al., *Mol. Microbiol.* 4(4):683-687 (1990)). The entire restriction map of the genome of *M. genitalium* has also been cloned in an ordered library of 20 overlapping cosmids and one  $\lambda$  clone (Lucier, T.S. et al., *Gene* 150:27-34 (1994)).

An initial study using random sequencing techniques to characterize the *M. genitalium* genome resulted in forty-four (44) random clones being partially sequenced; several long open reading frames were also found (Peterson, S.N. et al., *Nucleic Acids Res.* 19:6027-6031 (1991)). Subsequent work using random sequencing of 508 random nonidentical clones has allowed sequence information to be compiled for approximately seventeen percent (17%) (100,993 nucleotides) of the *M. genitalium* genome (Peterson, S.N. et al., *J. Bacteriol.* 175:7918-7930 (1993)). Sequence information indicates that the diminutive genome of *M. genitalium* contains numerous genes involved in various metabolic processes. The genome is estimated to encode approximately 390 proteins, indicating that *M. genitalium* makes very efficient use of its limited amount of DNA (Peterson, S.N. et al., *J. Bacteriol.* 175:7918-7930 (1993)).

Several studies have been undertaken to sequence and characterize individual genes identified in *M. genitalium*. In particular, the medically important aspects of *M. genitalium* have helped to direct interest to those genes which determine the degree of infectivity and the virulence characteristics of the organism. The nucleotide sequence and deduced amino acid sequence for the MgPa adhesin gene, i.e., the gene encoding the surface cytoadhesion protein of *M. genitalium*, indicates that the complete gene contains 4,335 nucleotides coding for a protein of 159,668 Da. (Dallo, S.F. et al., *Infect. Immun.* 57(4):1059-1065 (1989)). Furthermore, subsequent nucleotide sequencing of the *M. genitalium* MgPa adhesin gene revealed the specific codon order for this important gene (Inamine, J.M. et al., *Gene* 82:259-267 (1989)). The MgPa adhesin gene also has been shown to express restriction fragment length polymorphism (Dallo, S.F. et al., *Microbial Path.* 10:475-480 (1991)). Nucleotide homology to the well-known highly conserved procaryotic origin-of-replication gene (*gyrA*) was noted for *M. genitalium* (Bailey, C.C. et al., *J. Bacteriol.* 176:5814-5819 (1994)). The highly conserved procaryotic elongation factor, Tu, encoded by the *tuf* gene, has been noted and sequenced for *M. genitalium*, and was found to contain an open reading frame encoding a protein of approximately 393 amino acids (Loechel, S. et al., *Nucleic Acids Res.* 17(23):10127 (1989)). The *tuf* gene of *M. genitalium* has also been determined to use a signal other than a Shine-Delgarno (ribosomal binding site) sequence preceding the initiation codon (Loechel, S. et al., *Nucleic Acids Res.* 19:6905-6911 (1991)).

### Summary of the Invention

The present invention is based on the sequencing of the *Mycoplasma genitalium* genome. The primary nucleotide sequence which was generated is provided in SEQ ID NO:1.

The present invention provides the generated nucleotide sequence of the *Mycoplasma genitalium* genome, or a representative fragment thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, present invention is provided as a contiguous string of primary sequence information corresponding to the nucleotide sequence depicted in SEQ ID NO:1.

The present invention further provides nucleotide sequences which are at least 99.9% identical to the nucleotide sequence of SEQ ID NO:1.

The nucleotide sequence of SEQ ID NO:1, a representative fragment thereof, or a nucleotide sequence which is at least 99.9% identical to the nucleotide sequence of SEQ ID NO:1 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer read-

able media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Mycoplasma genitalium* genome.

Another embodiment of the present invention is directed to isolated fragments of the *Mycoplasma genitalium* genome. The fragments of the *Mycoplasma genitalium* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs), fragments which mediate the uptake of a linked DNA fragment into a cell, hereinafter uptake modulating fragments (UMFs), and fragments which can be used to diagnose the presence of *Mycoplasma genitalium* in a sample, hereinafter, diagnostic fragments (DFs).

Each of the ORF fragments of the *Mycoplasma genitalium* genome disclosed in Tables 1(a), 1(c) and 2, and the EMF found 5' to the ORF, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers for the presence of a specific microbe in a sample, for the production of commercially important pharmaceutical agents, and to selectively control gene expression.

The present invention further includes recombinant constructs comprising one or more fragments of the *Mycoplasma genitalium* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Mycoplasma genitalium* has been inserted.

The present invention further provides host cells containing any one of the isolated fragments of the *Mycoplasma genitalium* genome of the present invention. The host cells can be a higher eukaryotic host such as a mammalian cell, a lower eukaryotic cell such as a yeast cell, or can be a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated proteins encoded by the ORFs of the present invention. A variety of methodologies known in the art can be utilized to obtain any one of the proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. In an alternative method, the protein is purified from bacterial cells which naturally produce the protein. Lastly, the proteins of the present invention can alternatively be purified from cells which have been altered to express the desired protein.

The invention further provides methods of obtaining homologs of the fragments of the *Mycoplasma genitalium* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind one of the proteins of the present invention. Such antibodies include both monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples derived from cells which express one of the ORF of the present invention, or homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to a protein encoded by one of the ORFs of the present invention. Specifically, such agents include antibodies (described above), peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise the steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and
- (b) determining whether the agent binds to said protein.

The complete genomic sequence of *M. genitalium* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Mycoplasma genitalium* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Mycoplasma* researchers and for immediate commercial value for the production of proteins or to control gene expression. A specific example concerns PHA synthase. It has been reported that polyhydroxybutyrate is present in the membranes of *M. genitalium* and that the amount correlates with the level of competence for transformation. The PHA

synthase that synthesizes this polymer has been identified and sequenced in a number of bacteria, none of which are evolutionarily close to *M. genitalium*. This gene has yet to be isolated from *M. genitalium* by use of hybridization probes or PCR techniques. However, the genomic sequence of the present invention allows the identification of the gene by utilizing search means described below.

Developing the methodology and technology for elucidating the entire genomic sequence of bacterial and other small genomes has and will greatly enhance the ability to analyze and understand chromosomal organization. In particular, sequenced genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the ability to do comparative genomic and molecular phylogeny.

### Brief Description of the Figures

Figure 1 - EcoRI restriction map of the *Mycoplasma genitalium* genome.

Figure 2 - Block diagram of a computer system 102 that can be used to implement the computer-based systems of present invention.

Figure 3 - Summary of the *Mycoplasma genitalium* sequencing project.

Figure 4 - A circular representation of the *M. genitalium* chromosome. Outer concentric circle: Coding regions on the plus strand for which a gene identification was made. Each coding region location is coded as to role according to the color code in Figure 5. Second concentric circle: Coding regions on the minus strand for which a gene identification was made. Third concentric circle: The direction of transcription on each strand of the chromosome is depicted as a red arrow starting at the putative origin of replication. Fourth concentric circle: Coverage by cosmid and lambda clones (blue). Nineteen cosmid clones and one lambda clone were sequenced from each end to confirm the overall structure of the genome. Fifth concentric circle: The locations of the single ribosomal operon (blue) and the 33 tRNAs. The clusters of tRNAs (trnA, trnB, trnC, trnD and trnE) are indicated by the letters A-E with the number of tRNAs in each cluster listed in parentheses. Sixth concentric circle: Location of the MgPa operon (green) and MgPa repeat fragments (brown).

Figure 5 - Gene map of the *M. genitalium* genome. Predicted coding regions are shown on each strand. The rRNA operon and tRNA genes are shown as a line and as triangles, respectively. Genes are color-coded by the role category as described in the Figure key. Gene identification numbers correspond to those in Table 6. Where possible, three-letter designations are also provided.

Figure 6 - Location of the MgPa repeats in the *M. genitalium* genome. The structure of the MgPa operon (ORF1-MgPa gene-ORF3) in the *M. genitalium* genome is illustrated across the top. In addition to the complete operon, nine repetitive elements which are composites of particular regions of the MgPa operon were found. The coordinates of each repeat in the genome are indicated on the left and right end of each line. The repetitive elements are located directly below those regions in the operon for which there is sequence similarity. The percent of sequence identity between the repeat elements and the MgPa gene ranges from 78%-90%. In some of the repeats, the MgPa-related sequences are separated in the genome by a variable length, A-T rich spacer sequence (indicated in the figure by a line with the length of the spacer indicated in bp). In cases where no spacer sequence is shown, the composites of the operon are co-linear in the genome. In repeats 7 and 9, the order of the sequences in the repeats differs from that in the operon. In these cases, the order of the elements in each repeat in the genome is indicated numerically where element 1 is followed by element 2 which is followed by element 3, etc.

### Detailed Description of the Preferred Embodiments

The present invention is based on the sequencing of the *Mycoplasma genitalium* genome. The primary nucleotide sequence which was generated is provided in SEQ ID NO:1. As used herein, the "primary sequence" refers to the nucleotide sequence represented by the IUPAC nomenclature system.

The sequence provided in SEQ ID NO:1 is oriented relative to two genes (DNAA and DNA gyrase) known to flank the origin of replication of the *Mycoplasma genitalium* genome. A skilled artisan will readily recognize that this start/stop point was chosen for convenience and does not reflect a structural significance.

The present invention provides the nucleotide sequence of SEQ ID NO:1, or a representative fragment thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the sequence is provided as a contiguous string of primary sequence information corresponding to the nucleotide sequence provided in SEQ ID NO:1.

As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NO:1" refers to any portion of SEQ ID NO:1 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Mycoplasma genitalium* open reading frames, expression modulating fragments, uptake modulating fragments, and fragments which can be used to diagnose the presence of *Mycoplasma genitalium* in sample. A non-limiting identification of such preferred representative fragments is provided in Tables 1(a), 1(c) and 2.

The nucleotide sequence information provided in SEQ ID NO:1 was obtained by sequencing the *Mycoplasma genitalium* genome using a megabase shotgun sequencing method. The nucleotide sequence provided in SEQ ID NO:1 is a highly accurate, although not necessarily a 100% perfect, representation of the nucleotide sequence of the *Mycoplasma genitalium* genome.

As discussed in detail below, using the information provided in SEQ ID NO:1 and in Tables 1(a), 1(c) and 2 together with routine cloning and sequencing methods, one of ordinary skill in the art would be able to clone and sequence all "representative fragments" of interest including open reading frames (ORFs) encoding a large variety of *Mycoplasma genitalium* proteins. In very rare instances, this may reveal a nucleotide sequence error present in the nucleotide sequence disclosed in SEQ ID NO:1. Thus, once the present invention is made available (i.e., once the information in SEQ ID NO:1 and Tables 1(a), 1(c) and 2 have been made available), resolving a rare sequencing error in SEQ ID NO:1 would be well within the skill of the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler™ can be used as an aid during visual inspection of nucleotide sequences.

Even if all of the very rare sequencing errors in SEQ ID NO:1 were corrected, the resulting nucleotide sequence would still be at least 99.9% identical to the nucleotide sequence in SEQ ID NO:1.

The nucleotide sequences of the genomes from different strains of *Mycoplasma genitalium* differ slightly. However, the nucleotide sequence of the genomes of all *Mycoplasma genitalium* strains will be at least 99.9% identical to the nucleotide sequence provided in SEQ ID NO:1.

Thus, the present invention further provides nucleotide sequences which are at least 99.9% identical to the nucleotide sequence of SEQ ID NO:1 in a form which can be readily used, analyzed and interpreted by the skilled artisan. Methods for determining whether a nucleotide sequence is at least 99.9% identical to the nucleotide sequence of SEQ ID NO:1 are routine and readily available to the skilled artisan. For example, the well known *fasta* algorithm (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444 (1988)) can be used to generate the percent identity of nucleotide sequences.

#### Computer Related Embodiments

The nucleotide sequence provided in SEQ ID NO:1, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NO:1 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO:1, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NO:1. Such a manufacture provides the *Mycoplasma genitalium* genome or a subset thereof (e.g., a *Mycoplasma genitalium* open reading frame (ORF)) in a form which allows a skilled artisan to examine the manufacture using means not directly applicable to examining the *Mycoplasma genitalium* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO:1, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NO:1 in computer readable form, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames

(ORFs) within the *Mycoplasma genitalium* genome which contain homology to ORFs or proteins from other organisms. Such ORFs are protein encoding fragments within the *Mycoplasma genitalium* genome and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

5 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *Mycoplasma genitalium* genome.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means 10 of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means 15 for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data 20 storage means. Search means are used to identify fragments or regions of the *Mycoplasma genitalium* genome which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or 25 implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target 30 sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments of the *Mycoplasma genitalium* genome, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed 35 upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Mycoplasma genitalium* genome possessing varying degrees of homology to the target sequence or target motif. Such 40 presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *Mycoplasma genitalium* genome. In the present examples, implementing 45 software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) was used to identify open reading frames within the *Mycoplasma genitalium* genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

One application of this embodiment is provided in Figure 2. Figure 2 provides a block diagram of a computer system 102 that can be used to implement the present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, etc. A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic 55 tape, etc.) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the data from the removable medium storage device 114 once inserted in the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. Software for accessing and

processing the genomic sequence (such as search tools, comparing tools, etc.) reside in main memory 108 during execution.

### Biochemical Embodiments

Another embodiment of the present invention is directed to isolated fragments of the *Mycoplasma genitalium* genome. The fragments of the *Mycoplasma genitalium* genome of the present invention include, but are not limited to fragments which encode peptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs), fragments which mediate the uptake of a linked DNA fragment into a cell, hereinafter uptake modulating fragments (UMFs), and fragments which can be used to diagnose the presence of *Mycoplasma genitalium* in a sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Mycoplasma genitalium* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are normally associated with the composition. A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Mycoplasma genitalium* DNA can be mechanically sheared to produce fragments of 15-20 kb in length. These fragments can then be used to generate an *Mycoplasma genitalium* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF provided in Table 1(a), 1(c) or 2 can then be generated using nucleotide sequence information provided in SEQ ID NO:1. PCR cloning can then be used to isolate the ORF from the lambda DNA library. PCR cloning is well known in the art. Thus, given the availability of SEQ ID NO:1, Table 1(a), 1(c) and Table 2, it would be routine to isolate any ORF or other representative fragment of the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein. Tables 1(a), 1(b), 1(c) and 2 identify ORFs in the *Mycoplasma genitalium* genome. In particular, Table 1(a) indicates the location of ORFs (i.e., the addresses) within the *Mycoplasma genitalium* genome which encode the recited protein based on homology matching with protein sequences from the organism appearing in parentheses (see the fifth column of Table 1(a)).

The first column of Table 1(a) provides the "UID" (an arbitrary identification number) of a particular ORF. The second and third columns in Table 1(a) indicate an ORFs position in the nucleotide sequence provided in SEQ ID NO:1. One of ordinary skill in the art will recognize that ORFs may be oriented in opposite directions in the *Mycoplasma genitalium* genome. This is reflected in columns 2 and 3.

The fourth column of Table 1(a) provides the accession number of the database match for the ORF. As indicated above, the fifth column of Table 1(a) provides the name of the database match for the ORF.

The sixth column of Table 1(a) indicates the percent identity of the protein encoded for by an ORF to the corresponding protein from the organism appearing in parentheses in the fifth column. The seventh column of Table 1(a) indicates the percent similarity of the protein encoded for by an ORF to the corresponding protein from the organism appearing in parentheses in the fifth column. The concepts of percent identity and percent similarity of two polypeptide sequences are well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (e.g., at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (i.e., possessed similar biochemical characteristics). The eighth column in Table 1(a) indicates the length of the ORF in nucleotides.

Table 1(b) is a list of ORFs that have database matches to previously published *Mycoplasma genitalium* sequences over the full length of the ORF. The table headings for Table 1(b) are identical for Table 1(a) with the following two exceptions: (I) The heading for the eighth column in Table 1(a) (i.e., nucleotide length of the ORF) has been replaced with the following in Table 1(b): "Match\_info". "Match\_info" refers to the coordinates of the match of the ORF and the previously published *Mycoplasma genitalium* sequence. For example, "MG002 (1-930 of 930) GB:U09251 (298-1227 of 6140)," indicates that for ORF MG002, which is 930 nucleotides in length, there is a database match to accession number GB:U09251, which has a total length of 6140 nucleotides. The ORF matches this accession from position 298 to 1227. (II) Where an ORF shows homology matches for both a previously published *Mycoplasma genitalium* sequence and a previously published sequence from a different organism, columns 3, 4, 5, and 6 of Table 1(b) respectively provide the accession number, protein name (and organism in parentheses), percent identity and percent similarity for the "other organism," rather than for the previously published *Mycoplasma genitalium* sequence. (However, in this scenario, the accession number for the *Mycoplasma genitalium* sequence is still provided in column 8.)

Table 1(c) provides ORFs having database matches to previously published *Mycoplasma genitalium* sequences



but only over a portion of the ORF. The table headings are the same as above for Table 1(b).

In Tables 1(a), 1(b) and 1(c), unique identifiers are used to identify the recited ORFs, (e.g., "MG123"). In the parent application nos. 08/488,018 and 08/473,545, the recited ORFs are identified using the "MORF" identifier. Table 1(d) lists which of the new and old identifiers refer to the same ORF. For example, the first entry in Table 1(d) indicates that the ORF identified as MG001 in the current application is the same ORF which was previously identified as MORF-20072 in parent application nos. 08/488,018 and 08/473,545. Similarly, the third entry in Table 1(d) indicates that the ORF identified as MG003 in the current application is the same ORF which was previously identified as MORF-19818 and MORF-20073 in the parent applications.

Table 2 provides ORFs of the *Mycoplasma genitalium* genome which did not elicit a "homology match" with a known sequence from either *M. genitalium* or another organism.

Table 6 classifies each ORF according to its role category (adapted from Riley, M., *Microbiol. Rev.* 57:862 (1992)). The gene identification, the accession number from public archives that corresponds to the best match, the percent amino acid identity, and the length of the match in amino acids is also listed for each entry as above in Tables 1 (a-c). Those genes in *M. genitalium* that also match a gene in *H. influenzae* are indicated by an asterisk (\*) For the purposes of Tables 6 and 7 and Figure 4, each of the MgPa repetitive elements has been assigned an MG number, even though there is evidence to suggest that these repeats may not be transcribed.

Table 7 sorts the gene content in *H. influenzae* and *M. genitalium* by functional category. The number of genes in each category is listed for each organism. The number in parentheses indicates the percent of the putatively identified genes devoted to each functional category. For the category of unassigned genes, the percent of the genome indicated in parentheses represents the percent of the total number of putative coding regions.

Further details concerning the algorithms and criteria used for homology searches are provided in the Examples below.

A skilled artisan can readily identify ORFs in the *Mycoplasma genitalium* genome other than those listed in Tables 1(a), 1(b), 1(c) and 2, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.

As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are fragments which induce the expression or an operably linked ORF in response to a specific regulatory factor or physiological event. A review of known EMFs from *Mycoplasma* are described by (Tomb *et al. Gene* 104:1-10 (1991), Chandler, M. S., *Proc. Natl. Acad. Sci. USA* 89:1626-1630 (1992).

EMF sequences can be identified within the *Mycoplasma genitalium* genome by their proximity to the ORFs provided in Tables 1(a), 1(b), 1(c) and 2. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200 nucleotides in length, taken 5' from any one of the ORFs of Tables 1(a), 1(b), 1(c) or 2 will modulate the expression of an operably linked 3' ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to the fragments of the *Mycoplasma* genome which are between two ORF(s) herein described. Alternatively, EMFs can be identified using known EMFs as a target sequence or target motif in the computer-based systems of the present invention.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site 5' to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below.

A sequence which is suspected as being an EMF is cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host is examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

As used herein, an "uptake modulating fragment," UMF, means a series of nucleotide molecules which mediate the uptake of a linked DNA fragment into a cell. UMFs can be readily identified using known UMFs as a target sequence or target motif with the computer-based systems described above.

The presence and activity of a UMF can be confirmed by attaching the suspected UMF to a marker sequence. The resulting nucleic acid molecule is then incubated with an appropriate host under appropriate conditions and the uptake of the marker sequence is determined. As described above, a UMF will increase the frequency of uptake of a linked marker sequence. A review of DNA uptake in *Mycoplasma* is provided by Goodgall, S.H., *et al., J. Bact.* 172:5924-5928 (1990).

As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to

*Mycoplasma genitalium* sequences. DFs can be readily identified by identifying unique sequences within the *Mycoplasma genitalium* genome, or by generating and testing probes or amplification primers consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequence provided in SEQ ID NO: 1, a representative fragment thereof, or a nucleotide sequence at least 99.9% identical to SEQ ID NO:1 with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated.

Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (i.e., sequence both strands). Alternatively, error screening can be performed by sequencing correspond polynucleotides of *Mycoplasma genitalium* origin isolated by using part or all of the fragments in question as a probe or primer.

Each of the ORFs of the *Mycoplasma genitalium* genome disclosed in Tables 1(a), 1(b), 1(c) and 2, and the EMF found 5' to the ORF, can be used in numerous ways as polynucleotide reagents. The sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe, such as *Mycoplasma genitalium*, in a sample. This is especially the case with the fragments or ORFs of Table 2, which will be highly selective for *Mycoplasma genitalium*.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide.

The present invention further provides recombinant constructs comprising one or more fragments of the *Mycoplasma genitalium* genome of the present invention. The recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Mycoplasma genitalium* has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs and UMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF or UMF. Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Bacterial: pBs, phagescript, PsiX174, pBluescript SK, pBs, KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

The present invention further provides host cells containing anyone of the isolated fragments of the *Mycoplasma genitalium* genome of the present invention, wherein the fragment has been introduced into the host cell using known transformation methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or the host cell can be a procaryotic cell, such as a bacterial cell. Introduction of the recombinant construct into the host cell can be effected by calcium phosphate transfection, DEAE, dextran mediated transfection, or electroporation (Davis, L. *et al.*, *Basic Methods in Molecular Biology* (1986)).

The host cells containing one of the fragments of the *Mycoplasma genitalium* genome of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF.

The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ from a nucleic acid fragment of the present invention (e.g., an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence. Pre-



ferred nucleic acid fragments of the present invention are the ORFs depicted in Tables 1(a), 1(c) and 2.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Fragments are useful, for example, in generating antibodies against the native polypeptide. In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily follow known methods for isolating polypeptides and proteins in order to obtain one of the isolated polypeptides or proteins of the present invention. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention can alternatively be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. One skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, Cv-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (e.g., microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (e.g., yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, e.g., *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Mycoplasma genitalium* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

"Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, in *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, e.g., the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\alpha$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a

functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may, also be employed as a matter of choice.

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is derepressed by appropriate means (e.g., temperature shift or chemical induction) and cells are cultured for an additional period. Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described by Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Mycoplasma genitalium*, of the fragments of the *Mycoplasma genitalium* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Mycoplasma genitalium* is defined as a homolog of a fragment of the *Mycoplasma genitalium* genome or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Mycoplasma genitalium* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which process greater than 85% sequence (amino acid or nucleic acid) homology.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NO:1 or from a nucleotide sequence at least 99.9% identical to SEQ ID NO:1 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog using known methods (Innis *et al.*, *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NO:1 or from a nucleotide sequence at least 99.9% identical to SEQ ID NO:1, one skilled in the art will recognize that by employing high stringency conditions (e.g., annealing at 50-60°C) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (e.g., annealing at 35-37°C), sequences which are greater than 40-50% homologous to the primer will also be amplified.

When using DNA probes derived from SEQ ID NO:1 or from a nucleotide sequence at least 99.9% identical to SEQ ID NO:1 for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (e.g., hybridizing at 50-65°C in 5X SSPE and 50% formamide, and washing at 50-65°C in 0.5X SSPE), sequences having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (e.g., hybridizing at 35-37°C in 5X SSPE and 40-45% formamide, and washing at 42°C in SSPE), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Mycoplasma genitalium*.

## 5 Uses for the Compositions of the Invention

Each ORF provided in Table 1(a), 1(b) and 1(c) was assigned to biological role categories adapted from Riley, M., *Microbiology Reviews* 57(4):862 (1993)). This allows the skilled artisan to determine a use for each identified coding sequence. Tables 1(a), 1(b) and 1(c) further provides an identification of the type of polypeptide which is encoded for by each ORF. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and industrial purposes consistent with the type of putative identification of the polypeptide.

Such identifications permit one skilled in the art to use the *Mycoplasma genitalium* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. (For a review of enzymes used within the commercial industry, see *Biochemical Engineering and Biotechnology Handbook* 2nd, eds. Macmillan Publ. Ltd., NY (1991) and *Biocatalysts in Organic Syntheses*, ed. J. Tramper *et al.*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985)).

### 1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis. The various metabolic pathways present in *Mycoplasma* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1(a), 1(b) and 1(c).

Identified within the category of intermediary metabolism, a number of the proteins encoded by the identified ORFs in Tables 1(a), 1(b) and 1(c) are particularly involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Some of the enzymes identified include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided by Rombouts *et al.*, *Symbiosis* 21:79 (1986) and Voragen *et al.* in *Biocatalyst in Agricultural Biotechnology*, edited J.R. Whitaker *et al.*, *American Chemical Society Symposium Series* 389:93 (1989)).

The metabolism of glucose, galactose, fructose and xylose are important parts of the primary metabolism of *Mycoplasma*. Enzymes involved in the degradation of these sugars can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure (see Krueger *et al.*, *Biotechnology* 6(A), Rhine, H.J. *et al.*, eds., Verlag Press, Weinheim, Germany (1984)).

Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See Hartmeir *et al.*, *Biotechnology Letters* 1:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry (see Bigelis in *Gene Manipulations and Fungi*, Benett, J.W. *et al.*, eds., Academic Press, New York (1985), p. 357). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. See Owusu *et al.*, *Biochem. et Biophysica. Acta* 872:83 (1986).

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose-produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, *Starch* 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a

large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, *Acid Proteases Structure Function and Biology*, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, *Industrial Enzymes*, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, *Report Industrial Enzymes* by 1990, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases identified in Tables 1(a), 1(b) and 1(c) (see Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London* 310:227 (1985) and Poserke, *Journal of the American Oil Chemist Society* 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction. When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other hand, has been described in detail by Bud *et al.*, *Chemistry in Britain* (1987), p. 127.

Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo-selective synthesis of only *L*-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

## 2. Generation of Antibodies

As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and hybridomas which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Method* 35:1-21 (1980); Kohler and Milstein, *Nature* 256:495-497 (1975)), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985), pp. 77-96).

Any animal (mouse, rabbit, etc.) which is known to produce antibodies can be immunized with the pseudogene polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin or  $\beta$ -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175:109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using proce-

dures known in the art (Campbell, A.M., *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

Techniques described for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of the present invention.

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

The present invention further provides the above-described antibodies in detectably labelled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, etc.), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, etc.) fluorescent labels (such as FITC or rhodamine, etc.), paramagnetic atoms, etc. Procedures for accomplishing such labelling are well-known in the art, for example see (Sternberger, L.A. *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer, E.A. *et al.*, *Meth. Enzym.* 62:308 (1979); Engval, E. *et al.*, *Immunol.* 109:129 (1972); Goding, J.W. *J. Immunol. Meth.* 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues in which a fragment of the *Mycoplasma genitalium* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir, D.M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W.D. *et al.*, *Meth. Enzym.* 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as for immunoaffinity purification of the proteins of the present invention.

### 3. Diagnostic Assays and Kits

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample, using one of the DFs or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the DFs of the present invention and assaying for binding of the DFs or antibodies to components within the test sample.

Conditions for incubating a DF or antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the DFs or antibodies of the present invention. Examples of such assays can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G.R. *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the DFs or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound DF or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound antibody or DF.

Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alternative, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with the labelled antibody. One skilled in the art will readily recognize that the disclosed DFs and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Mycoplasma* genome herein described.

In detail, said method comprises the steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Mycoplasma* genome; and
- (b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, Application of Synthetic Peptides: Antisense Peptides," In *Synthetic Peptides, A User's Guide*, W.H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry* 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix formation by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulphhydryl or polymeric derivatives which have base attachment capacity.

Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251: 1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the sequences of the present invention is necessary for the design of an antisense or triple helix oligonucleotide and other DNA binding agents.

Agents which bind to a protein encoded by one of the ORFs of the present invention can be used as a diagnostic agent, in the control of bacterial infection by modulating the activity of the protein encoded by the ORF. Agents which bind to a protein encoded by one of the ORFs of the present invention can be formulated using known techniques to generate a pharmaceutical composition for use in controlling *Mycoplasma* growth and infection.

#### 5. Vaccine and Pharmaceutical Composition

The present invention further provides pharmaceutical agents which can be used to modulate the growth of *Mycoplasma genitalium*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulated the growth of *Mycoplasma sp.*, or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of the organism in question. The pharmaceutical agents of the present invention can modulate the growth of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological activity of the protein, while other agents may bind to a component of the outer surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alterna-



tively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components, such as the LPS, are well known in the art.

As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organism do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 10  $\mu\text{g/kg}$  body weight and in most cases they will be administered in an amount not in excess of about 8 mg/Kg body weight per day. In most cases, the dosage is from about 10  $\mu\text{g/kg}$  to about 1 mg/kg body weight daily, taking into account the routes of administration, symptoms, etc.

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Moieties capable of mediating such effects are disclosed in *Remington's Pharmaceutical Sciences* (1980).

For example, a change in the immunological character of the functional derivative, such as affinity for a given antibody, is measured by a competitive type immunoassay. Changes in immunomodulation activity are measured by the appropriate assay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers are assayed by methods well known to the ordinarily skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (i.e., inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled.

To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, etc. In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s) serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to the mammal in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, e.g., human serum albumin, are described, for example, in *Remington's Pharmaceutical Sciences* (16th ed., Osol, A., Ed., Mack, Easton PA (1980)). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together

with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences* (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

## Experimental

### Example 1

#### Overview of Experimental Design and Methods

##### 1. Shotgun Sequencing Strategy

The overall strategy for a shotgun approach to whole genome sequencing is outlined in Table 3. The theory of shotgun sequencing follows from the application of the equation for the Poisson distribution  $p_x = m^x e^{-m} / x!$ , where  $x$  is the number of occurrences of an event and  $m$  is the mean number of occurrences. To determine the probability that any given base is not sequenced after a certain amount of random sequence has been generated, if  $L$  is the genome length,  $n$  is the number of clone insert ends sequenced, and  $w$  is the sequencing read length, then  $m = nw/L$ , and the probability that no clone originates at any of the  $w$  bases preceding a given base, i.e., the probability that the base is not sequenced, is  $p_0 = e^{-m}$ . Using the fold coverage as the unit form, one sees that after 580 kb of sequence has been randomly generated,  $m = 1$ , representing 1X coverage. In this case,  $p_0 = e^{-1} = 37\%$ , thus approximately 37% is unsequenced. A 5X coverage (approximately 3150 clones sequenced from both insert ends) yields  $p_0 = e^{-5} = 0.0067$ , or .67% unsequenced. The total gap length is  $Le^{-m}$ , and the average gap size is  $L/n$ . 5X coverage would leave about 48 gaps averaging about 80 bp in size. The treatment is essentially that of Lander and Waterman. Table 4 illustrates a computer simulation of a random sequencing experiment for coverage of a 580 kb genome with an average fragment size of 400 bp.

##### 2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragment is required. *M. genitalium* genomic chromosomal DNA was mechanically sheared, digested with BAL31 nuclease to produce blunt-ends, and size-fractionated by agarose gel electrophoresis. Fragments in the 2.0 kb size range were excised and recovered. These fragments were ligated to Smal-cut, phosphatased pUC18 vector and the ligated products were fractionated on an agarose gel. The linear vector plus insert band was excised and recovered. The ends of the linear recombinant molecules were repaired with T4 polymerase treatment and the molecules were then ligated into circles. This two-stage procedure resulted in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<1%). Deviation from randomness is most likely to occur during cloning. *E. coli* host cells deficient in all recombinant and restriction functions were used to prevent rearrangements, deletions, and loss of clones by restriction. Transformed cells were plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells. All colonies were picked for template preparation regardless of size. Only clones lost due to "poison" DNA or deleterious gene products would be deleted from the library, resulting in a slight increase in gap number over that expected.

In order to evaluate the quality of the *M. genitalium* random insert library, sequence data was obtained from approx-



imately 2000 templates using the M13F primer. The random sequence fragments were assembled using The Institute for Genomic Research (TIGR) autoassembler software after obtaining 500, 1000, 1500, and 2000 sequence fragments, and the number of unique assembled base pairs was determined. The progression of assembly was plotted using the actual data obtained from the assembly of up to 2000 sequence fragments and compared the data that is provided in the ideal plot. There was essentially no deviation of the actual assembly data from the ideal plot, indicating that we had constructed close to an ideal random library with minimal contamination from double insert chimeras and free of vector.

### 3. Random DNA Sequencing

Five-thousand seven hundred and sixty (5,760) plasmid templates were prepared using a "boiler bead" preparation method developed in collaboration with AGTC (Gaithersburg, MD), as suggested by the manufacturer. The AGTC method is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration was determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations were not adjusted and low-yielding templates were identified and not sequenced where possible. Sequencing reactions were carried out on plasmid templates using the AB Catalyst Lab station or Perkin-Elmer 9600 Thermocyclers with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (-21M13) and the M13 reverse (RP1) primers. Dye terminator sequencing reactions were carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. Nine-thousand eight hundred and forty-six (9,846) sequencing reactions were performed during the random phase of the project by 4 individuals using an average of 10 AB373 DNA Sequencers over a 2 month period. All sequencing reactions were analyzed using the Stretch modification of the AB373, primarily using a 36cm well-to-read distance. The overall sequencing success rate for M13-21 sequences was 88% and 84% for M13RP1 sequences. The average usable read length for M13-21 sequences was 485 and 441 for M13RP1 sequences.

The art has described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects. A skilled artisan must balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths and lower success rates for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. For this project, essentially all of the templates were sequenced from both ends.

### 4. Protocol for Automated Cycle Sequencing

The sequencing consisted of using five (5) ABI Catalyst robots and ten (10) ABI 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the *Taq* thermostable DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates were combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (e.g., one primer synthesis) steps were performed including denaturation, annealing of primer and template, and extension of DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevented evaporation without the need for an oil overlay.

Two sequencing protocols were used: dye-labelled primers and dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR-generated templates with both dye-primers and dye-terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions were loaded per 373 Sequencer each day, for a total of 960 samples. Electrophoresis was run overnight following the manufacture's protocols, and the data was collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking was confirmed visually. Each sequence electropherogram (or fluorescence lane trace) was inspected visually and assessed for quality. Trailing sequences of low quality were removed and the sequence itself was loaded via software a Sybase database (archived daily to a 8mm tape). Leading vector polylinker sequence was removed automatically by software program. The average edited lengths of sequences from the ABI 373 Sequencers converted to Stretch Liners were approximately 460 bp.

## Informatics

### 1. Data Management

5 A number of information management systems (LIMS) for a large-scale sequencing lab have been developed. A system was used which allowed an automated data flow wherever possible to reduce user error. The system used to collect and assemble the sequence information obtained is centered upon a relational data management system built using the Sybase RDBMS. The database is designed to store and correlate all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the AB 373 Sequencers is based on a Macintosh platform and the data management system chosen is based on a Unix platform, it was necessary to design and implement a variety of multi-user, client server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

### 2. Assembly

15 The sequence data from 8,472 sequence fragments was used to assemble the *M. genitalium* genome. The assembly was performed by using a new assembly engine (TIGR Assembler - previously designated ASMG) developed at TIGR. The TIGR Assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the necessary speed, the TIGR Assembler builds a hash table of 10bp oligonucleotide subsequences to generate a list of potential sequence fragment. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, the TIGR Assembler extends the current contig by attempting to add the best matching fragment based on oligonucleotide content. The current contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gap alignments. The current contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the TIGR Assembler in regions of minimal coverage and raised in regions with a good chance of containing repetitive elements. Potentially chimeric fragments and fragments representing the boundaries of repetitive elements are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. The TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. The TIGR Assembler enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library). Assembly of the 8,472 sequence fragments of *M. genitalium* required 10 hours of CPU time on a SPARCcenter 2000. All contigs were loaded into a Sybase structure representing the location of each fragment in the contig and extensive information about the consensus sequence itself. The result of this process was approximately 40 contigs ordered into 2 groups (See below). Because of the high stringency of the TIGR Assembler process it was found to be useful to perform a FASTA (GRATA) alignment of all contigs built by the TIGR Assembler process against each other. In this way additional overlaps were detected which enabled compression of the data set into 26 contigs in 2 groups.

### 40 Achieving Closure

The complete genome sequence was obtained by sequencing across the gaps between contigs. While gap filling has occupied a major portion of the time and expense of other genome sequencing projects, it was minimal in the present invention. This was primarily due to 1) saturation of the genome as a result of the number of random clones and sequencing reactions performed, 2) the longer read lengths obtained from the Stretch Liners, 3) the anchored ends which were obtain for joining contigs, and 4) the overall capacity and efficiency of the high throughput sequencing facility.

Gaps occurred on a predicted random basis, as shown in Table 4, which illustrates simulated random sequencing. These gaps generally were less than 200 bp in size. All of the gaps were closed by sequencing further on the templates bordering the gaps. In these cases, oligo primers for extension of the sequence from both ends of the gap were generated using techniques known in the art. This gave a double standard coverage across the gap areas.

The high redundancy of sequence information that was obtained from the shotgun approach gave a highly accurate sequence. Our sequence accuracy was confirmed by comparing the sequence information obtained against known *M. genitalium* genes present in the GenBank database. The accuracy of our chromosome structure was confirmed by comparison of restriction digests to the known restriction map of *M. genitalium*. The EcoRI restriction map of *M. genitalium* is shown in Figure 1 and expressed in tabular form in Table 5.

## Identifying Genes

*M. genitalium* ORFs were initially defined by evaluating their coding potential with the program Gene Works using composition matrices specific to *Mycoplasma* genomic DNA. The ORF sequences (plus 300 bp of flanking sequence) were used in searches against a database of non-redundant bacterial proteins (NRBP). Redundancy was removed from NRBP at two stages. (1) All DNA coding sequences were extracted from GenBank (release 85), and sequences from the same species were searched against each other. Sequences having >97% similarity over regions >100 nucleotides were combined. (2) The sequences were translated and used to protein comparisons with all sequences in Swiss-Prot (release 30). Sequences belonging to the same species and having >98% similarity over 33 amino acids were combined. NRBP is composed of 21445 sequences from 23751 GenBank sequences and 11183 Swiss-Prot sequences from 1099 different species.

Searches were performed using an algorithm that (1) translates the query DNA sequence in all six reading frames for searching against a protein database, (2) identifies the protein sequences that match the query, and (3) aligns the protein-protein matches using a modified Smith-Waterman algorithm. In cases where insertion or deletions in the DNA sequence produced a frame shift error, the alignment algorithm started with protein regions of maximum similarity and extended the alignment to the same database match using the 300 bp flanking region. Regions known to contain frame shift errors were saved to the database and evaluated for possible correction. The role categories were adopted from those previously defined by Riley *et al.* for *E. coli* gene products. Role assignments were made to *M. genitalium* ORFs at the protein sequence level by linking the protein sequence of the ORFs with the Swiss-Prot sequences in the Riley database.

## Detailed Description of Sequencing the *Mycoplasma genitalium* Genome, Genome Analysis and Comparative Genomics

We have determined the complete nucleotide sequence (580,071 bp) of the *Mycoplasma genitalium* genome using the approach of whole chromosome shotgun sequencing and assembly, which has successfully been applied to the analysis of the *Haemophilus influenzae* genome (R. Fleischmann *et al.*, *Science* 269:496 (1995)). These data, together with the description of the complete genome sequence (1.83 Mb) of the eubacterium *Haemophilus influenzae*, have provided the opportunity for comparative genomics on a whole genome level for the first time. Our initial whole genome comparisons reveal fundamental differences in genome content which are reflected in different physiological and metabolic capacities of *M. genitalium* and *H. influenzae*.

The strategy and methodology for whole genome shotgun sequencing and assembly was similar to that previously described for *H. influenzae* (R. Fleischmann *et al.*, *Science* 269:496 (1995)). In particular, a total of 50 µg of purified *M. genitalium* strain G-37 DNA (ATCC No. 33530) was isolated from cells grown in Hayflick's medium. A mixture (990 µl) containing 50 µg of DNA, 300 mM sodium acetate, 10 mM Tris HCl, 1 mM EDTA, and 30 percent glycerol was chilled to 0°C in a nebulizer chamber and sheared at 4 lbs/in<sup>2</sup> for 60 seconds. The DNA was precipitated in ethanol and redissolved in 50 µl of Tris-EDTA (TE) buffer to create blunt ends; a 40 µl portion was digested for 10 minutes at 30°C in 85 µl of BAL31 buffer with 2 units of BAL 31 nuclease (New England BioLabs). The DNA was extracted with phenol, precipitated in ethanol, dissolved in 60 µl of TE buffer, and fractionated on a 1.0 percent low melting agarose gel. A fraction (2.0 kb) was excised, extracted with phenol, and redissolved in 20 µl of TE buffer. A two-step ligation procedure was used to produce a plasmid library in which 99% of the recombinants contained inserts, of which >99% were single inserts. The first ligation mixture (50 µl) contained approximately 2 µg DNA fragments, 2 µg of SmaI + bacterial alkaline phosphatase pUC 18 DNA (Pharmacia), and 10 units of T4 DNA ligase (GIBCO/BRL), and incubation was for 5 hours at 4°C. After extraction with phenol and ethanol precipitation, the DNA was dissolved in 20 µl of TE buffer and separated by electrophoresis on a 1.0 percent low melting agarose gel. A ladder of ethidium bromide-stained, linearized DNA bands, identified by size as insert (i), vector (v), v + i, v + 2i, v + 3i, etc. was visualized by 360 nm ultraviolet light. The v + i DNA was excised and recovered in 20 µl of TE buffer. The v + i DNA was blunt-ended by T4 polymerase treatment for 5 minutes at 37°C in a reaction mixture (50 µl) containing the linearized v + i fragments, four deoxynucleotide triphosphates (dNTPs) (25 µM each), and 3 units of T4 polymerase (New England Biolabs) under buffer conditions recommended by the supplier. After phenol extraction and ethanol precipitation, the repaired v + i linear pieces were dissolved in 20 µl of TE. The final ligation to produce circles was carried out in a 50 µl reaction containing 5 µl of v + i DNA and 5 units of T4 ligase at 15°C overnight. The reaction mixture was heated at 67°C for 10 minutes and stored at -20°C.

For transformation, a 100 µl portion of Epicurian SURE 2 Supercompetent Cells (Stratagene 200152) was thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7 µl volume of 1.42M β-mercaptoethanol was added to the cells to a final concentration of 25 mM. Cells were incubated on ice for 10 minutes. A 1 µl sample of the final ligation mix was added to the cells and incubated on ice for 30 minutes. The cells were heat-treated for 30 seconds at 42°C and placed back on ice for 2 minutes. The outgrowth period in liquid culture was omitted to minimize the preferential growth of any transformed cell. Instead, the transformed cells were plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (1.5 percent SOB agar consisted of 20 g of tryptone, 5g of yeast extract, 0.5 g of NaCl,

and 1.5 percent Difco agar/liter). The 5 ml bottom layer was supplemented with 0.4 ml of ampicillin (50 mg/ml) per 100 ml of SOB agar. The 15 ml top layer of SOB agar was supplemented with 1 ml of  $MgCl_2$  (1M) and 1 ml of  $MgSO_4$  (1M) per 100 ml of SOB agar. The 15 ml top layer was poured just before plating. The titer of the library was approximately 100 colonies per 10  $\mu$ l aliquot of transformation.

One of the lessons learned from sequencing and assembly of the complete *H. influenzae* genome was that contig ordering and gap closure is most efficient if the random sequencing phase of the project is continued until at least 99.8%-99.9% of the genome is sequenced with at least 6-fold coverage. To calculate the number of random sequencing reactions necessary to obtain this coverage for the *M. genitalium* genome, we made use of the Lander and Waterman [E.S. Lander and M.S. Waterman, *Genomics* 2:231 (1988)] application of the Poisson distribution, where  $p_x = e^{-nw/L}$ .  $p_x$  is the probability that any given base is not sequenced,  $n$  is the number of clone insert ends sequenced,  $w$  is the average read length of each template in bp, and  $L$  is the size of the genome in bp. For a genome of 580 kb with an average sequencing read length of 450 bp after editing, approximately 8650 sequencing reactions (or 4325 clones sequenced from both ends) should theoretically provide 99.85% coverage of the genome. This level of coverage should leave approximately 10 gaps with an average size of 70 bp unsequenced.

To evaluate the quality of the *M. genitalium* library, sequence data were obtained from both ends of approximately 600 templates using both the M13 forward (M13-21) and the M13 reverse (M13RP1) primers. Sequence fragments were assembled using the TIGR ASSEMBLER and found to approximate a Poisson distribution of fragments with an average read length of 450 bp for a 580 kb library, indicating that the library was essentially random.

For this project, a total of 5760 double-stranded DNA plasmid templates were prepared in a 96-well format using a boiling bead method. Ninety-four percent of the templates prepared yielded a DNA concentration  $\geq 30$  ng/ $\mu$ l and were used for sequencing reactions. To facilitate ordering of contigs each template was sequenced from both ends. Reactions were carried out on using the AB Catalyst LabStation with Applied Biosystems PRISM Ready reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers. The success rate and average read length after editing with the M13-21 primer were 88 percent and 444 bp, respectively, and 84 percent and 435 bp, respectively, with the M13RP1 primer. All data from template preparation to final analysis of the project were stored in a relational data management system developed at TIGR [A.R. Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Science* (IEEE Computer Society Press, Washington, D.C., 1993), p. 585]. To facilitate ordering of contigs each template was sequenced from both ends. A total of 9846 sequencing reactions were performed by five individuals using an average of 8 AB 373 DNA Sequencers per day for a total of 8 weeks. Assembly of 8472 high quality *M. genitalium* sequence fragments along with 299 random genomic sequences from Peterson *et al.* (S.N. Peterson *et al.*, *J. Bacteriol.* 175:7918 (1993)) was performed with the TIGR ASSEMBLER. The assembly process generated 39 contigs (size range: 606 to 73,351 bp) which contained a total of 3,806,280 bp of primary DNA sequence data. Contigs were ordered by ASM\_ALIGN, program which links contigs based on information derived from forward and reverse sequencing reactions from the same clone.

ASM\_ALIGN analysis revealed that all 39 gaps were spanned by an existing template from the small insert genomic DNA library (i.e., there were no physical gaps in the sequence assembly). The order of the contigs was confirmed by comparing the order of the random genomic sequences from Peterson *et al.* (S.N. Peterson *et al.*, *J. Bacteriol.* 175:7918 (1993)) that were incorporate into the assembly with their known position on the physical map of the *M. genitalium* chromosome (T.S. Lucier *et al.*, *Gene* 150:27 (1994); Peterson *et al.*, *J. Bacteriol.* 177:3199 (1995)). Because of the high stringency of the TIGR ASSEMBLER, the 39 contigs were searched against each other with GRASTA (a modified FASTA (B. Brutlag *et al.*, *Comp. Chem.* 1:203 (1993))). The BLOSUM 60 amino acid substitution matrix was used in all protein-protein comparisons [S. Henikoff and J.G. Henikoff, *Proc. Natl. Acad. Sci. USA* 89:1091 (1992)] to detect overlaps (< 30 bp) that would have been missed during the initial assembly process. Eleven overlaps were detected with this approach which reduced the total number of gaps from 39 to 28.

Templates spanning each of the sequence gaps were identified and oligonucleotide primers were designed from the sequences at the end of each contig. All gaps were less than 300 bp; thus a primer walk from both ends of each template was sufficient for closure. All electropherograms were visually inspected with TIGR EDITOR (R. Fleischmann *et al.*, *Science* 269:496 (1995)) for initial sequence editing. Where a discrepancy could not be resolved or a clear assignment made, the automatic base calls were left unchanged.

Several criteria for determination of sequence completion were established for the *H. influenzae* genome sequencing project and these same criteria were applied to this study. Across the assembled *M. genitalium* genome there is an average sequence redundancy of 6.5-fold. The completed sequence contains less than 1% single sequence coverage. For each of the 53 ambiguities remaining after editing and the 25 potential frameshifts found after sequence-similarity searching, the appropriate template was resequenced with an alternative sequencing chemistry (dye terminator vs. dye primer) to resolve ambiguities. Although it is extremely difficult to assess sequence accuracy, we estimate our error rate to be less than 1 base in 10,000 based upon frequency of shifts in open reading frames, unresolved ambiguities, overall quality of raw data, and fold coverage.

A direct cost estimate for sequencing, assembly, and annotation of the *M. genitalium* genome was determined by summing reagent and labor costs for library construction, template preparation and sequencing, gap closure, sequence

confirmation, annotation, and preparation for publication, and dividing by the size of the genome in base pairs. This yielded a final cost of 30 cents per finished base pair.

### Genomic Analysis

The *M. genitalium* genome is a circular chromosome of 580,071 bp. The overall G+C content is 32% (A, 34%; C, 16%; G, 16%; and T, 34%). The G+C content across the genome varies between 27 and 37% (using a window of 5000 bp), with the regions of lowest G+C content flanking the presumed origin of replication of the organism. As in *H. influenzae* (Fleischmann, R. *et al.*, *Science* 269:496 (1995)), the rRNA operon in *M. genitalium* contains a higher G+C content (44%) than the rest of the genome, as do the tRNA genes (52%). The higher G+C content in these regions may reflect the necessity of retaining essential G+C base pairing for secondary structure in rRNAs and tRNAs (Rogers, M.J. *et al.*, *Isr. J. Med. Sci.* 20:768 (1984)).

The genome of *M. genitalium* contains 74 *EcoRI* fragments, as predicted by cosmid mapping data (Lucier, T.S. *et al.*, *Gene* 150:27 (1994); Peterson *et al.*, *J. Bacteriol.* 177:3199 (1995)). The order and sizes of the *EcoRI* fragments determined from sequence analysis are in agreement with those previously reported (Lucier, T.S. *et al.*, *Gene* 150:27 (1994); Peterson *et al.*, *J. Bacteriol.* 177:3199 (1995)), with one apparent discrepancy between coordinates 62,708 and 94,573 in the sequence. However, re-evaluation of cosmid hybridization data in light of results from genome sequence analysis confirms that the sequence data are correct, and the extra 4.0 kb *EcoRI* fragment in this region of the cosmid map reflects a misinterpretation of the overlap between cosmids J-8 and 21 (Lucier, T.S., unpublished observation). The ends of each clone from the ordered cosmid library were sequenced and are shown on the circular chromosome in Figure 4. The order of the cosmids based on sequence analysis is in complete agreement with that determined by physical mapping (Lucier, T.S. *et al.*, *Gene* 150:27 (1994); Peterson *et al.*, *J. Bacteriol.* 177:3199 (1995)).

We defined the first bp of the chromosomal sequence of *M. genitalium* based on the putative origin of replication (Bailey & Bott, *J. Bacteriol.* 176:5814 (1994)). Studies of origins of replication in some prokaryotes have shown that DNA synthesis is initiated in an untranscribed AT rich region between *dnaA* and *dnaN* (Ogasawara, N. *et al.*, in *The Bacterial Chromosome*, Krlica & Riley, eds., American Society for Microbiology, Washington, DC (1990), pp. 287-295; Ogasawara & Yoshikawa, *Mol. Microbiol.* 6:629 (1992)). A search of the *M. genitalium* sequence for "DnaA boxes" around the putative origin of replication with consensus "DnaA boxes" from *Escherichia coli*, *Bacillus subtilis*, and *Pseudomonas aeruginosa* revealed no significant matches. Although we have not been able to precisely localize the origin, the co-localization of *dnaA* and *dnaN* to a 4000 bp region of the chromosome lends support to the hypothesis that it is the functional origin of replication in *M. genitalium* (Ogasawara, N. *et al.*, in *The Bacterial Chromosome*, Krlica & Riley, eds., American Society for Microbiology, Washington, DC (1990), pp. 287-295; Ogasawara & Yoshikawa, *Mol. Microbiol.* 6:629 (1992); Miyata, M. *et al.*, *Nucleic Acids Res.* 21:4816 (1993)). We have chosen an untranscribed region between *dnaA* and *dnaN* so that *dnaN* is numbered as the first open reading frame in the genome. As seen in Figure 4, genes to the right of this region are preferentially transcribed from the plus strand and to the left of this region, are preferentially transcribed from the minus strand. The apparent polarity in gene transcription is maintained across each half of the genome (Figures 4 and 5). This stands in marked contrast to *H. influenzae* which displays no apparent polarity of transcription around the origin of replication. The significance of this observation remains to be determined.

The predicted coding regions of *M. genitalium* were initially defined by searching the entire genome for open reading frames greater than 100 amino acids. Translations were made using the genetic code for mycoplasma species in which UGA encodes tryptophan. All open reading frames were searched with BLAZE (Brutlag, D. *et al.*, *Comp. Chem.* 1:203 (1993)). The BLOSUM 60 amino acid substitution matrix was used in all protein-protein comparisons (Henikoff, S. and Henikoff, J.G., *Proc. Natl. Acad. Sci. USA* 89:1091 (1992)) against a non-redundant bacterial protein database (NRBP) (Fleischmann, R. *et al.*, *Science* 269:496 (1995)) developed at TIGR on a MasPar MP-2 massively parallel computer with 4096 microprocessors. Protein matches were aligned with PRAZE, a modified Smith-Waterman (Waterman, M.S., *Methods Enzymol.* 164:765 (1988)) algorithm. Segments between predicted coding regions of the genome were used in additional searches against all protein sequences from GenPept, Swiss-Prot, and PIR. Pairwise alignments between *M. genitalium* predicted open reading frames and sequences from the public archives were examined. Motif matches were annotated in cases where sequence similarity was confined to short domains in the predicted coding region. The coding potential of 170 unidentified open reading frames was analyzed with GeneMark (Borodovsky & McIninch, *ibid.*, p. 123) which had been trained with 308 *M. genitalium* sequences. Open reading frames that had low coding potential (based on the GeneMark analysis) and were smaller than 100 nucleotides (a total of 53) were removed from the final set of putative coding regions. In a separate analysis, open reading frames were searched against the complete set of translated sequences from *H. influenzae* (GSDB accession L42023, see (Fleischmann, R. *et al.*, *Science* 269:496 (1995))). In total, these processes resulted in the identification of 482 predicted coding regions, of which 365 were putatively identified (Twenty-three of the protein matches in Table 6 were annotated as motifs. These data matches were not full-length protein matches, but nonetheless displayed regions of significant amino acid similarity) and 117 had no matches to protein sequences from any other organism.

The 365 predicted coding regions that matched protein sequences from the public sequence archives were

assigned biological roles. The role classifications were developed from Riley (Riley, M., *Microbiol. Rev.* 57:862 (1992)) and identical to those used in *H. influenzae* assignments (Fleischmann, R. et al., *Science* 269:496 (1995)). A separate search procedure was used in cases where we were unable to detect genes in the *M. genitalium* genome. Query peptide sequences that were available from eubacteria such as *E. coli*, *B. subtilis*, *M. capricolum*, and *H. influenzae* were used in searches against all six reading frame translations of the entire genome sequence, and the alignments were examined. The possibility remains that current searching methods, an incomplete set of query sequences, or the subjective analysis of the database matches, are not sensitive enough to identify certain *M. genitalium* gene sequences.

One-half of all predicted coding regions in *M. genitalium* for which a putative identification could be assigned display the greatest degree of similarity to a protein from either a gram-positive organism (e.g., *B. subtilis*) or a *Mycoplasma* species. The significance of this finding is underscored by the fact that NRBP contained 3885 sequences from *E. coli* and only 1975 sequences from *B. subtilis*. In the majority of cases where *M. genitalium* coding regions matched sequences from both *E. coli* and *Bacillus* species, the better match was to a sequence from *Bacillus* (average of 62 percent similarity) rather than to a sequence from *E. coli* (average of 56 percent similarity). The evolutionary relationship between *Mycoplasma* and the *Lactobacillus*-*Clostridium* branch of the gram-positive phylum has been deduced from small subunit rRNA sequences (Maidak, B.L. et al., *Nucleic Acids Research* 22:3485 (1994)). Our data from whole genome analysis support this hypothesis.

### Comparative Genomics: *M. genitalium* and *H. influenzae*

A survey of the genes and their organization in *M. genitalium* makes possible the description of a minimal set of genes required for survival. One would predict that a minimal cell must contain genes for replication and transcription, at least one rRNA operon and a set of ribosomal proteins, tRNAs and tRNA synthetases, transport proteins to derive nutrients from the environment, biochemical pathways to generate ATP and reducing power, and mechanisms for maintaining cellular homeostasis. Comparison of the genes identified in *M. genitalium* with those in *H. influenzae* allows for identification of a basic complement of genes conserved in these two species and provides insights into physiological differences between one of the simplest self-replicating prokaryotes and a more complex, gram-negative bacterium.

The *M. genitalium* genome contains 482 predicted coding sequences (Table 6) as compared to 1,727 identified in *H. influenzae* (Fleischmann, R. et al., *Science* 269:496 (1995)). Table 7 summarizes the gene content of both organisms sorted by functional category. The percent of the total genome in *M. genitalium* and *H. influenzae* encoding genes involved in cell envelope, cellular processes, energy metabolism, purine and pyrimidine metabolism, replication, transcription, transport, and other categories is similar; although the total number of genes in these categories is considerably fewer in *M. genitalium*. A smaller percentage of the *M. genitalium* genome encodes genes involved in amino acid biosynthesis, biosynthesis of co-factors, central intermediary metabolism, fatty acid and phospholipid metabolism, and regulatory functions as compared with *H. influenzae*. A greater percentage of the *M. genitalium* genome encodes proteins involved in translation than in *H. influenzae*, as shown by the similar numbers of ribosomal proteins and tRNA synthetases in both organisms.

The 482 predicted coding regions in *M. genitalium* (average size of 1100 bp) cover 85% of the genome (on average, one gene every 1169 bp), a value similar to that found in *H. influenzae* where 1727 predicted coding regions (average size of 900 bp) cover 91% of the genome (one gene every 1042 bp). These data indicate that the reduction in genome size that has occurred within *Mycoplasma* has not led to an increase in gene density or a decrease in gene size (Bork, P. et al., *Mol. Microbiol.* 16:955 (1995)). A global search of *M. genitalium* and *H. influenzae* genomes reveals short regions of conservation of gene order, particularly two clusters of ribosomal proteins.

**Replication.** Two major protein complexes are formed during replication: the primosome and the replisome. We have identified genes encoding many of the essential proteins in the replication process, including *M. genitalium* isologs of the primosome proteins DnaA, DnaB, GyrA, GyrB, a single stranded DNA binding protein, and the primase protein, DnaE. DnaJ and DnaK, heat shock proteins that may function in the release of the primosome complex, are also found in *M. genitalium*. A gene encoding the DnaC protein, responsible for delivery of DnaB to the primosome, has yet to be identified.

Genes encoding most of the essential subunit proteins for DNA polymerase III in *M. genitalium* were also identified. The *polC* gene encodes the  $\alpha$  subunit which contains the polymerase activity. We have also identified the isolog of *dnaH* in *B. subtilis* (*dnaX* in *E. coli*) which encodes the  $\gamma$  and  $\epsilon$  subunits as alternative products from the same gene. These proteins are necessary for the processivity of DNA polymerase III. An isolog of *dnaN* which encodes the  $\beta$  subunit was previously identified in *M. genitalium* (Bailey & Bott, *J. Bacteriol.* 176:5814 (1994)) and is involved in the process of clamping the polymerase to the DNA template. While we have yet to identify a gene encoding the  $\epsilon$  subunit responsible for the 3'-5' proofreading activity, it is possible that this activity is encoded in the  $\alpha$  subunit as has been previously described (Sanjanwala, B. and Ganesa, A.T., *Mol. Gen. Genet.* 226:467 (1991); Sanjanwala, B. and Ganesan, A.T., *Proc. Natl. Acad. Sci. USA* 86:4421 (1989)). Finally, we have identified a gene encoding a DNA ligase, necessary for the joining of the Okazaki fragments formed during synthesis of the lagging strand.

While we have identified genes encoding many of the isologs thought to be essential for DNA replication, some



genes encoding proteins with key functions have yet to be identified. Examples of these are the DnaC protein mentioned above as well as Dna $\theta$  and Dna $\delta$  whose functions are less well understood but are thought to be involved in the assembly and processivity of polymerase III. Also apparently absent is a specific RNaseH protein responsible for the hydrolysis of the RNA primer synthesized during lagging strand synthesis.

**DNA Repair.** It has been suggested that in *E. coli* as many as 100 genes are involved in DNA repair (Kornberg, A. and Baker, T.A., *DNA Replication-2nd Ed.*, W.H. Freeman and Co., New York (1992)), and in *H. influenzae* the number of putatively identified DNA repair enzymes is approximately 30 (Fleischmann, R. *et al.*, *Science* 269:496 (1995)). Although *M. genitalium* appears to have the necessary genes to repair many of the more common lesions in DNA, the number of genes devoted to the task is much smaller. Excision repair of regions containing missing bases (apurinic/apyriminic (AP) sites) can likely occur by a pathway involving endonuclease IV (info), Pol I, and ligase. The *ung* gene which encodes uracil-DNA glycosylase is present. This activity removes uracil residues from DNA which usually arise by spontaneous deamination of cytosine. This produces an AP site which could then be repaired as described above.

All three genes necessary for production of the uvr ABC exonuclease are present, and along with Pol I, helicase II, and ligase should provide a mechanism for repair of damage such as cross-linking, which requires replacement of both strands. Although *recA* is present, which in *E. coli* is activated as it binds to single strand DNA, thereby initiating the SOS response, we find no evidence for a *lexA* gene which encodes the repressor which regulates the SOS genes. We have not identified photolyase (*phr*) in *M. genitalium* which repairs UV-induced pyrimidine dimers, or other genes involved in reversal of DNA damage rather than excision and replacement of the lesion.

**Transcription.** The critical components for transcription were identified in *M. genitalium*. In addition to the  $\alpha$ ,  $\beta$ , and  $\beta'$  subunits of the core RNA polymerase, *M. genitalium* appears to encode a single  $\sigma$  factor, whereas *E. coli* and *B. subtilis* encode at least six and seven, respectively. We have not detected a homolog of the Rho termination factor gene, so it seems likely that a mechanism similar to Rho-independent termination in *E. coli* operates in *M. genitalium*. We have clear evidence for homologs of only two other genes which modulate transcription, *nusA* and *nusG*.

**Translation.** *M. genitalium* possesses a single rRNA operon which contains three rRNA subunits in the order: 16S rRNA (1518 bp)-spacer (203 bp)-23S rRNA (2905 bp)-spacer (56 bp)-5S rRNA (103 bp). The small subunit rRNA sequence was compared with the Ribosomal Database Project's (Maidak, B.L. *et al.*, *Nucleic Acids Research* 22:3485 (1994)) prokaryote database with the program "similarity\_yank." Our sequence is identical to the *M. genitalium* (strain G37) sequence deposited there, and the 10 most similar taxa returned by this search are also in the genus *Mycoplasma*.

A total of 33 tRNA genes were identified in *M. genitalium*, these were organized into five clusters plus nine single genes. In all cases, the best match for each tRNA gene in *M. genitalium* was the corresponding gene in *M. pneumoniae* (Simoneau, P. *et al.*, *Nuc. Acid Res.* 21:4967 (1993)). Furthermore, the grouping of tRNAs into clusters (trnA, trnB, trnC, trnD, and trnE) was identical in *M. genitalium* and *M. pneumoniae* as was gene order within the cluster (Simoneau, P. *et al.*, *Nuc. Acids Res.* 21:4967 (1993)). The only difference between *M. genitalium* and *M. pneumoniae* observed with regard to tRNA gene organization was an inversion between trnD and GTG. In contrast to *H. influenzae* and many other eubacteria, no tRNAs were found in the spacer region between the 16S and 23S rRNA genes in the rRNA operon of *M. genitalium*, similar to what has been reported for *M. capricolum* (Sawada, M. *et al.*, *Mol. Gen. Genet.* 182:502 (1981)).

A search of the *M. genitalium* genome for tRNA synthetase genes identified all of the expected genes with the exception of glutamyl tRNA synthetase. We expect that this gene is present in the *M. genitalium* genome, but we have not been able to identify it by similarity searches. The latest GenBank release (release 89) contains only a single entry for a glutamyl tRNA synthetase from a bacterial species; this was from *E. coli*, a gram-negative organism only distantly related to *Mycoplasma*. In general, tRNA synthetase sequences from gram-positive organisms such as *B. subtilis* displayed greater similarity to those from *M. genitalium* than the corresponding sequences from *E. coli*, lending support to the notion that the similarity between the *E. coli* and *M. genitalium* glutamyl tRNA synthetase may not have been high enough to be detected.

**Metabolic pathways.** The reduction in genome size among *Mycoplasma* species is associated with a marked reduction in the number and components of biosynthetic pathways in these organisms, requiring them to use metabolic products from their hosts. In the laboratory, *M. genitalium* has not been grown in a chemically defined medium. The complex growth requirements of this organism can be explained by the almost complete lack of enzymes involved in amino acid biosynthesis, *de novo* nucleotide biosynthesis, and fatty acid biosynthesis (Table 6 and Figure 5). When the number of genes in the categories of central intermediary metabolism, energy metabolism, and fatty acid and phospholipid metabolism are summed, marked differences in gene content between *H. influenzae* and *M. genitalium* are apparent. For example, whereas the *H. influenzae* genome contains 68 genes involved in amino acid biosynthesis, the *M. genitalium* genome contains only one. In total, the *H. influenzae* genome has 167 genes associated with metabolic pathways whereas the *M. genitalium* genome has just 42. A recent analysis of 214 kb of sequence from *Mycoplasma capricolum* (Bork, P. *et al.*, *Mol. Microbiol.* 16:955 (1995)), a related organism whose genome size is twice as large as that of *M. genitalium*, reveals that *M. capricolum* contains a number of biosynthetic enzymes not present in *M. genitalium*. This observation suggests that *M. capricolum*'s larger genome confers a greater anabolic capacity.

*M. genitalium* is a facultative anaerobe that ferments glucose and possibly other sugars via glycolysis to lactate and acetate. Genes that encode all the enzymes of the glycolytic pathway were identified, including genes for components of the pyruvate dehydrogenase complex, phosphotransacetylase, and acetate kinase. The major route for ATP synthesis may be through substrate level phosphorylation since no cytochromes are present. *M. genitalium* also lacks all the components of the tricarboxylic acid cycle. None of the genes coding for glycogen or poly-beta-hydroxybutyrate production were identified, indicating limited capacity for carbon and energy storage. The pentose phosphate pathway also appears limited since only genes encoding 6-phosphogluconate dehydrogenase and transketolase were identified. The limited metabolic capacity of *M. genitalium* sharply contrasts with the complexity of catabolic pathways in *H. influenzae*, reflecting the four-fold greater number of genes involved in energy metabolism found in *H. influenzae*.

**Transport.** The transporters identified in *H. influenzae* are specific for a range of nutritional substrates. Using protein transport as an example, both oligopeptide and amino acid transporters are represented. One interesting peptide transporter has homology to a lactococcal transporter (lcnDR3) and related bacteriocin transporters, suggesting the *M. genitalium* may export a small peptide with antibacterial activity. The *H. influenzae* isolog of the *M. hyorhinis* p37 high-affinity transport system also has a conserved lipid modification site, providing further evidence that the *Mycoplasma* binding-protein dependent transport systems are organized in a manner analogous to gram positive bacteria (Gilson, E. et al., *EMBO J.* 7:3971 (1988)).

Genes encoding proteins that function in the transport of glucose via the phosphoenolpyruvate:sugar transferase system (PTS) have been identified in *M. genitalium*. These include enzyme I (EI), HPr and sugar specific enzyme IIs (EII) (Postma, P.W. et al., *Microbiol. Rev.* 57:543 (1993)). EIIs consist of a complex of at least three domains, EIIA, EIIB and EIIC. In some bacteria (eg, *E. coli*), EIIA is a soluble protein, while in others (*Bacillus subtilis*), a single membrane protein contains all three domains, EIIA, B and C. These variations in the proteins that make up the EII complex are due to fusion or splitting of domains during evolution and are not considered to be mechanistic differences (Postma, P.W. et al., *Microbiol. Rev.* 57:543 (1993)). In *M. genitalium* EIIA, B, and C are located in a single protein similar to the protein found in *B. subtilis*. In *Mycoplasma capricolum* ptsH, the gene which encodes for HPr, is located on a monocistronic transcriptional unit while genes encoding EI (ptsI) and EIIA (crr) are located on a dicistronic operon (Zhu, P.P. et al., *Protein Sci.* 3:2115 (1994); Zhu, P.P. et al., *J. Biol. Chem.* 268:26531 (1993)). In most bacterial species studied to date, ptsI, ptsH, and crr are part of a polycistronic operon (pts operon). In *M. genitalium* ptsH, ptsI and the gene encoding EIIABC reside at different locations of the genome and thus each of these genes may constitute monocistronic transcriptional units. We have also identified EIIBC component for uptake of fructose; however, other components of the fructose PTS were not found. Thus, *M. genitalium* may be limited to the use of glucose as a energy source. In contrast, *H. influenzae* has the ability to use at least six different sugars as a source of carbon and energy.

**Regulatory Systems.** It appears that regulatory systems found in other bacteria are absent in *M. genitalium*. For instance, although two component systems have been described for a number of gram-positive organisms, no sensor or response regulator genes are found in the *M. genitalium* genome. Furthermore, the lack of a heat shock  $\sigma$  factor raises the question of how the heat shock response is regulated. Another stress faced by all metabolically active organisms is the generation of reactive oxygen intermediates such as superoxide anions and hydrogen peroxide. Although *H. influenzae* has a oxyR homologue, as well as catalase and superoxide dismutase, *M. genitalium* appears to lack these genes as well as an NADH peroxidase. The importance of these reactive intermediate molecules in host cell damage suggests that some as yet unidentified protective mechanism may exist within the cell.

**Antigenic variation.** Numerous examples exist of microbial pathogens expressing outer membrane proteins that vary due to DNA rearrangements as a mechanism for providing antigenic and functional variations that influence virulence potential (Bergstrom, S. et al., *Proc. Natl. Acad. Sci. USA* 83:3890 (1986); Meier, J.T. et al., *Cell* 47:61 (1986); Majiwa, P.A.O. et al., *Nature* 297:514 (1982)). Because humans are the natural host for both *M. genitalium* and *H. influenzae*, it was of interest to compare mechanisms for generating antigenic variation in these organisms. In *H. influenzae*, a number of virulence-related genes encoding membrane proteins contain tandem tetramer repeats that undergo frequent addition and deletion of one or more repeat units during replication, such that the reading frame of the gene is changed and its expression altered (Weiser, J.N. et al., *Cell* 59:657 (1989)).

*M. genitalium* appears to use a different system for evading host immune responses. The 140 kDa adhesion protein of *M. genitalium* is densely clustered at a differentiated tip of this organism and elicits a strong immune response in humans and experimentally infected animals (Collier, A.M. et al., *Zbl. Bkt. Suppl.* 20:73 (1992)). The adhesion protein (MgPa) operon in *M. genitalium* contains a 29 kDa ORF, the MgPa protein (160 kDa) and a 114 kDa ORF with intervening regions of 6 and 1 nt, respectively (Inamine, J.M. et al., *Gene* 82:259 (1989)). Based on hybridization experiments (Dallo, S.F. and Baseman, J.B., *Microb. Pathog.* 8:371 (1990)), multiple copies of regions of the *M. genitalium* MgPa gene and the 114 kDa ORF are known to exist throughout the genome.

The availability of the complete genomic sequence from *M. genitalium* has allowed a comprehensive mapping of the MgPa repeats (Figures 4 and 6). In addition to the complete operon, nine repetitive elements which are composites of particular regions of the MgPa operon were found. The percent of sequence identity between the repeat elements and the MgPa gene ranges from 78%-90%. In some of the repeats, the MgPa-related sequences are separated in the genome by a variable length, A-T rich spacer sequence, as has previously been described (Peterson, S.N., PhD dis-



sertation, Univ. No. Carolina 1992, Univ. Mi. Dissertation Services #6246). The sequences contained in the MgPa operon and the nine repeats scattered throughout the chromosome represent 4.5% of the total genomic sequence. At first glance this might appear to contradict the expectation for a minimal genome. However, recent evidence for recombination between the repetitive elements and the MgPa operon has been reported (Peterson, S.N. *et al.*, *Proc. Natl. Acad. Sci. USA*, in press (1995)). Such recombination may allow *M. genitalium* to evade the host immune response through mechanisms that induce antigenic variation within the population. Since *M. genitalium* survives in nature by obtaining essential nutrients from its mammalian host, a efficient mechanism to evade the immune response may be a necessary part of this minimal genome.

The *M. genitalium* genome contains 93 putatively identified genes that are apparently not present in *H. influenzae*. Almost 60% of these genes have database matches to known or hypothetical proteins from gram-positive bacteria or other *Mycoplasma* species, suggesting that these genes may encode proteins with a restricted phylogenetic distribution. One hundred seventeen potential coding regions in *M. genitalium* have no database match to any sequences in public archives including the entire *H. influenzae* genome; therefore, these likely represent novel genes in *M. genitalium*, and related organisms.

The predicted coding sequences of the hypothetical ORFs, the ORFs with motif matches and the ORFs that have no similarities to known peptide sequences were analyzed. The two programs used were the Kyte-Doolittle algorithm (Kyte, J. and Doolittle, R.F., *J. Mol. Biol.* 157:105 (1982)) with a range of 11 residues, and PSORT which is available on the WWW site <http://psort.nibb.ac.jp>. PSORT predicts the presence of signal sequences by the methods of McGeoch (McGeoch, D.J., *Virus Res.* 3:271 (1985)) and von Heijne (von Heijne, G., *Nucl. Acids Res.* 14:4683 (1986)), and detects potential transmembrane domains by the method of Klein *et al.* (Klein, P. *et al.*, *Biochim. Biophys. Acta* 815:468 (1985)). Of a total of 201 ORFs examined, 90 potential membrane proteins were found. Eleven of them are predicted to have type I signal peptides, and five type II signal peptides. Using this approach, at least fifty potential membrane proteins were identified from the list of ORFs with known functions. This brings the total number of membrane proteins in *M. genitalium* to approximately 140.

To manage these putative membrane proteins, *M. genitalium* has at its disposal a minimal secretory machinery composed of seven functions: three chaperoning GroEL, DnaK and the trigger factor Tlg (Pugsley, A.P., *Microbiol. Rev.* 57:50 (1993); Guthrie, B. and Wickner, W., *J. Bacteriol.* 172:5555 (1990), an ATPase pilot protein SecA, one integral membrane protein translocase (SecY), a signal recognition particle protein (Ffh) and a lipoprotein-specific signal peptidase LspA (Pugsley, A.P., *Microbiol. Rev.* 57:50 (1993)). Perhaps the lack of other known translocases like SecE, SecD, and SecF which are present in *E. coli* and *H. influenzae*, is related to the fact that *M. genitalium* has a one-layer cell envelope. Also, the absence of a SecB homologue, the secretory chaperonin of *E. coli*, in *M. genitalium* (it is also absent in *B. subtilis* (Collier, D.N. *J. Bacteriol.* 176:4937 (1994))) might reflect a difference between gram negative and wall-less Mollicutes in handling nascent proteins destined for the general secretory pathway. Considering the presence of several putative membrane proteins that contain type I signal peptides, the absence of a signal peptidase I (*lepB*) is most surprising. A direct electronic search for the *M. genitalium lepB* gene using the *E. coli lepB* and the *B. subtilis sipS* (van Dijl, J.M. *et al.*, *EMBO J.* 11:2819 (1992)) as queries did not reveal any significant similarities.

There are a number of possible explanations as to why genes encoding some of the proteins thought to be essential for a self-replicating organism appear to be absent in *M. genitalium*. One possibility is that a limited number of proteins may have adapted to take on other functions. A second possibility is that certain proteins thought to be essential for life based on studies in *E. coli* are not required in a simpler prokaryote like *M. genitalium*. Finally, it may be that sequences from *M. genitalium* have such a low similarity to known sequences from other species that matches are not detectable above a reasonable confidence threshold.

Determination of the complete genome sequence of *M. genitalium* provides a new starting point in understanding the biology of this and related organisms. Comparison of the genes expressed in *M. genitalium*, a simple prokaryote, with those in *H. influenzae*, a more complex organism, has revealed a myriad of differences between these species. Fifty-six percent of the genes in *M. genitalium* have apparent isoforms in *H. influenzae*, suggesting that this subset of the *M. genitalium* genome may encode the genes that are truly essential for a self-replicating organism. Notable among the genes that are conserved between *M. genitalium* and *H. influenzae* are those involved in DNA replication and repair, transcription and translation, cell division, and basic energy metabolism via glycolysis. Isoforms of these genes are found in eukaryotes as well.

## Example 2

### Production of an Antibody to a *Mycoplasma genitalium* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the

protein can then be prepared as follows:

### Monoclonal Antibody Production by Hybridoma Fusion

5 Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells  
10 destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use.  
15 Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* Basic Methods in Molecular Biology Elsevier, New York. Section 21-2 (1989).

### Polyclonal Antibody Production by Immunization

20 Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than other and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive  
25 doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall (See Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973)). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12  $\mu$ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, (eds.), Amer. Soc. For Microbio., Washington, D.C. (1980).  
30

35 Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample.

### Example 3

40

#### Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Mycoplasma genitalium* genome, such as those disclosed in Tables 1a, 1b, 1c and 2 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the examples that follow.  
45

### Example 4

50

#### Gene expression from DNA Sequences Corresponding to ORFs

A fragment of the *Mycoplasma genitalium* genome provided in Tables 1a, 1b, 1c and 2 is introduced into a expression vector using conventional technology (techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art). Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U.S. Pat. No. 5,082,767, which is hereby incorporated by ref-  
55

erence.

The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Mycoplasma* genome fragment. Since the ORF lacks a poly A sequence because of the bacterial origin of the ORF, this sequence can be added to the construct by, for example, splicing out the poly A sequence from pSG5 (Stratagene) using *Bgl*I and *Sal*I restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Mycoplasma* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Mycoplasma* DNA and containing restriction endonuclease sequences for *Pst*I incorporated into the 5' primer and *Bgl*II at the 5' end of the corresponding *Mycoplasma* DNA 3' primer, taking care to ensure that the *Mycoplasma* DNA is positioned such that its followed with the poly A sequence. The purified fragment obtained from the resulting PCR reaction is digested with *Pst*I, blunt ended with a exonuclease, digested with *Bgl*II, purified and ligated to pXT1, now containing a poly A sequence and digested *Bgl*II.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface.

Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *Mycoplasma* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Mycoplasma* DNA.

If antibody production is not possible, the *Mycoplasma* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as a chimeric with, for example,  $\beta$ -globin. Antibody to  $\beta$ -globin is used to purify the chimeric. Corresponding protease cleavage sites engineered between the  $\beta$ -globin gene and the *Mycoplasma* DNA are then used to separate the two polypeptide fragments from one another after translation. One useful expression vector for generating  $\beta$ -globin chimerics is pSG5 (Stratagene). This vector encodes rabbit  $\beta$ -globin. Intron II of the rabbit  $\beta$ -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis et al. and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from either construct using in vitro translation systems such as In vitro Express™ Translation Kit (Stratagene).

Table 1(a)

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG006	8552	9181	SP-P00572	thymidylate kinase (CDC8) {Saccharomyces cerevisiae}	27.5862	51.7241	630
MG009	11252	12037	GB:D26185_1 02	hypothetical protein (GB:D26185_102) {Bacillus subtilis}	35.4331	55.1181	786
MG010	12069	12722	SP:P33655	DNA primase (dnaE) {Clostridium acetobutylicum}	25.731	53.2164	654
MG012	14247	13573	SP:P17116	ribosomal protein S6 modification protein (rimK) {Escherichia coli}	31.4961	54.3307	675
MG013	15217	14399	GB:D10588_1	5,10-methylene-tetrahydrofolate dehydrogenase (folD) {Escherichia coli}	33.0472	53.2189	819
MG015	17474	19240	SP:P27299	transport ATP-binding protein (msbA) {Escherichia coli}	32.2382	57.4949	1767
MG023	26478	27341	GB:M22039_4	fructose-bisphosphate aldolase (tsr) {Bacillus subtilis}	45.9649	65.9649	864
MG024	27345	28445	GP:U02423_1	GTP-binding protein (gtp1) {Escherichia coli}	46.8401	67.658	1101
MG032	36978	38975	GB:M63489_1	ATP-dependent nuclease (addA) {Bacillus subtilis}	26.8293	54.2683	1998
MG033	39242	39901	GB:M99611_2	glycerol uptake facilitator (glpF) {Bacillus subtilis}	35.8974	55.3846	660
MG034	40514	39876	GB:M97678_5	thymidine kinase (tdk) {Bacillus subtilis}	48.1283	69.5187	639
MG035	40543	41784	GB:U00011_2	histidyl-tRNA synthetase (hisS) {Mycobacterium leprae}	30.7107	50.7614	1242

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG038	46277	44754	GB:L19201_68	glycerol kinase (glpK) {Escherichia coli}	46.8254	70.2381	1524
MG039	47422	46271	PIR:S48379	glycerol-3-phosphate dehydrogenase (GUT2) {Saccharomyces cerevisiae}	43.2099	60.4938	1152
MG041	49377	49640	GB:L22432_2	phosphohistidinoprotein-hexose phosphotransferase (ptsH) {Mycoplasma capricolum}	48.8636	70.4545	264
MG042	50060	51517	GB:M64519_1	spermidine/putrescine transport ATP-binding protein (potA) {Escherichia coli}	41.9231	65.3846	1458
MG043	51525	52379	GB:M64519_2	spermidine/putrescine transport system permease protein (potB) {Escherichia coli}	26.5116	57.2093	855
MG044	52366	53217	GB:M64519_3	spermidine/putrescine transport system permease protein (potC) {Escherichia coli}	29.4574	58.1395	852
MG046	54658	55602	GB:M62364_1	sialoglycoprotease (gcp) {Pasteurella haemolytica}	36.6013	59.4771	945
MG048	58310	56973	SP:P37105	signal recognition particle protein (ffh) {Bacillus subtilis}	43.0206	66.1327	1338
MG049	58117	59076	GB:U14003_2 95	purine-nucleoside phosphorylase (deoD) {Escherichia coli}	44.7826	63.0435	960
MG050	59083	59751	GB:X13544_1	deoxyribose-phosphate aldolase (deoC) {Mycoplasma pneumoniae}	83.0357	91.5179	669

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG056	65731	64901	GB:D26185_9	hypothetical protein (GB:D26185_99) {Bacillus subtilis}	30.2583	54.6125	831
MG057	66249	65716	GB:D26185_104	hypothetical protein (GB:D26185_104) {Bacillus subtilis}	28.9017	28.9017	534
MG067	81047	82594	GB:D00730_1	glutamic acid specific protease (SPase) {Staphylococcus aureus}	28.8462	48.0769	1548
MG070	91065	91916	SP:P34831	ribosomal protein S2 (rpS2) {Spirulina platensis}	34.8	55.2	852
MG077	10310	104324	SP:P24138	oligopeptide transport system permease protein (oppB) {Bacillus subtilis}	28.0528	58.4158	1221
MG078	104320	105447	SP:P26904	oligopeptide transport system permease protein (dciAC) {Bacillus subtilis}	33.4572	55.0186	1128
MG079	105452	106657	SP:P18765	oligopeptide transport ATP-binding protein (amiE) {Streptococcus pneumoniae}	47.9412	67.9412	1206
MG081	109262	109672	SP:P29395	ribosomal protein L11 (RPL11) {Thermotoga maritima}	51.7986	71.9424	411
MG085	111790	112722	PIR:S24760	hydroxymethylglutaryl-CoA reductase (NADPH) {Nicotiana sylvestris}	23.3216	49.1166	933
MG086	112718	113863	GB:L13259_2	prolipoprotein diacylglycerol transferase (lgt) {Salmonella typhimurium}	29.1262	53.8835	1146

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG091	11755 3	118032	GB:U04997_2	single-stranded DNA binding protein (ssb) {Haemophilus influenzae}	21.7949	41.6667	480
MG092	11802 5	118339	GB:U14003_1 14	ribosomal protein S18 (rpS18) {Escherichia coli}	45.4545	68.1818	315
MG093	11834 5	118794	GB:M57623_1	ribosomal protein L9 (rpL9) {Bacillus stearothermophilus}	32.8859	56.3758	450
MG099	12585 2	127282	GB:M61151_1	hydrolase (aux2) {Agrobacterium rhizogenes}	32.1212	51.8182	1431
MG106	13482 6	134149	SP:P27251	formylmethionine deformylase (def) {Escherichia coli}	36.9369	68.4685	678
MG107	13455 8	135334	GB:L10328_14	5'guanylate kinase (gmk) {Escherichia coli}	42.623	65.0273	777
MG114	14134 5	142052	GB:M12299_2	phosphatidylglycerophosphate synthase (pgsA) {Escherichia coli}	29.2994	57.3248	708
MG118	14393 5	144954	SP:P09147	UDP-glucose 4-epimerase (galE) {Escherichia coli}	34.0557	53.87	1020
MG121	14823 8	149155	SP:P32720	hypothetical protein (SP:P32720) {Escherichia coli}	30.8824	50.7353	918

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG125	15308 1	153935	GB:L10328_61	hypothetical protein (GB:L10328_61) {Escherichia coli}	31.9149	48.227	855
MG126	15496 2	153922	GB:M24068_1	tryptophanyl-tRNA synthetase (trpS) {Bacillus subtilis}	41.1585	61.5854	1041
MG127	15499 8	155432	SP:P19434	hypothetical protein (SP:P19434) {Streptomyces viridochromogenes}	25.9615	49.0385	435
MG128	15544 3	156219	GB:U00021_1 9	hypothetical protein (GB:U00021_19) {Mycobacterium leprae}	27.7027	49.3243	777
MG129	15622 2	156572	GB:U12340_1	PTS glucose-specific permease {Bacillus stearothermophilus}	25.4545	51.8182	351
MG130	15656 5	158016	GB:M91593_1	hypothetical protein (GB:M91593_1) {Mycoplasma mycoides}	30.6773	55.7769	1452
MG131	15802 2	158243	GB:M31161_3	hypothetical protein (GB:M31161_3) {Spiroplasma citri}	21.5909	56.8182	222
MG132	15900 5	158583	SP:P32083	hypothetical protein (SP:P32083) {Mycoplasma hyorhinis}	30.0971	56.3107	423
MG136	16096 2	162431	GB:D26185_1 44	lysyl-tRNA synthetase (lysS) {Bacillus subtilis}	45.6212	68.4318	1470



UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG137	16237 6	163587	GP:L41518_4	dTDP-4-dehydrorhamnose reductase (rfbD) {Klebsiella pneumoniae}	32.1622	55.9459	1212
MG139	16547 0	167176	GB:L18927_2	hypothetical protein (GB:L18927_2) {Buchnera aphidicola}	28.5714	62.8571	1707
MG143	18285 3	183188	SP:P09170	hypothetical protein (SP:P09170) {Escherichia coli}	25	53.7037	336
MG145	18405 5	184861	GB:M35367_1	protein X {Pseudomonas fluorescens}	29.0698	48.4496	807
MG148	18730 4	188530	GB:L18965_6	hypothetical protein (GB:L18965_6) {Thermophilic bacterial sp.}	25.2874	52.8736	1227
MG150	19004 8	190365	SP:P38518	ribosomal protein S10 (rpS10) {Thermotoga maritima}	48.913	71.7391	318
MG152	19114 5	191777	SP:P28601	ribosomal protein L4 (rpL4) {Bacillus stearothermophilus}	39.2345	63.1579	633
MG153	19178 4	192101	SP:P04454	ribosomal protein L23 (rpL23) {Bacillus stearothermophilus}	38.7097	62.3656	318
MG154	19210 4	192958	SP:P04257	ribosomal protein L2 (rpL2) {Bacillus stearothermophilus}	58.7814	72.4014	855

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG155	19296 1	193221	GB:X02613_6	ribosomal protein S19 (rpS19) {Escherichia coli}	58.6207	77.0115	261
MG156	19322 7	193658	GB:M74770_4	ribosomal protein L22 (rpL22) {Mycoplasma-like organism}	49.0385	67.3077	432
MG157	19366 4	194467	SP:P02353	ribosomal protein S3 (rpS3) {Mycoplasma capricolum}	46.729	67.2897	804
MG158	19447 6	194889	SP:P02415	ribosomal protein L16 (rpL16) {Mycoplasma capricolum}	63.5037	78.1022	414
MG159	19489 2	195491	SP:P38514	ribosomal protein L29 (rpL29) {Thermotoga maritima}	41.6667	65	600
MG160	19549 4	195748	SP:P10131	ribosomal protein S17 (rpS17) {Mycoplasma capricolum}	51.1905	67.8571	255
MG161	19575 5	196120	SP:P04450	ribosomal protein L14 (rpL14) {Bacillus stearothermophilus}	63.1148	86.0656	366
MG162	19612 3	196446	SP:P04455	ribosomal protein L24 (rpL24) {Bacillus stearothermophilus}	44.5783	66.2651	324
MG163	19645 5	196994	SP:P08895	ribosomal protein L5 (rpL5) {Bacillus stearothermophilus}	57.5419	77.095	540

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG164	19700 0	197182	GB:X06414_1 5	ribosomal protein S14 (rpS14) {Mycoplasma capricolum}	70.4918	83.6066	183
MG165	19717 9	197601	SP:P04446	ribosomal protein S8 (rpS8) {Mycoplasma capricolum}	46.875	71.0938	423
MG166	19761 1	198162	SP:P04448	ribosomal protein L6 (rpL6) {Mycoplasma capricolum}	46.9945	66.6667	552
MG167	19816 7	198511	GB:M57624_1	ribosomal protein L18 (rpL18) {Bacillus stearothermophilus}	42.9825	57.8947	345
MG169	19916 0	199609	SP:P10138	ribosomal protein L15 (rpL15) {Mycoplasma capricolum}	41.8919	66.2162	450
MG170	19961 2	201036	SP:P10250	preprotein translocase sec Y subunit (sec Y) {Mycoplasma capricolum}	38.7892	68.1614	1425
MG171	20103 3	201674	GB:M88104_2	adenylate kinase (adk) {Bacillus stearothermophilus}	32.2115	57.6923	642
MG172	20168 0	202423	GB:D00619_5	methionine amino peptidase (map) {Bacillus subtilis}	36.2903	58.4677	744
MG173	20242 6	202635	GB:M26414_1	initiation factor 1 (infA) {Bacillus subtilis}	48.5294	67.6471	210

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG174	20264 9	202759	SP:P38015	ribosomal protein L36 (rpL36) {Chlamydia trachomatis}	78.3784	83.7838	111
MG177	20351 6	204499	GB:M26414_5	RNA polymerase alpha core subunit (rpoA) {Bacillus subtilis}	39.3939	65.9933	984
MG178	20451 5	204515	GB:M26414_6	ribosomal protein L17 (rpL17) {Bacillus subtilis}	34.7826	59.1304	369
MG179	20487 3	205694	SP:P11599	haemolysin secretion ATP-binding protein (hlyB) {Proteus vulgaris}	34.5992	62.0253	822
MG187	21676 2	218516	GB:M77351_7	ATP-binding protein (msmK) {Streptococcus mutans}	40.5325	65.6805	1755
MG188	21852 2	219508	GB:M77351_4	membrane protein (msmF) {Streptococcus mutans}	22.4719	51.6854	987
MG189	21943 5	220436	GB:M77351_5	membrane protein (msmG) {Streptococcus mutans}	27.1429	52.8571	1002
MG196	23563 5	236057	GB:X16188_1	translation initiation factor IF3 (infC) {Bacillus stearothermophilus}	31.3433	62.6866	423
MG197	23606 3	236239	PIR:S05347	ribosomal protein L35 (rpL35) {Bacillus stearothermophilus}	60	72.7273	177

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG198	23624 5	236616	SP:Q05427	ribosomal protein L20 (rpL20) {Mycoplasma fermentans}	57.5221	73.4513	372
MG201	23916 3	239813	GB:M84964_2	heat shock protein (grpE) {Bacillus subtilis}	31.677	49.6894	651
MG205	24559 6	244568	GB:M84964_1	hypothetical protein (GB:M84964_1) {Bacillus subtilis}	30.9942	58.1871	1029
MG213	25257 9	253991	GB:L09228_16	hypothetical protein (GB:L09228_16) {Bacillus subtilis}	27.1186	54.661	1413
MG214	25397 8	254598	GB:L09228_17	hypothetical protein (GB:L09228_17) {Bacillus subtilis}	34.8571	59.4286	621
MG215	25462 0	255588	SP:P20275	6-phosphofructokinase (pfk) {Spiroplasma citri}	39.441	63.0435	969
MG217	25804 0	259155	SP:P29126	bifunctional endo-1,4-beta-xylanase xyla precursor (xynA) {Ruminococcus flavefaciens}	37.5839	48.9933	1116
MG219	26559 6	266039	GB:M87491_1	IgA1 protease {Haemophilus influenzae}	32.2314	51.2397	444
MG220	26638 2	266077	GB:Z26883_1	pre-procytotoxin (vacA) {Helicobacter pylori}	36.1446	51.8072	306

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG222	26708 0	268006	GB:D10483_6 3	hypothetical protein (GB:D10483_63) {Escherichia coli}	35.1974	56.5789	927
MG224	26924 9	270355	GB:U06462_1	cell division protein (ftsZ) {Staphylococcus aureus}	30.8824	50.7353	1107
MG234	27949 1	279802	GB:K02665_2	ribosomal protein L27 (rpL27) {Bacillus subtilis}	64.3678	80.4598	312
MG235	27979 8	280670	SP:P12638	endonuclease IV (nfo) {Escherichia coli}	29.368	51.3011	873
MG245	29344 6	293940	GB:M12965_1	hypothetical protein (GB:M12965_1) {Escherichia coli}	33.8462	56.9231	495
MG247	29548 4	294768	SP:P31056	hypothetical protein (SP:P31056) {Escherichia coli}	32.973	56.2162	717
MG248	29612 7	295474	GP:U17284_2	major sigma factor (rpoD) {Listeria monocytogenes}	28.4848	51.5152	654
MG251	30080 2	299465	GB:L08106_1	glycyl-tRNA synthetase {Bombyx mori}	35.8974	56.1772	1338
MG252	30155 0	300825	GP:Z33076_2	rRNA methylase {Mycoplasma capricolum}	38.8626	59.7156	726

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG253	30283 9	301556	GB:D26185_1 56	cysteinyI-tRNA synthetase (cysS) {Bacillus subtilis}	34.3458	56.3084	1284
MG257	30763 5	307925	GB:L19201_78	ribosomal protein L31 (rpL31) {Escherichia coli}	37.3134	61.194	291
MG258	30792 8	309004	GB:M11519_1	peptide chain release factor 1 (RF-1) {Escherichia coli}	43.1677	66.4596	1077
MG259	30900 8	310375	GB:D28567_2	protoporphyrinogen oxidase (hemK) {Escherichia coli}	30.5732	54.1401	1368
MG260	31050 9	312803	GB:Z32651_1	hypothetical protein (GB:Z32651_1) {Mycoplasma pneumoniae}	57.1429	71.4286	2295
MG262	31833 0	319202	GB:L11920_1	DNA polymerase I (polI) {Mycobacterium tuberculosis}	29.9419	47.9651	873
MG264	32104 4	321637	GB:M64324_1	6-phosphogluconate dehydrogenase (gnd) {Escherichia coli}	29.8507	47.7612	594
MG265	32241 2	321579	GB:L10328_61	hypothetical protein (GB:L10328_61) {Escherichia coli}	27.193	48.6842	834
MG268	32587 7	325194	GB:U01881_2	deoxyguanosine/deoxyadenosine kinase(I) subunit 2 {Lactobacillus acidophilus}	29.5181	49.3976	684



UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG270	32844 2	327435	GB:U14003_2 97	hypothetical protein (GB:U14003_297) {Escherichia coli}	38.2838	57.7558	1008
MG272	33098 4	329833	GB:M81753_3	dihydrolipoamide acetyltransferase (pdhC) {Acholeplasma laidlawii}	45.1524	62.0499	1152
MG273	33221 4	331237	GB:M81753_2	pyruvate dehydrogenase E1-beta subunit (pdhB) {Acholeplasma laidlawii}	55.0314	76.7296	978
MG274	33330 8	332235	GB:M81753_1	pyruvate dehydrogenase E1-alpha subunit (pdhA) {Acholeplasma laidlawii}	42.9825	61.1111	1074
MG277	33832 3	335414	GB:L16960_2	spore germination apparatus protein (gerBB) {Bacillus subtilis}	31.2	55.2	2910
MG280	34192 0	341177	GB:Z35086_1	sensory rhodopsin II transducer (htrII) {Natronobacterium pharaonis}	15.7143	46.6667	744
MG288	35303 4	351793	GB:L04466_1	protein L {Peptostreptococcus magnus}	31.1475	50.8197	1242
MG290	35511 9	355853	SP:P15361	ATP-binding protein P29 {Mycoplasma hyorhinis}	32.3009	58.8496	735
MG292	36059 2	357893	GB:J01581_1	alanyl-tRNA synthetase (alaS) {Escherichia coli}	33.8403	55.64	2700

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG295	36402 2	362922	SP:P25745	hypothetical protein (SP:P25745) {Escherichia coli}	34.7107	57.0248	1101
MG299	36969 4	368735	SP:P39646	phosphotransacetylase (pta) {Clostridium acetobutylicum}	44.6541	63.522	960
MG303	37399 8	372928	GB:M61017_1	membrane transport protein (glnQ) {Bacillus stearothermophilus}	31.982	54.955	1071
MG304	37474 1	373983	GB:U13043_1	membrane associated ATPase (cbiO) {Propionibacterium freudenreichii}	30.0448	53.8117	759
MG310	38646 2	387265	GB:D11037_1	proline iminopeptidase (pip) {Bacillus coagulans}	29.2079	51.4851	804
MG311	38789 2	387278	GB:M59358_1	ribosomal protein S4 (rpS4) {Bacillus subtilis}	43	65.5	615
MG313	39202 3	391397	GP:L38997_5	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}	53.8462	79.8077	627
MG315	39455 0	393660	GP:L38997_3	cytadherence accessory protein (hmw1) {Mycoplasma pneumoniae}	44.3878	69.898	891
MG316	39558 3	394477	GB:L15202_4	competence locus E (comE3) {Bacillus subtilis}	30.4933	52.4664	1107

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG322	40539 8	403725	GB:D17462_1 1	Na <sup>+</sup> ATPase subunit J (ntpJ) {Enterococcus hirae}	31.0811	56.3063	1674
MG323	40545 5	406135	GB:D37799_6	hypothetical protein (GB:D37799_6) {Bacillus subtilis}	27.5701	54.2056	681
MG325	40895 3	408795	SP:P23375	ribosomal protein L33 (rpL33) {Bacillus stearothermophilus}	58.1395	69.7674	159
MG326	40985 7	408973	GB:Z18629_1	hypothetical protein (GB:Z18629_1) {Bacillus subtilis}	27.0758	52.7076	885
MG329	41431 8	412975	GB:U00021_5	hypothetical protein (GB:U00021_5) {Mycobacterium leprae}	32.1839	54.2529	1344
MG332	41632 9	415613	GB:D10165_3	hypothetical protein (GB:D10165_3) {Escherichia coli}	26.9231	49.1453	717
MG346	44392 2	444419	GB:M65289_3	hypothetical protein (GB:M65289_3) {Bacillus stearothermophilus}	37.9747	60.1266	498
MG347	44441 3	445042	SP:P32049	hypothetical protein (SP:P32049) {Escherichia coli}	28.4615	46.9231	630
MG351	44966 5	450216	SP:P37981	inorganic pyrophosphatase (ppa) {Thermoplasma acidophilum}	38.8535	61.7834	552

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG355	45375 7	451616	GB:M29364_2	ATP-dependent protease binding subunit (clpB) {Escherichia coli}	47.7337	70.6799	2142
MG356	45475 3	453914	GB:M27280_1	lic-1 operon protein (licA) {Haemophilus influenzae}	27.7778	56.25	840
MG359	45734 7	458267	GB:M21298_2	Holliday junction DNA helicase (ruvB) {Escherichia coli}	34.6939	64.966	921
MG360	45949 5	458263	SP:P14303	UV protection protein (mucB) {Salmonella typhimurium}	22.0859	48.1595	1233
MG363	46049 7	460667	GB:M29698_2	ribosomal protein L32 (rpL32) {Escherichia coli}	48.1481	62.963	171
MG364	46101 5	461686	GB:M95954_1	mobilization protein (mob13) {Leuconostoc oenos}	30.8725	53.6913	672
MG367	46543 4	464649	GB:X02673_1	ribonuclease III (rnc) {Escherichia coli}	30.1724	65.5172	786
MG380	47899 9	479574	GB:L10328_10 5	glucose inhibited division protein (gidB) {Escherichia coli}	24.8276	51.7241	576
MG382	48069 1	481329	SP:P31218	uridine kinase (udk) {Escherichia coli}	34.4828	62.5616	639

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG383	48207 5	481332	GB:M15811_1	sporulation protein (outB) {Bacillus subtilis}	36.3636	54.9784	744
MG384	48336 9	482071	GB:M24537_2	GTP-binding protein (obg) {Bacillus subtilis}	39.627	62.0047	1299
MG387	49071 1	489842	SP:P37214	GTP-binding protein era homolog (spg) {Streptococcus mutans}	27.3859	51.0373	870
MG396	50071 9	500264	GB:M80797_2	galactosidase acetyltransferase (lacA) {Streptococcus mutans}	40.5797	57.971	456
MG398	50282 3	502425	SP:P33255	ATP synthase epsilon chain (atpC) {Mycoplasma gallisepticum}	36.9231	55.3846	399
MG402	50720 1	506674	SP:P33254	ATP synthase delta chain (atpH) {Mycoplasma gallisepticum}	33.9181	58.4795	528
MG403	50782 0	507197	SP:P33256	ATP synthase B chain (atpF) {Mycoplasma gallisepticum}	36.5979	66.4948	624
MG404	50813 1	507826	SP:P33258	ATP synthase C chain (atpE) {Mycoplasma gallisepticum}	50	74.359	306
MG407	51083 6	509463	GB:L29475_4	enolase (eno) {Bacillus subtilis}	54.0793	74.1259	1374

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG408	51090 3	511373	SP:P14930	pilin repressor (pilB) {Neisseria gonorrhoeae}	49.2188	68.75	471
MG409	51205 0	511376	GB:L10328_88	peripheral membrane protein U (phoU) {Escherichia coli}	27.027	48.6486	675
MG420	52414 4	523365	GB:D26185_8 3	DNA polymerase III subunit (dnaH) {Bacillus subtilis}	49.115	68.5841	780
MG424	53147 9	531222	SP:P05766	ribosomal protein S15 (BS18) {Bacillus stearothermophilus}	48.1481	71.6049	258
MG426	53304 0	533231	GB:L12244_2	ribosomal protein L28 (rpL28) {Bacillus subtilis}	36.0656	59.0164	192
MG429	53603 6	534321	GB:M69050_2	PEP-dependent HPr protein kinase phosphoryltransferase (ptsI) {Staphylococcus carnosus}	46.4789	66.5493	1716
MG430	53756 3	536043	GB:L29475_3	phosphoglycerate mutase (pgm) {Bacillus subtilis}	45.1866	62.4754	1521
MG432	53954 6	538353	SP:P27712	hypothetical protein (SP:P27712) {Spiroplasma citri}	28.436	48.8152	1194
MG433	53963 2	540525	GB:M31161_2	elongation factor Ts (tsf) {Spiroplasma citri}	39.0572	62.6263	894

UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG434	54084 8	541237	GB:D26562_5 6	mukB suppressor protein (smbA) {Escherichia coli}	40.8696	61.7391	390
MG435	54124 0	541788	GB:D26562_5 7	ribosome releasing factor (frn) {Escherichia coli}	34.9112	57.3965	549
MG438	54300 4	544152	GB:J01631_1	restriction-modification enzyme EcoD specificity subunit (hsdS) {Escherichia coli}	24.5734	45.7338	1149
MG442	54769 0	546881	GB:U00021_5	hypothetical protein (GB:U00021_5) {Mycobacterium leprae}	26.8966	42.069	810
MG443	54884 9	547665	GB:D16311_1	hypothetical protein (GB:D16311_1) {Bacillus subtilis}	26.1818	52	1185
MG444	54922 4	548868	SP:P30529	ribosomal protein L19 (rpL19) {Bacillus stearothermophilus}	49.1071	69.6429	357
MG445	54990 3	549211	SP:P36245	tRNA (guanine-N1)-methyltransferase (trmD) {Salmonella typhimurium}	40.8072	64.1256	693
MG446	55017 2	549906	SP:P21474	ribosomal protein S16 (BS17) {Bacillus subtilis}	48.7805	64.6341	267
MG448	55289 7	552448	GB:Z33052_1	pilin repressor (pilB) {Mycoplasma capricolum}	53.4884	72.093	450



UID	end5	end3	db_match	db_match name	per_id	per_si m	gene_len
MG454	55777 0	557306	SP:P23929	osmotically inducible protein (osmC) {Escherichia coli}	28.4091	51.1364	465
MG457	56260 2	560497	GB:D26185_1 32	cell division protein (ftsH) {Bacillus subtilis}	49.7445	68.1431	2106
MG461	56620 3	564929	GB:X73124_9 4	hypothetical protein (GB:X73124_94) {Bacillus subtilis}	40	64.2857	1275
MG464	56955 4	568400	GB:D14982_3	hypothetical protein (GB:D14982_3) {Mycoplasma capricolum}	32.3699	53.7572	1155
MG465	56991 2	569529	GB:D14982_2	RNaseP C5 subunit (rnpA) {Mycoplasma capricolum}	40	58.75	384
MG466	57002 7	569884	GB:L10328_67	ribosomal protein L34 (rpL34) {Escherichia coli}	67.3913	80.4348	144
MG470	58003 0	579224	GB:D26185_5 5	SpoOJ regulator {Bacillus subtilis}	27.8884	53.3865	807

Table 1(b)

UID	end5	end3	db_match	db_match name	per_sim	per_id	match_info
MG002	1829	2758	SP:P35514	heat shock protein (dnaJ) (Lactococcus lactis)	40	61.6667	MG002(1 - 930 of 930) GB:U09251(298 - 1227 of 6140)
MG003	2846	4795	GB:U09251_3	DNA gyrase subunit B (gyrB) (Mycoplasma genitalium)	99.3846	99.3846	MG003(1 - 1950 of 1950) GB:U09251(1315 - 3264 of 6140)
MG004	4813	7320	GB:U09251_4	DNA gyrase subunit A (gyrA) (Mycoplasma genitalium)	99.8804	99.8804	MG004(1 - 2508 of 2508) GB:U09251(3282 - 5789 of 6140)
MG191	221571	225902	SP:P20796	attachment protein, MgPa operon (mgp) (Mycoplasma genitalium)	100	100	MG191(1 - 4332 of 4332) GB:M31431(1066 - 5397 of 8760)
MG192	225907	229062	SP:P22747	114 kDa protein, MgPa operon (mgp) (Mycoplasma genitalium)	100	100	MG192(1 - 3156 of 3156) GB:M31431(3402 - 8557 of 8760)
MG232	278904	279203	SP:P26908	ribosomal protein L21 (rpL21) (Bacillus subtilis)	37.8947	65.2632	MG232(1 - 300 of 300) GB:U02141(138 - 437 of 827)
MG233	279199	279495	GP:U02141_2	ribosomal protein L21 homolog (Mycoplasma genitalium)	100	100	MG233(1 - 297 of 297) GB:U02141(433 - 729 of 827)
MG287	348882	349133	SP:P04686	nodulation protein F (nodF) (Rhizobium leguminosarum)	34.9398	56.6265	MG287(1 - 252 of 252) GB:U01810(152 - 403 of 917)
MG417	521868	521473	SP:P07842	ribosomal protein S9 (rpS9) (Bacillus stearothermophilus)	51.9685	71.6535	MG417(1 - 396 of 396) GB:U01744(127 - 522 of 620)

Table 1(c)

UID	end5	end3	db_match	db_match name	per_slim	per_id	match_info
MG001	1026	1826	GB:U09251_1	DNA polymerase III beta subunit (dnaN) (Mycoplasma genitalium)	100	100	MG001(507 - 801 of 801) GB:U09251(1 - 295 of 6140)
MG005	7295	8545	GB:D26185_77	seryl-tRNA synthetase (serS) (Bacillus subtilis)	42.615	66.3438	MG005(1 - 377 of 1251) GB:U09251(5764 - 6140 of 6140)
MG005	7295	8545	GB:D26185_77	seryl-tRNA synthetase (serS) (Bacillus subtilis)	42.615	66.3438	MG005(16 - 337 of 1251) GB:U02210(1 - 322 of 322)
MG007	9157	9918	GB:D26185_83	DNA polymerase III subunit (dnaH) (Bacillus subtilis)	22.695	45.3901	MG007(762 - 711 of 762) GB:U02216(270 - 321 of 321)
MG008	9924	11249	GB:D26185_60	thiophene and furan oxidizer (tdhF) (Bacillus subtilis)	31.9101	59.7753	MG008(264 - 1 of 1326) GB:U02216(1 - 264 of 321)
MG011	13565	12705	-	-	-	-	MG011(473 - 767 of 861) GB:U02257(2 - 296 of 296)
MG014	15556	17424	SP:P27299	transport ATP-binding protein (msbA) (Escherichia coli)	28.0702	52.6316	MG014(1005 - 678 of 1869) GB:U02235(1 - 326 of 326)
MG018	21063	22343	SP:P32333	helicase (mot1) (Saccharomyces cerevisiae)	36.6972	60.0917	MG018(1281 - 1067 of 1281) GB:U01723(89 - 304 of 304)
MG018	21063	22343	SP:P32333	helicase (mot1) (Saccharomyces cerevisiae)	36.6972	60.0917	MG018(409 - 105 of 1281) GB:U02179(1 - 305 of 305)
MG018	21063	22343	SP:P32333	helicase (mot1) (Saccharomyces cerevisiae)	36.6972	60.0917	MG018(592 - 896 of 1281) GB:U01757(1 - 305 of 305)

5

10

15

20

25

30

35

40

45

50

55

MG019	22388	23554	SP:P35514	heat shock protein (dnaJ) {Lactococcus lactis}	33.9779	51.105	MG019(44 - 1 of 1167) GB:U01723(1 - 44 of 304)
MG020	23541	24464	GB:Z25461_2	proline iminopeptidase (pip) {Neisseria gonorrhoeae}	37.5439	55.7895	MG020(723 - 924 of 924) GB:U02229(1 - 202 of 333)
MG021	24467	26002	GB:D26185_101	methionyl-tRNA synthetase (metS) {Bacillus subtilis}	37.5494	58.8933	MG021(1 - 129 of 1536) GB:U02229(205 - 333 of 333)
MG021	24467	26002	GB:D26185_101	methionyl-tRNA synthetase (metS) {Bacillus subtilis}	37.5494	58.8933	MG021(1318 - 1527 of 1536) GB:X61513(1 - 209 of 209)
MG022	26035	26469	GB:M21677_1	RNA polymerase delta subunit (rpoE) {Bacillus subtilis}	28.6765	49.2647	MG022(254 - 1 of 435) GB:U01721(1 - 254 of 299)
MG025	28651	29544	GP:Z47767_4	TrsB {Yersinia enterocolitica}	27.551	54.0816	MG025(514 - 894 of 894) GB:U02253(1 - 381 of 649)
MG026	29551	30120	GB:U14003_62	elongation factor P (efp) {Escherichia coli}	26.3804	47.2393	MG026(1 - 262 of 570) GB:U02253(388 - 649 of 649)
MG029	31702	31145	GB:L19300_1	hypothetical protein (GB:L19300_1) {Staphylococcus aureus}	27.027	45.045	MG029(1 - 93 of 558) GB:U01773(210 - 302 of 302)
MG030	32324	31707	GB:Z27121_3	uracil phosphoribosyltransferase (upp) {Mycoplasma hominis}	44.9275	66.6667	MG030(414 - 618 of 618) GB:U01773(1 - 205 of 302)
MG031	36713	32361	GB:U06833_1	DNA polymerase III (polC) {Mycoplasma pulmonis}	38.0303	59.3182	MG031(1473 - 1701 of 4353) GB:U01807(1 - 229 of 229)
MG031	36713	32361	GB:U06833_1	DNA polymerase III (polC) {Mycoplasma pulmonis}	38.0303	59.3182	MG031(2923 - 3309 of 4353) GB:U01712(1 - 387 of 387)
MG031	36713	32361	GB:U06833_1	DNA polymerase III (polC) {Mycoplasma pulmonis}	38.0303	59.3182	MG031(3330 - 3676 of 4353) GB:U02208(1 - 347 of 347)

55	50	45	40	35	30	25	20	15	10	5
MG036	41777	43426	SP:P36419		aspartyl-tRNA synthetase (aspS) {Thermus aquaticus}		40.8582	62.8731	MG036(1115 - 1650 of 1650) GB:U01814(1 - 532 of 1006)	
MG036	41777	43426	SP:P36419		aspartyl-tRNA synthetase (aspS) {Thermus aquaticus}		40.8582	62.8731	MG036(1407 - 1638 of 1650) GB:X61511(1 - 232 of 232)	
MG036	41777	43426	SP:P36419		aspartyl-tRNA synthetase (aspS) {Thermus aquaticus}		40.8582	62.8731	MG036(1412 - 1160 of 1650) GB:X61523(1 - 252 of 252)	
MG037	43402	44751	GP:U02020_1		pre-B cell enhancing factor (PBEF) {Homo sapiens}		34.3164	52.2788	MG037(1 - 500 of 1350) GB:U01814(508 - 1006 of 1006)	
MG040	47581	49353	SP:P29724		membrane lipoprotein (tmpC) {Treponema pallidum}		30.8594	48.0469	MG040(1341 - 1552 of 1773) GB:U02125(1 - 212 of 212)	
MG045	53205	54653	-		-		-	-	MG045(381 - 4 of 1449) GB:U02166(1 - 378 of 378)	
MG047	55589	56737	SP:P30869		S-adenosylmethionine synthetase 2 (metX) {Escherichia coli}		43.6111	60.5556	MG047(787 - 1070 of 1149) GB:U02123(1 - 284 of 284)	
MG051	59741	61003	GB:L13289_3		thymidine phosphorylase (deoA) {Mycoplasma pirum}		52.7316	73.6342	MG051(1161 - 1263 of 1263) GB:U02191(1 - 103 of 183)	
MG052	61015	61404	GB:L13289_4		cytidine deaminase (cdd) {Mycoplasma pirum}		38.2114	64.2276	MG052(1 - 69 of 390) GB:U02191(115 - 183 of 183)	
MG052	61015	61404	GB:L13289_4		cytidine deaminase (cdd) {Mycoplasma pirum}		38.2114	64.2276	MG052(320 - 390 of 390) GB:U02108(1 - 71 of 212)	
MG053	61407	63056	GB:L13289_5		phosphomannomutase (cpsG) {Mycoplasma pirum}		38.7868	58.0882	MG053(1 - 140 of 1650) GB:U02108(74 - 212 of 212)	
MG054	63986	63039	GB:D13303_4		transcription antitermination factor (nusG) {Bacillus subtilis}		30.8571	51.4286	MG054(688 - 44 of 948) GB:U01710(1 - 645 of 645)	

MG054	63986	63039	GB:D13303_4	transcription antitermination factor (nusG) {Bacillus subtilis}	30.8571	51.4286	MG054(948 - 719 of 948) GB:U02236(45 - 274 of 276)
MG055	64361	63993	-	-	-	-	MG055(1 - 326 of 369) GB:U02240(23 - 348 of 348)
MG058	67121	66231	GB:D26185_114	phosphoribosylpyrophosphate synthetase (prs) {Bacillus subtilis}	44.4089	63.5783	MG058(72 - 1 of 891) GB:U01693(1 - 72 of 350)
MG059	67644	67210	GB:D12501_1	small protein (smpB) {Escherichia coli}	32.5581	62.0155	MG059(435 - 247 of 435) GB:U01693(161 - 350 of 350)
MG060	67651	68541	SP:P26401	lipopolysaccharide biosynthesis protein (rfbV) {Salmonella typhimurium}	36.0656	59.8361	MG060(723 - 396 of 891) GB:U02262(1 - 328 of 328)
MG061	69908	68526	GB:M89480_4	hexosephosphate transport protein (uhpT) {Salmonella typhimurium}	30.9091	57.2727	MG061(1273 - 613 of 1383) GB:U01705(1 - 661 of 661)
MG062	70531	72570	SP:P20966	fructose-permease IIBC component (fruA) {Escherichia coli}	42.723	60.5634	MG062(439 - 761 of 2040) GB:U02138(1 - 323 of 323)
MG063	72668	73432	SP:P23539	1-phosphofructokinase (fruK) {Escherichia coli}	26.3158	51.5038	MG063(363 - 626 of 765) GB:U01777(1 - 264 of 264)
MG065	77686	79083	GB:X75422_1	heterocyst maturation protein (devA) {Anabaena sp.}	35.2941	59.7285	MG065(1398 - 1176 of 1398) GB:U02154(133 - 354 of 354)
MG066	79090	81033	SP:P27302	transketolase 1 (TK 1) (ktA) {Escherichia coli}	32.5617	54.9383	MG066(126 - 1 of 1944) GB:U02154(1 - 126 of 354)
MG068	82621	84042	-	-	-	-	MG068(1244 - 919 of 1422) GB:U02162(1 - 326 of 326)
MG069	88228	90951	SP:P20166	phosphotransferase enzyme II, ABC component (ptsG) {Bacillus subtilis}	43.1596	61.0749	MG069(1127 - 849 of 2724) GB:U02207(1 - 279 of 279)

MG071	91924	94545	SP:P37278	cation-transporting ATPase (pacL) { <i>Synechococcus</i> sp.}	34.3897	57.277	MG071(1470 - 1209 of 2622) GB:X61532(1 - 262 of 262)
MG072	94535	96952	GB:D10279_2	preprotein translocase (secA) { <i>Bacillus subtilis</i> }	43.6601	66.7974	MG072(2269 - 2418 of 2418) GB:U01743(1 - 150 of 365)
MG073	96933	98900	SP:P07025	excinuclease ABC subunit B (uvrB) { <i>Escherichia coli</i> }	47.9751	67.2897	MG073(1 - 235 of 1968) GB:U01743(131 - 365 of 365)
MG073	96933	98900	SP:P07025	excinuclease ABC subunit B (uvrB) { <i>Escherichia coli</i> }	47.9751	67.2897	MG073(1584 - 1240 of 1968) GB:U01698(1 - 345 of 345)
MG073	96933	98900	SP:P07025	excinuclease ABC subunit B (uvrB) { <i>Escherichia coli</i> }	47.9751	67.2897	MG073(305 - 694 of 1968) GB:U02119(1 - 391 of 391)
MG074	98906	99316	-	-	-	-	MG074(369 - 411 of 411) GB:U01715(1 - 43 of 576)
MG075	99383	102454	-	-	-	-	MG075(1 - 467 of 3072) GB:U01715(110 - 576 of 576)
MG075	99383	102454	-	-	-	-	MG075(1206 - 804 of 3072) GB:U02251(1 - 403 of 403)
MG075	99383	102454	-	-	-	-	MG075(1927 - 2210 of 3072) GB:U01749(1 - 284 of 284)
MG075	99383	102454	-	-	-	-	MG075(2841 - 2422 of 3072) GB:U01775(1 - 420 of 420)
MG080	106660	109203	SP:P18766	oligopeptide transport ATP-binding protein (amiF) { <i>Sireptococcus pneumoniae</i> }	46.6403	67.1937	MG080(2268 - 1934 of 2544) GB:U02129(1 - 315 of 315)
MG080	106660	109203	SP:P18766	oligopeptide transport ATP-binding protein (amiF) { <i>Sireptococcus pneumoniae</i> }	46.6403	67.1937	MG080(951 - 646 of 2544) GB:U01758(1 - 306 of 306)



MG082	109675	110352	SP:P04447	ribosomal protein L1 (rpL1) (Bacillus stearothermophilus)	48.1982	67.5676	MG082(446 - 170 of 678) GB:U02113(1 - 278 of 278)
MG083	110355	110921	GB:L32144_1	peptidyl-tRNA hydrolase homolog (pth) (Borrelia burgdorferi)	38.2166	57.3248	MG083(567 - 220 of 567) GB:U02185(26 - 373 of 373)
MG084	110917	111786	SP:P37563	hypothetical protein (SP:P37563) (Bacillus subtilis)	28.125	46.3542	MG084(30 - 1 of 870) GB:U02185(1 - 30 of 373)
MG084	110917	111786	SP:P37563	hypothetical protein (SP:P37563) (Bacillus subtilis)	28.125	46.3542	MG084(794 - 870 of 870) GB:U01783(1 - 77 of 269)
MG087	113895	114311	SP:P09901	ribosomal protein S12 (rpS12) (Bacillus stearothermophilus)	75.3731	82.0896	MG087(417 - 349 of 417) GB:U02212(326 - 394 of 394)
MG088	114331	114795	SP:P22744	ribosomal protein S7 (rpS7) (Bacillus stearothermophilus)	64.9351	81.1688	MG088(305 - 1 of 465) GB:U02212(2 - 306 of 394)
MG089	114808	116871	SP:P13551	elongation factor G (fus) (Thermus aquaticus)	59.2105	78.0702	MG089(1878 - 1540 of 2064) GB:U02180(1 - 339 of 340)
MG089	114808	116871	SP:P13551	elongation factor G (fus) (Thermus aquaticus)	59.2105	78.0702	MG089(1885 - 2064 of 2064) GB:U02136(1 - 180 of 410)
MG089	114808	116871	SP:P13551	elongation factor G (fus) (Thermus aquaticus)	59.2105	78.0702	MG089(687 - 1374 of 2064) GB:U01722(1 - 688 of 688)
MG090	116926	117549	SP:P02358	ribosomal protein S6 (rpS6) (Escherichia coli)	23.8636	44.3182	MG090(1 - 176 of 624) GB:U02136(235 - 410 of 410)
MG094	118847	120184	SP:P03005	replicative DNA helicase (dnaB) (Escherichia coli)	33.105	55.0228	MG094(1068 - 731 of 1338) GB:U01803(1 - 336 of 336)
MG094	118847	120184	SP:P03005	replicative DNA helicase (dnaB) (Escherichia coli)	33.105	55.0228	MG094(228 - 1 of 1338) GB:U02158(1 - 228 of 301)

5  
10  
15  
20  
25  
30  
35  
40  
45  
50  
55

MG095	120191	121384	-	-	uracil DNA glycosylase (ung) {Escherichia coli}	32.5688	51.8349	MG097(220 - 694 of 735) GB:U02201(1 - 475 of 475)	MG095(355 - 759 of 1194) GB:U01787(1 - 403 of 403)
MG096	121939	123519	-	-	p48 eggshell protein (p48) {Schistosoma mansoni}	23.0769	47.9853	MG098(1260 - 831 of 1431) GB:U01782(1 - 431 of 431)	MG096(1 - 309 of 1581) GB:U01713(58 - 366 of 366)
MG096	121939	123519	-	-	p48 eggshell protein (p48) {Schistosoma mansoni}	23.0769	47.9853	MG098(134 - 467 of 1431) GB:U01701(1 - 334 of 334)	MG096(361 - 531 of 1581) GB:U01762(1 - 171 of 171)
MG097	123579	124313	GB:D13169_3	-	PET112 protein (Saccharomyces cerevisiae)	30.8696	54.1304	MG100(533 - 238 of 1431) GB:U01799(1 - 296 of 296)	MG100(533 - 238 of 1431) GB:U01799(1 - 296 of 296)
MG098	124416	125846	GP:M74170_2	-	thioredoxin reductase (trxR) {Escherichia coli}	-	-	MG101(89 - 398 of 666) GB:U02103(1 - 309 of 309)	MG101(89 - 398 of 666) GB:U02103(1 - 309 of 309)
MG098	124416	125846	GP:M74170_2	-	virulence associated protein homolog (vacB) {Escherichia coli}	38.5906	59.396	MG102(45 - 367 of 945) GB:U02197(1 - 322 of 322)	MG102(45 - 367 of 945) GB:U02197(1 - 322 of 322)
MG100	127278	128708	GP:L22072_1	-	protein phosphatase 2C homolog (ptc1) {Saccharomyces cerevisiae}	-	-	MG103(623 - 256 of 840) GB:U02170(1 - 368 of 369)	MG103(623 - 256 of 840) GB:U02170(1 - 368 of 369)
MG101	128686	129351	-	-		29.2335	52.2282	MG104(215 - 491 of 2175) GB:U01795(1 - 277 of 277)	MG104(215 - 491 of 2175) GB:U01795(1 - 277 of 277)
MG102	129347	130291	GB:J03762_1	-		27.5362	52.1739	MG108(780 - 598 of 780) GB:U02111(33 - 215 of 215)	MG108(780 - 598 of 780) GB:U02111(33 - 215 of 215)
MG103	130284	131123	-	-					
MG104	131384	133538	GB:U14003_91	-					
MG108	135337	136116	SP:P35182	-					

MG109	136179	137264	PIR:S36944	protein serine/threonine kinase {Arabidopsis thaliana}	33.7398	52.0325	MG109(425 - 786 of 1086) GB:U01720(1 - 362 of 362)
MG109	136179	137264	PIR:S36944	protein serine/threonine kinase {Arabidopsis thaliana}	33.7398	52.0325	MG109(781 - 1084 of 1086) GB:U01748(1 - 303 of 303)
MG110	137380	138087	GB:U14003_76	hypothetical protein (GB:U14003_76) {Escherichia coli}	28.5714	54.1126	MG110(140 - 242 of 708) GB:X61518(1 - 102 of 102)
MG110	137380	138087	GB:U14003_76	hypothetical protein (GB:U14003_76) {Escherichia coli}	28.5714	54.1126	MG110(670 - 378 of 708) GB:U01714(1 - 293 of 293)
MG111	138105	139403	SP:P13376	phosphoglucose isomerase B (pgiB) {Bacillus stearothermophilus}	34.8235	53.6471	MG111(1 - 98 of 1299) GB:U01747(38 - 135 of 135)
MG112	139396	140022	GB:M64173_3	D-ribulose-5-phosphate 3 epimerase (cfxEc) {Alcaligenes eutrophus}	33.1361	53.8462	MG112(207 - 473 of 627) GB:U02181(1 - 267 of 267)
MG113	140039	141406	GB:M33145_1	asparaginyl-tRNA synthetase (asnS) {Escherichia coli}	41.4579	64.2369	MG113(1231 - 941 of 1368) GB:U01692(1 - 291 of 291)
MG115	142314	142550	SP:P31131	hypothetical protein (SP:P31131) {Escherichia coli}	32.6087	50	MG115(198 - 237 of 237) GB:U02127(1 - 40 of 234)
MG116	142562	143314	-	-	-	-	MG116(1 - 183 of 753) GB:U02127(52 - 234 of 234)
MG119	144972	146663	GB:M59444_2	methylgalactoside permease ATP-binding protein (mgIA) {Escherichia coli}	33.1984	57.6923	MG119(1660 - 1692 of 1692) GB:U02147(1 - 33 of 301)
MG119	144972	146663	GB:M59444_2	methylgalactoside permease ATP-binding protein (mgIA) {Escherichia coli}	33.1984	57.6923	MG119(192 - 1 of 1692) GB:U02149(1 - 192 of 681)
MG120	146673	148232	SP:P36948	ribose transport system permease protein (rbsC) {Bacillus subtilis}	27.4809	51.9084	MG120(1 - 259 of 1360) GB:U02147(43 - 301 of 301)

MG122	149198	151324	GB:L27797_2	DNA topoisomerase I (topA) (Bacillus subtilis)	38.9222	59.7305	MG122(1193 - 1443 of 2127) GB:U02134(1 - 251 of 251)
MG122	149198	151324	GB:L27797_2	DNA topoisomerase I (topA) (Bacillus subtilis)	38.9222	59.7305	MG122(1578 - 1971 of 2127) GB:U02242(1 - 394 of 394)
MG123	151305	152717	GB:M91593_1	hypothetical protein (GB:M91593_1) (Mycoplasma mycoides)	23.9837	50.4065	MG123(1413 - 1236 of 1413) GB:U01796(114 - 291 of 291)
MG124	152767	153072	GB:J03294_1	thioredoxin (trx) (Bacillus subtilis)	36.0825	65.9794	MG124(64 - 1 of 306) GB:U01796(1 - 64 of 291)
MG133	159669	158986	-	-	-	-	MG133(1 - 110 of 684) GB:U02144(237 - 345 of 345)
MG133	159669	158986	-	-	-	-	MG133(435 - 673 of 684) GB:X61537(1 - 238 of 238)
MG134	159797	160096	GB:M38777_3	hypothetical protein (GB:M38777_3) (Escherichia coli)	28.5714	57.1429	MG134(109 - 1 of 300) GB:U02144(1 - 109 of 345)
MG135	160913	160074	PIR:E22845	hypothetical protein 4 (GP:Z33006_1) (Trypanosoma brucei)	30.7692	55.9441	MG135(485 - 782 of 840) GB:U02114(1 - 298 of 298)
MG138	163590	165383	GB:K00426_1	GTP-binding membrane protein (lepA) (Escherichia coli)	47.5465	70.5584	MG138(1237 - 938 of 1794) GB:U02133(2 - 301 of 301)
MG138	163590	165383	GB:K00426_1	GTP-binding membrane protein (lepA) (Escherichia coli)	47.5465	70.5584	MG138(1318 - 1794 of 1794) GB:U01745(1 - 477 of 524)
MG138	163590	165383	GB:K00426_1	GTP-binding membrane protein (lepA) (Escherichia coli)	47.5465	70.5584	MG138(323 - 591 of 1794) GB:X61521(1 - 269 of 269)
MG140	175807	179145	-	-	-	-	MG140(1 - 41 of 3339) GB:U02110(178 - 218 of 218)

MG140	175807	179145	.	.	MG140(2727 - 2429 of 3339) GB:U01730(1 - 297 of 297)
MG140	175807	179145	.	.	MG140(3302 - 2994 of 3339) GB:U02156(1 - 308 of 308)
MG140	175807	179145	.	.	MG140(382 - 834 of 3339) GB:U01729(1 - 454 of 454)
MG140	175807	179145	.	.	MG140(834 - 616 of 3339) GB:X61512(1 - 220 of 220)
MG140	175807	179145	.	.	MG140(880 - 1182 of 3339) GB:U01742(1 - 303 of 303)
MG141	179153	180745	SP:P32727	30.8743 53.8251	MG141(223 - 871 of 1593) GB:U01778(1 - 652 of 652)
MG142	181007	182863	GB:M34836_1	46.0292 64.6677	MG142(265 - 393 of 1857) GB:U01765(1 - 129 of 129)
MG144	183216	184052	.	.	MG144(190 - 420 of 837) GB:U02121(1 - 231 of 231)
MG146	184877	186148	GB:X73141_2	26.2712 52.1186	MG146(1272 - 1174 of 1272) GB:U02223(19 - 117 of 117)
MG149	188609	189451	.	.	MG149(843 - 765 of 843) GB:U02135(182 - 260 of 260)
MG151	190372	191142	SP:P10134	42.5926 61.5741	MG151(528 - 1 of 771) GB:U02153(1 - 527 of 543)
MG168	198519	199151	GB:M57621_1	55.9748 72.327	MG168(505 - 633 of 633) GB:U01726(1 - 129 of 260)

N-utilization substance protein A homolog (nusA) {Bacillus subtilis}

protein synthesis initiation factor 2 (infB) {Bacillus subtilis}

hemolysin (llyC) {Serpulina hyodysenteriae}

ribosomal protein L3 (rpL3) {Mycoplasma capricolum}

ribosomal protein S5 (rpS5) {Bacillus stearothermophilus}

5

10

15

20

25

30

35

40

45

50

55

MG175	202762	203133	GB:M26414_3	ribosomal protein S13 (rpS13) {Bacillus subtilis}	63.3333	82.5	MG175(22 - 372 of 372) GB:U01733(1 - 351 of 600)
MG176	203136	203528	GB:X02543_2	ribosomal protein S11 (rpS11) {Escherichia coli}	47.7876	69.9115	MG176(1 - 247 of 393) GB:U01733(354 - 600 of 600)
MG180	205682	206593	GB:M61017_1	membrane transport protein (glnQ) {Bacillus stearothermophilus}	37.3832	63.0841	MG180(249 - 1 of 912) GB:U01754(1 - 248 of 265)
MG180	205682	206593	GB:M61017_1	membrane transport protein (glnQ) {Bacillus stearothermophilus}	37.3832	63.0841	MG180(912 - 784 of 912) GB:U01750(167 - 295 of 295)
MG181	206589	207848	.	.	.	.	MG181(171 - 1 of 1260) GB:U01750(1 - 171 of 295)
MG182	207844	208575	SP:P07649	pseudouridylylate synthase I (hisT) {Escherichia coli}	27.0042	45.1477	MG182(1 - 308 of 732) GB:U02176(70 - 377 of 377)
MG182	207844	208575	SP:P07649	pseudouridylylate synthase I (hisT) {Escherichia coli}	27.0042	45.1477	MG182(732 - 383 of 732) GB:U02100(31 - 380 of 380)
MG183	208568	210388	GB:Z32522_1	oligoendopeptidase F (pepF) {Lactococcus lactis}	30	50.6667	MG183(27 - 335 of 1821) GB:U02198(1 - 309 of 309)
MG183	208568	210388	GB:Z32522_1	oligoendopeptidase F (pepF) {Lactococcus lactis}	30	50.6667	MG183(38 - 1 of 1821) GB:U02100(1 - 38 of 380)
MG184	210392	211342	GB:M97479_2	methyltransferase (ssolM) {Shigella sonnei}	42.5249	67.4419	MG184(520 - 719 of 951) GB:U02115(1 - 200 of 201)
MG190	220479	221561	PIR:JS0068	29 kDa protein, MgPa operon (mgp) {Mycoplasma genitalium}	62.0833	82.0833	MG190(28 - 1083 of 1083) GB:M3143(1 - 1056 of 8760)
MG194	232007	233029	GB:Y00291_5	phenylalanyl-tRNA synthetase beta-subunit (pheS) {Escherichia coli}	35.0769	56.3077	MG194(194 - 359 of 1023) GB:U02120(1 - 166 of 166)

MG195	233036	235453	SP:P17922	phenylalanyl-tRNA synthetase beta chain (pheT) {Bacillus subtilis}	25.4597	49.0806	MG195(2044 - 2396 of 2418) GB:U02173(1 - 353 of 353)
MG200	237346	239148	GB:L36455_1	heat shock protein (dnaJ) {Coxiella burnetii}	33.5938	51.5625	MG200(842 - 1227 of 1803) GB:U02163(2 - 387 of 387)
MG203	240322	242220	GB:U25549_1	topoisomerase IV subunit B (parE) {Mycoplasma genitalium}	100	100	MG203(1216 - 1899 of 1899) GB:U25549(1 - 684 of 2124)
MG204	242223	244565	GB:U25549_2	topoisomerase IV subunit A (parC) {Mycoplasma genitalium}	99.7912	99.7912	MG204(1 - 1438 of 2343) GB:U25549(687 - 2124 of 2124)
MG204	242223	244565	GB:U25549_2	topoisomerase IV subunit A (parC) {Mycoplasma genitalium}	99.7912	99.7912	MG204(1950 - 1641 of 2343) GB:U02155(1 - 308 of 308)
MG206	246127	247422	SP:P14951	excinuclease ABC subunit C (uvrC)	28.0872	51.0896	MG206(738 - 399 of 1296) GB:U02182(1 - 341 of 341)
MG208	248492	247905	-	-	-	-	MG208(585 - 162 of 588) GB:U01785(1 - 423 of 423)
MG209	249402	248479	SP:P23851	hypothetical protein (SP:P23851) {Escherichia coli}	30.4498	55.0173	MG209(730 - 372 of 924) GB:U02214(1 - 359 of 359)
MG210	249947	249405	GB:M83994_1	prolipoprotein signal peptidase (lsp) {Staphylococcus aureus}	32.3944	52.1127	MG210(1 - 116 of 543) GB:U01759(196 - 311 of 311)
MG212	251780	252583	GB:L32861_1	1-acyl-sn-glycerol-3-phosphate acetyltransferase (plsC) {Borrelia burgdorferi}	32.1429	60.7143	MG212(7 - 315 of 804) GB:U02160(3 - 313 of 313)
MG216	255594	257117	GB:L07920_2	pyruvate kinase (pyk) {Lactococcus lactis}	35.3319	57.6017	MG216(1118 - 790 of 1524) GB:U01798(1 - 329 of 329)
MG218	259176	264590	PIR:S37536	no score generated - score shown is bogus	-1	-1	MG218(1669 - 1977 of 5415) GB:U02165(1 - 309 of 309)



MG221	266626	267087	SP:P22186	hypothetical protein (SP:P22186) {Escherichia coli}	28.8732	56.338	MG221(137 - 49 of 462) GB:U02195(1 - 290 of 290)
MG225	270404	271870	GB:U14003_71	hypothetical protein (GB:U14003_71) {Escherichia coli}	21.9565	48.0435	MG225(1467 - 1409 of 1467) GB:U02264(289 - 347 of 347)
MG226	271938	273314	GB:D26562_11	aromatic amino acid transport protein (aroP) {Escherichia coli}	24.5902	47.2131	MG226(221 - 1 of 1377) GB:U02264(1 - 221 of 347)
MG227	273789	274649	SP:P13954	thymidylate synthase (thyA) {Staphylococcus aureus}	56.5972	75.3472	MG227(577 - 861 of 861) GB:U01718(1 - 285 of 439)
MG228	274652	275131	GB:X60681_1	dihydrofolate reductase (dhfr) {Lactococcus lactis}	33.1288	59.5092	MG228(480 - 385 of 480) GB:U02137(174 - 269 of 269)
MG229	275140	276159	SP:P17424	ribonucleotide reductase 2 (nrdF) {Salmonella typhimurium}	50	70.0637	MG229(1020 - 697 of 1020) GB:U01739(22 - 344 of 344)
MG231	276646	278808	GB:X73226_1	ribonucleoside-diphosphate reductase (nrdE) {Salmonella typhimurium}	54.1193	73.1534	MG231(2122 - 2163 of 2163) GB:U02141(1 - 42 of 827)
MG237	281078	281959	.	.	.	.	MG237(647 - 882 of 882) GB:U01774(1 - 236 of 289)
MG238	281992	283323	GB:M34066_1	trigger factor (tig) {Escherichia coli}	24.6193	47.9695	MG238(420 - 648 of 1332) GB:U01772(1 - 229 of 229)
MG239	283395	285779	SP:P37945	ATP-dependent protease (lon) {Bacillus subtilis}	43.6268	65.8344	MG239(1818 - 1449 of 2385) GB:U02148(1 - 370 of 370)
MG240	286657	285782	GB:M91593_1	hypothetical protein (GB:M91593_1) {Mycoplasma mycoides}	27.8195	53.3835	MG240(876 - 598 of 876) GB:U01734(27 - 305 of 305)
MG242	288752	290641	.	.	.	.	MG242(886 - 543 of 1890) GB:U02194(1 - 344 of 344)

MG244	291332	293440	GB:M99049_1	DNA helicase II (mulB1) {Haemophilus influenzae}	36.0078	55.9687	MG244(829 - 1035 of 2109) GB:X61517(1 - 207 of 207)
MG249	297604	296114	SP:P33656	RNA polymerase sigma-A factor (sigA) {Clostridium acetobutylicum}	43.6842	66.0526	MG249(970 - 666 of 1491) GB:X61535(1 - 306 of 306)
MG250	299472	297652	GB:M10040_1	DNA primase (dnaE) {Bacillus subtilis}	27.2727	52.2078	MG250(1530 - 1821 of 1821) GB:U01771(1 - 292 of 572)
MG250	299472	297652	GB:M10040_1	DNA primase (dnaE) {Bacillus subtilis}	27.2727	52.2078	MG250(648 - 231 of 1821) GB:U02146(1 - 418 of 418)
MG254	304823	302847	GB:M24278_1	DNA ligase (lig) {Escherichia coli}	38.2263	59.3272	MG254(1429 - 1722 of 1977) GB:U02152(1 - 294 of 294)
MG254	304823	302847	GB:M24278_1	DNA ligase (lig) {Escherichia coli}	38.2263	59.3272	MG254(37 - 367 of 1977) GB:U01761(1 - 330 of 330)
MG255	304999	306093	-	-	-	-	MG255(726 - 1095 of 1095) GB:U02164(1 - 370 of 370)
MG255	304999	306093	-	-	-	-	MG255(729 - 400 of 1095) GB:U02174(1 - 333 of 333)
MG261	315699	318320	GB:M19334_4	DNA polymerase III alpha subunit (dnaE) {Escherichia coli}	31.9115	55.7662	MG261(2442 - 2159 of 2622) GB:U01738(1 - 284 of 284)
MG263	320175	321047	GB:L10328_61	hypothetical protein (GB:L10328_61) {Escherichia coli}	27.8008	47.7178	MG263(828 - 489 of 873) GB:U01764(1 - 340 of 340)
MG266	324809	322434	GB:M88581_1	leucyl-tRNA synthetase (leuS) {Bacillus stearothermophilus}	43.401	64.2132	MG266(78 - 287 of 2376) GB:U01780(1 - 210 of 210)
MG266	324809	322434	GB:M88581_1	leucyl-tRNA synthetase (leuS) {Bacillus stearothermophilus}	43.401	64.2132	MG266(957 - 622 of 2376) GB:U02167(1 - 336 of 336)

MG269	127050	326031	GB:D90354_1	surface protein antigen precursor (pag) (Streptococcus sobrinus)	25.5144	47.3251	MG269(239 - 1 of 1020) GB:U02215(1 - 239 of 366)
MG271	329826	328456	SP:P11959	dihydrolipoamide dehydrogenase (pdhD) (Bacillus stearothermophilus)	38.3592	62.306	MG271(914 - 1214 of 1371) GB:U01784(1 - 301 of 301)
MG275	334772	333339	SP:P37061	NADH oxidase (nox) (Enterococcus faecalis)	39.229	62.1315	MG275(81 - 1 of 1434) GB:U01786(4 - 84 of 280)
MG276	335397	334858	GB:M14040_1	adenine phosphoribosyltransferase (apt) (Escherichia coli)	34.3373	58.4337	MG276(540 - 430 of 540) GB:U01786(170 - 280 of 280)
MG278	338366	340525	GB:X72832_5	stringent response-like protein (rel) (Streptococcus equisimilis)	29.1339	55.1181	MG278(391 - 697 of 2160) GB:U01770(1 - 308 of 308)
MG281	343702	342035	-	-	-	-	MG281(748 - 1051 of 1668) GB:U01706(1 - 303 of 303)
MG282	344849	344367	SP:P27640	transcription elongation factor (greA) (Rickettsia prowazekii)	40.146	65.6934	MG282(483 - 356 of 483) GB:U02104(187 - 314 of 314)
MG283	345181	346629	GB:M97858_1	prolyl-tRNA synthetase (proS) (Escherichia coli)	22.6562	46.0938	MG283(839 - 1183 of 1449) GB:U02205(1 - 346 of 346)
MG285	347214	348254	-	-	-	-	MG285(315 - 493 of 1041) GB:U02266(1 - 180 of 180)
MG289	354023	355126	SP:P15363	high affinity transport system protein P37 (P37) (Mycoplasma hyorhinis)	35.7798	58.4098	MG289(105 - 1 of 1104) GB:U02132(1 - 105 of 571)
MG291	355846	357474	SP:P15362	transport system permease protein P69 (P69) (Mycoplasma hyorhinis)	27.9159	54.8757	MG291(1216 - 1629 of 1629) GB:U01768(1 - 415 of 705)
MG291	355846	357474	SP:P15362	transport system permease protein P69 (P69) (Mycoplasma hyorhinis)	27.9159	54.8757	MG291(279 - 1 of 1629) GB:U02171(1 - 279 of 346)

MG293	361384	360653	SP:P37965	glycero-phosphoryl diester phosphodiesterase (g(pQ) { <i>Bacillus subtilis</i> })	30.3965	55.9471	MG293(357 - 41 of 732) GB:U02118(1 - 317 of 317)
MG294	362801	361380	GB:L19201_18	hypothetical protein (GB:L19201_18) { <i>Escherichia coli</i> }	23.1013	46.2025	MG294(256 - 592 of 1422) GB:U02243(1 - 337 of 337)
MG297	365574	364537	GB:U00039_18	cell division protein (ftsY) { <i>Escherichia coli</i> }	36.1371	57.9439	MG297(1 - 57 of 1038) GB:U02177(215 - 271 of 271)
MG298	368529	365584	GB:M34956_1	115 kDa protein (p115) { <i>Mycoplasma hyorhinis</i> }	33.4059	57.5626	MG298(2743 - 2946 of 2946) GB:U02177(1 - 205 of 271)
MG300	370962	369715	SP:P36204	phosphoglycerate kinase (pgk) { <i>Thermotoga maritima</i> }	51.2887	70.6186	MG300(1 - 167 of 1248) GB:U02178(167 - 333 of 333)
MG300	370962	369715	SP:P36204	phosphoglycerate kinase (pgk) { <i>Thermotoga maritima</i> }	51.2887	70.6186	MG300(935 - 609 of 1248) GB:U02226(1 - 326 of 326)
MG300	370962	369715	SP:P36204	phosphoglycerate kinase (pgk) { <i>Thermotoga maritima</i> }	51.2887	70.6186	MG300(939 - 1243 of 1248) GB:U02234(1 - 305 of 305)
MG301	371962	370952	GB:X72219_1	glyceraldehyde-3-phosphate dehydrogenase (gap) { <i>Clostridium pasteurianum</i> }	56.0606	73.0303	MG301(244 - 1 of 1011) GB:U02213(1 - 244 of 364)
MG301	371962	370952	GB:X72219_1	glyceraldehyde-3-phosphate dehydrogenase (gap) { <i>Clostridium pasteurianum</i> }	56.0606	73.0303	MG301(835 - 1011 of 1011) GB:U02178(1 - 177 of 333)
MG302	372946	371996	-	-	-	-	MG302(951 - 865 of 951) GB:U02213(278 - 364 of 364)
MG305	376705	374921	GB:D30690_3	heat shock protein 70 (hsp70) { <i>Staphylococcus aureus</i> }	57.4359	75.8974	MG305(1382 - 1055 of 1785) GB:U02204(1 - 327 of 327)
MG307	381507	377977	-	-	-	-	MG307(3175 - 2042 of 3531) GB:U01767(1 - 1134 of 1134)

MG308	382724	381495	SP:P23304	ATP-dependent RNA helicase (dead) ( <i>Escherichia coli</i> )	23.0986	48.169	MG308(1 - 89 of 1230) GB:U02200(276 - 364 of 364)
MG309	386408	382734	-	-	-	-	MG309(3410 - 3675 of 3675) GB:U02200(1 - 266 of 364)
MG312	391334	387918	GB:U11381_1	cytadherence-accessory protein (hmw1) ( <i>Mycoplasma pneumoniae</i> )	39.3235	60.6765	MG312(2541 - 2160 of 3417) GB:U02261(1 - 382 of 382)
MG314	393633	392305	GP:L38997_4	hypothetical protein (GP:L38997_4) ( <i>Mycoplasma pneumoniae</i> )	51.4477	71.4922	MG314(514 - 206 of 1329) GB:U02151(1 - 309 of 309)
MG317	397423	395627	GB:M82965_1	cytadherence-accessory protein (hmw3) ( <i>Mycoplasma pneumoniae</i> )	41.1458	59.8958	MG317(1329 - 1542 of 1797) GB:U02267(1 - 214 of 214)
MG317	397423	395627	GB:M82965_1	cytadherence-accessory protein (hmw3) ( <i>Mycoplasma pneumoniae</i> )	41.1458	59.8958	MG317(509 - 169 of 1797) GB:U02224(1 - 341 of 341)
MG317	397423	395627	GB:M82965_1	cytadherence-accessory protein (hmw3) ( <i>Mycoplasma pneumoniae</i> )	41.1458	59.8958	MG317(73 - 1 of 1797) GB:U01716(1 - 73 of 325)
MG318	398280	397441	GB:J04151_1	fibrinectin-binding protein (fnbA) ( <i>Staphylococcus aureus</i> )	24.6154	43.0769	MG318(840 - 604 of 840) GB:U01716(91 - 325 of 325)
MG319	398833	398300	-	-	-	-	MG319(423 - 1 of 534) GB:U01769(1 - 426 of 541)
MG320	399797	398940	-	-	-	-	MG320(371 - 781 of 858) GB:U01700(1 - 410 of 410)
MG324	408792	407731	GB:D00398_1	aminopeptidase P (pepP) ( <i>Escherichia coli</i> )	30.531	54.4248	MG324(883 - 1062 of 1062) GB:U01717(1 - 181 of 223)
MG324	408792	407731	GB:D00398_1	aminopeptidase P (pepP) ( <i>Escherichia coli</i> )	30.531	54.4248	MG324(889 - 1062 of 1062) GB:U01755(2 - 175 of 217)

MG327	410676	409873	SP:P26174	magnesium-chelatase 30 kDa subunit (bchO) {Rhodobacter capsulatus}	26.7281	51.1521	MG327(782 - 533 of 804) GB:U022332(1 - 250 of 250)
MG328	412933	410666	GB:X62467_1	protein V (fcrV) {Streptococcus sp.}	27.5434	48.3871	MG328(339 - 53 of 2268) GB:U02188(1 - 287 of 287)
MG328	412933	410666	GB:X62467_1	protein V (fcrV) {Streptococcus sp.}	27.5434	48.3871	MG328(817 - 462 of 2268) GB:U022203(1 - 356 of 356)
MG330	414975	414325	SP:P38493	cytidylate kinase (cmk) {Bacillus subtilis}	40.3756	61.0329	MG330(537 - 226 of 651) GB:U022241(1 - 312 of 314)
MG334	419480	416970	SP:Q05873	valyl-tRNA synthetase (valS) {Bacillus subtilis}	38.5629	60.5988	MG334(1109 - 781 of 2511) GB:U022202(1 - 330 of 330)
MG334	419480	416970	SP:Q05873	valyl-tRNA synthetase (valS) {Bacillus subtilis}	38.5629	60.5988	MG334(2400 - 2511 of 2511) GB:U02249(1 - 112 of 305)
MG335	420045	419473	SP:P38424	hypothetical protein (SP:P38424) {Bacillus subtilis}	34.5238	61.3095	MG335(1 - 95 of 573) GB:U02190(200 - 294 of 294)
MG336	421467	422690	GB:U00013_6	nitrogen fixation protein (nifS) {Mycobacterium leprae}	26.2295	47.2678	MG336(990 - 719 of 1224) GB:U02256(1 - 272 of 272)
MG337	422697	423110	-	-	-	-	MG337(414 - 151 of 414) GB:U01709(35 - 297 of 297)
MG338	426915	423103	-	-	-	-	MG338(1 - 251 of 3813) GB:U02269(65 - 315 of 315)
MG338	426915	423103	-	-	-	-	MG338(1304 - 917 of 3813) GB:U02221(1 - 388 of 388)
MG338	426915	423103	-	-	-	-	MG338(3342 - 3067 of 3813) GB:U01809(1 - 276 of 276)

MG338	426915	423103	.	.	MG338(3772 - 3813 of 3813) GB:U01709(1 - 42 of 297)
MG339	428115	427096	GB:L25893_1	recombination protein (recA) (Staphylococcus aureus)	MG339(372 - 93 of 1020) GB:U01704(1 - 279 of 279)
MG340	434458	430583	SP:P00577	DNA-directed RNA polymerase beta' chain (rpoC) (Escherichia coli)	MG340(1294 - 999 of 3876) GB:X61534(1 - 295 of 295)
MG340	434458	430583	SP:P00577	DNA-directed RNA polymerase beta' chain (rpoC) (Escherichia coli)	MG340(1519 - 1289 of 3876) GB:X61528(1 - 231 of 231)
MG340	434458	430583	SP:P00577	DNA-directed RNA polymerase beta' chain (rpoC) (Escherichia coli)	MG340(3444 - 3083 of 3876) GB:U02169(1 - 361 of 361)
MG340	434458	430583	SP:P00577	DNA-directed RNA polymerase beta' chain (rpoC) (Escherichia coli)	MG340(3772 - 3876 of 3876) GB:U01766(1 - 105 of 467)
MG340	434458	430583	SP:P00577	DNA-directed RNA polymerase beta' chain (rpoC) (Escherichia coli)	MG340(426 - 66 of 3876) GB:U01797(1 - 361 of 361)
MG341	438640	434471	GB:L24376_3	RNA polymerase beta subunit (rpoB) (Bacillus subtilis)	MG341(1 - 107 of 4170) GB:U02230(217 - 323 of 323)
MG341	438640	434471	GB:L24376_3	RNA polymerase beta subunit (rpoB) (Bacillus subtilis)	MG341(1932 - 1595 of 4170) GB:U01737(1 - 338 of 338)
MG341	438640	434471	GB:L24376_3	RNA polymerase beta subunit (rpoB) (Bacillus subtilis)	MG341(2833 - 3201 of 4170) GB:U01735(1 - 369 of 369)
MG342	439236	438733	-	-	MG342(381 - 504 of 504) GB:U02230(1 - 124 of 323)
MG342	439236	438733	-	-	MG342(386 - 65 of 504) GB:U02231(1 - 322 of 322)

MG343	440355	439318	.	.	MG343(108 - 452 of 1038) GB:U01811(1 - 345 of 345)
MG344	441180	440362	GP:U17036_2	lipase-esterase (lip1) {Mycoplasma mycoides}	MG344(575 - 767 of 819) GB:U02222(1 - 193 of 193)
MG345	443878	441194	SP:P00956	isoleucyl-tRNA synthetase (ileS) {Escherichia coli}	MG345(1115 - 782 of 2685) GB:U02196(1 - 334 of 334)
MG345	443878	441194	SP:P00956	isoleucyl-tRNA synthetase (ileS) {Escherichia coli}	MG345(1811 - 2134 of 2685) GB:U02254(1 - 324 of 324)
MG348	446165	445200	.	.	MG348(166 - 459 of 966) GB:U01781(1 - 292 of 292)
MG352	450222	450719	GB:U11883_2	hypothetical protein (GB:U11883_2) {Bacillus subtilis}	MG352(366 - 498 of 498) GB:U02237(1 - 133 of 310)
MG353	451048	450722	.	.	MG353(327 - 153 of 327) GB:U02237(136 - 309 of 310)
MG357	455947	454769	GB:L17320_2	acetate kinase (ackA) {Bacillus subtilis}	MG357(342 - 131 of 1179) GB:X61531(1 - 211 of 211)
MG358	456590	457369	GB:M21298_1	Holliday junction DNA helicase (ruvA) {Escherichia coli}	MG358(350 - 87 of 780) GB:U02233(1 - 265 of 265)
MG361	459615	460100	SP:P29394	ribosomal protein L10 (rpL10) {Thermotoga maritima}	MG361(274 - 486 of 486) GB:U02206(1 - 213 of 345)
MG362	460126	460491	SP:P02394	ribosomal protein L7/L12 ('A' type) (rpL7/L12) {Bacillus subtilis}	MG362(1 - 107 of 366) GB:U02206(239 - 345 of 345)
MG365	461682	462614	GB:X63666_2	methionyl-tRNA formyltransferase (fmt) {Escherichia coli}	MG365(292 - 1 of 933) GB:U02238(1 - 292 of 349)



MG368	466410	463427	GB:M96793_1	fatty acid/phospholipid synthesis protein (plsX) {Escherichia coli}	28.972	52.3364	MG368(227 - 1 of 984) GB:U01791(1 - 227 of 326)
MG369	468083	466413	-	-	-	-	MG369(1146 - 1446 of 1671) GB:U01763(1 - 300 of 300)
MG370	469123	468155	SP:P23851	hypothetical protein (SP:P23851) {Escherichia coli}	26.9531	48.8281	MG370(240 - 599 of 969) GB:U02220(1 - 360 of 360)
MG371	470084	469113	GB:D26185_10	hypothetical protein (GB:D26185_10) {Bacillus subtilis}	25.8065	47.0046	MG371(349 - 689 of 972) GB:U02263(1 - 341 of 341)
MG374	472891	472070	-	-	-	-	MG374(1 - 178 of 822) GB:U02250(159 - 337 of 337)
MG375	474578	472887	GB:M36594_1	threonyl-tRNA synthetase (thrSv) {Bacillus subtilis}	38.7097	60.7527	MG375(1048 - 1389 of 1692) GB:U02130(1 - 342 of 342)
MG375	474578	472887	GB:M36594_1	threonyl-tRNA synthetase (thrSv) {Bacillus subtilis}	38.7097	60.7527	MG375(1530 - 1692 of 1692) GB:U02250(1 - 163 of 337)
MG378	477139	475529	SP:P35868	arginyl-tRNA synthetase (argS) {Corynebacterium glutamicum}	33.6406	56.9124	MG378(1364 - 1047 of 1611) GB:U01740(1 - 319 of 319)
MG378	477139	475529	SP:P35868	arginyl-tRNA synthetase (argS) {Corynebacterium glutamicum}	33.6406	56.9124	MG378(765 - 456 of 1611) GB:U02168(1 - 309 of 309)
MG379	477168	479003	GB:L10328_106	glucose inhibited division protein (gidA) {Escherichia coli}	40.7346	61.9366	MG379(900 - 1184 of 1836) GB:U01812(1 - 285 of 285)
MG385	484699	483992	-	-	-	-	MG385(234 - 6 of 708) GB:U02112(1 - 229 of 229)
MG385	484699	483992	-	-	-	-	MG385(523 - 708 of 708) GB:U02239(1 - 186 of 320)

MG385	484699	483992	-	.					MG385(528 - 259 of 708) GB:U02246(1 - 270 of 270)
MG386	489552	484705	GB:U11381_1	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}					31.1755 49.4037 MG386(1294 - 1628 of 4848) GB:U02175(1 - 335 of 335)
MG386	489552	484705	GB:U11381_1	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}					31.1755 49.4037 MG386(2274 - 1991 of 4848) GB:X61519(1 - 283 of 284)
MG386	489552	484705	GB:U11381_1	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}					31.1755 49.4037 MG386(3247 - 3420 of 4848) GB:U02126(1 - 174 of 174)
MG386	489552	484705	GB:U11381_1	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}					31.1755 49.4037 MG386(3842 - 4196 of 4848) GB:U02192(1 - 355 of 355)
MG386	489552	484705	GB:U11381_1	cytadherence-accessory protein (hmw1) {Mycoplasma pneumoniae}					31.1755 49.4037 MG386(767 - 1281 of 4848) GB:U02245(2 - 515 of 515)
MG388	491004	490702	GB:U00016_19	hypothetical protein (GB:U00016_19) {Mycobacterium leprae}					30.9278 56.701 MG388(285 - 1 of 303) GB:U02265(1 - 285 of 339)
MG389	491530	491150	-	-					- MG389(320 - 129 of 381) GB:U01813(1 - 192 of 192)
MG390	493516	491537	SP:P37608	lactococcin transport ATP-binding protein (lcnDR3) {Lactococcus lactis}					22.3421 46.5331 MG390(1393 - 1744 of 1980) GB:U02218(1 - 350 of 350)
MG390	493516	491537	SP:P37608	lactococcin transport ATP-binding protein (lcnDR3) {Lactococcus lactis}					22.3421 46.5331 MG390(1400 - 1174 of 1980) GB:U02248(1 - 227 of 227)
MG391	494967	493627	GB:D17450_1	aminopeptidase {Mycoplasma salivarium}					41.2921 60.3933 MG391(1 - 217 of 1341) GB:U02268(256 - 472 of 472)
MG391	494967	493627	GB:D17450_1	aminopeptidase {Mycoplasma salivarium}					41.2921 60.3933 MG391(412 - 735 of 1341) GB:U01801(1 - 324 of 324)

MG391	494967	493627	GB:D17450_1	aminopeptidase (Mycoplasma salivarium)		41.2921	60.3933	MG391(412 - 735 of 1341) GB:U01802(1 - 324 of 324)
MG392	496615	494987	GB:L10132_2	heat shock protein (groEL) (Bacillus stearothermophilus)		51.5209	71.4829	MG392(1394 - 1629 of 1629) GB:U02268(1 - 236 of 472)
MG392	496615	494987	GB:L10132_2	heat shock protein (groEL) (Bacillus stearothermophilus)		51.5209	71.4829	MG392(181 - 1 of 1629) GB:U02252(1 - 181 of 296)
MG393	496960	496631	GB:D17398_1	heat shock protein 60-like protein (PgGroES) (Porphyromonas gingivalis)		39.5604	54.9451	MG393(330 - 231 of 330) GB:U02252(197 - 296 of 296)
MG394	498306	497089	SP:P06192	serine hydroxymethyltransferase (glyA) (Salmonella typhimurium)		55.303	70.7071	MG394(328 - 683 of 1218) GB:U02131(1 - 356 of 356)
MG395	499890	498319	-	-		-	-	MG395(457 - 116 of 1572) GB:U02260(1 - 342 of 342)
MG395	499890	498319	-	-		-	-	MG395(763 - 979 of 1572) GB:X61530(1 - 217 of 217)
MG399	503976	502831	SP:P33253	ATP synthase beta chain (atpD) (Mycoplasma gallisepticum)		80.9524	89.418	MG399(447 - 852 of 1146) GB:U01752(1 - 406 of 406)
MG400	503099	504263	SP:P33257	ATP synthase gamma chain (atpG) (Mycoplasma gallisepticum)		37.9433	62.0567	MG400(160 - 711 of 837) GB:U01703(1 - 552 of 552)
MG401	506655	505102	SP:P33252	ATP synthase alpha chain (atpA) (Mycoplasma gallisepticum)		63.3911	79.5761	MG401(973 - 1554 of 1554) GB:U01727(1 - 583 of 598)
MG405	509012	508137	GB:X64256_2	adenosinetriphosphatase (atpB) (Mycoplasma gallisepticum)		36.4261	63.9175	MG405(75 - 1 of 876) GB:U01728(1 - 75 of 299)
MG406	509319	508981	SP:P15362	transport system permease protein P69 (P69) (Mycoplasma hyorhinis)		40	57.1429	MG406(339 - 84 of 339) GB:U01728(44 - 299 of 299)

MG410	513042	512056	GB:L10328_89	peripheral membrane protein B (pstB) (Escherichia coli)	50.813	70.3252	MG410(301 - 941 of 987) GB:U01707(1 - 640 of 640)
MG411	514991	513030	GB:X75297_1	periplasmic phosphate permease homolog (AG88) (Mycobacterium tuberculosis)	30.7692	56.2753	MG411(406 - 632 of 1962) GB:U01746(1 - 227 of 229)
MG412	516124	514994	-	-	-	-	MG412(252 - 1 of 1131) GB:U01702(1 - 252 of 313)
MG412	516124	514994	-	-	-	-	MG412(675 - 563 of 1131) GB:U02101(1 - 113 of 113)
MG413	518389	516248	GB:L22432_4	hypothetical protein (GB:L22432_4) (Mycoplasma capricolum)	25	54.1667	MG413(1179 - 701 of 2142) GB:U01699(1 - 480 of 480)
MG413	518389	516248	GB:L22432_4	hypothetical protein (GB:L22432_4) (Mycoplasma capricolum)	25	54.1667	MG413(1535 - 1230 of 2142) GB:U01804(1 - 305 of 305)
MG414	519355	516248	-	-	-	-	MG414(438 - 154 of 917) GB:U01695(1 - 285 of 285)
MG416	521414	520371	-	-	-	-	MG416(1 - 39 of 1044) GB:U01744(580 - 618 of 620)
MG416	521414	520371	-	-	-	-	MG416(7 - 351 of 1044) GB:U02102(1 - 345 of 345)
MG418	522314	521877	SP:P02410	ribosomal protein L13 (rpL13) (Escherichia coli)	41.3043	70.2899	MG418(321 - 438 of 438) GB:U01744(1 - 118 of 620)
MG421	526696	524153	SP:P07671	exonuclease ABC subunit A (uvrA) (Escherichia coli)	47.7541	68.5579	MG421(1693 - 1393 of 2544) GB:X61514(1 - 301 of 301)
MG422	529493	526989	-	-	-	-	MG422(2274 - 2101 of 2505) GB:U02117(1 - 174 of 174)

5

10

15

20

25

30

35

40

45

50

55

MG422	529493	526989	-	-	MG422(2439 - 2505 of 2505) GB:U02172(1 - 67 of 318)
MG422	529493	526989	-	-	MG422(35 - 1 of 2505) GB:U02228(1 - 35 of 304)
MG423	531216	529534	-	-	MG423(1434 - 1197 of 1683) GB:X61510(1 - 238 of 238)
MG423	531216	529534	-	-	MG423(161 - 413 of 1683) GB:X61524(1 - 252 of 255)
MG423	531216	529534	-	-	MG423(1683 - 1455 of 1683) GB:U02228(76 - 304 of 304)
MG425	531668	533014	SP:P23304	32.4121 58.0402	MG425(989 - 769 of 1347) GB:U01805(1 - 220 of 220)
MG431	538290	537559	GB:L27492_1	39.7541 61.8852	MG431(463 - 732 of 732) GB:U02109(1 - 270 of 277)
MG437	542067	542981	GB:M11330_1	38.0165 55.3719	MG437(679 - 378 of 915) GB:U02189(2 - 303 of 303)
MG441	546707	546300	-	-	MG441(20 - 318 of 408) GB:U02128(1 - 299 of 299)
MG447	552444	550804	GB:L08897_1	34.058 55.0725	MG447(319 - 645 of 1641) GB:U01788(1 - 327 of 327)
MG451	555612	554431	SP:P13927	100 100	MG451(927 - 586 of 1182) GB:U02255(1 - 342 of 342)
MG453	556435	557310	GB:L12272_1	48.0287 65.233	MG453(491 - 181 of 876) GB:U02258(1 - 311 of 311)

ATP-dependent RNA helicase (deaD) (Escherichia coli)

triosephosphate isomerase (tim) (Thermotoga maritima)

CDP-diglyceride synthetase (cdsA) (Escherichia coli)

hypothetical protein (GB:L08897\_1) (Mycoplasma gallisepticum)

elongation factor TU (tuf) (Mycoplasma genitalium)

UDP-glucose pyrophosphorylase (gluB) (Bacillus subtilis)

MG455	557724	558944	GB:M77668_1	tyrosyl tRNA synthetase (tyrS) (Bacillus stearothermophilus)	38.539	61.7128	MG455(604 - 362 of 1221) GB:U02247(5 - 247 of 247)
MG456	559941	558940	-	-	-	-	MG456(256 - 568 of 1002) GB:U01790(1 - 312 of 312)
MG458	563307	562783	SP:Q02522	hypoxanthine-guanine phosphoribosyltransferase (hpt) (Lactococcus lactis)	38.3721	66.8605	MG458(295 - 24 of 525) GB:U02193(1 - 272 of 272)
MG459	563818	563312	GB:M64978_2	surface exclusion protein (prgA) (Plasmid pCF10) (Enterococcus faecalis)	28.3582	49.2537	MG459(330 - 1 of 507) GB:U01725(1 - 330 of 638)
MG460	563991	564926	SP:P33572	L-lactate dehydrogenase (ldh) (Mycoplasma hyopneumoniae)	50.3226	67.7419	MG460(1 - 136 of 936) GB:U01725(503 - 638 of 638)
MG462	567638	566187	GB:M55072_1	glutamyl-tRNA synthetase (gluX) (Bacillus stearothermophilus)	42.887	65.272	MG462(1452 - 1081 of 1452) GB:U02122(9 - 379 of 379)
MG463	568404	567628	GB:D26185_105	high level kasamycin resistance (ksgA) (Bacillus subtilis)	35.6164	53.8813	MG463(777 - 409 of 777) GB:U01719(36 - 405 of 405)
MG467	570988	570056	GB:X75422_1	heterocyst maturation protein (devA) (Anabaena sp.)	39.899	63.1313	MG467(40 - 352 of 933) GB:U01741(1 - 313 of 313)
MG469	578578	577268	SP:P34028	chromosomal replication initiator protein (dnaA) (Spiroplasma citri)	30.9469	57.2748	MG469(845 - 547 of 1311) GB:U02259(1 - 299 of 299)
MG469	578578	577268	SP:P34028	chromosomal replication initiator protein (dnaA) (Spiroplasma citri)	30.9469	57.2748	MG469(855 - 1206 of 1311) GB:U02145(1 - 352 of 352)

Table 1(d)

5

UID Old\_id(s)

MG001 MORF-20072

MG002 MORF-19817

10

MG003 MORF-19818 MORF-20073

MG004 MORF-19819 MORF-20074

MG005 MORF-20075

15

MG006 MORF-20076

MG007 MORF-19820

MG008 MORF-20077

MG009 MORF-20078

20

MG010 MORF-20079

MG011 MORF-19821 MORF-19822

MG012 MORF-20080

25

MG013 MORF-19823 MORF-20080 MORF-20081

MG014 MORF-20082

MG015 MORF-20084

MG016 MORF-19824

30

MG017 MORF-19825

MG018 MORF-20085

MG019 MORF-20086

35

MG020 MORF-20088

MG021 MORF-20089

MG022 MORF-20091

MG023 MORF-20092

40

MG024 MORF-19826 MORF-20093

MG025 MORF-20094

MG026 MORF-20095

45

MG027 MORF-19827

MG028 MORF-19828

MG029 MORF-19829

MG030 MORF-20096

50

MG031 MORF-19830 MORF-20097

MG032 MORF-20099

55

EP 0 756 006 A2

MG033 MORF-20100  
MG034 MORF-20101  
MG035 MORF-20102  
MG036 MORF-20103  
MG037 MORF-20104  
MG038 MORF-20105  
MG039 MORF-19831 MORF-20106  
MG040 MORF-20107  
MG042 MORF-19832 MORF-20108  
MG043 MORF-20110  
MG044 MORF-20111  
MG045 MORF-19833  
MG046 MORF-20112  
MG047 MORF-20113  
MG048 MORF-19834 MORF-20114 MORF-20115  
MG049 MORF-20114 MORF-20115  
MG050 MORF-20117  
MG051 MORF-19835 MORF-20118  
MG052 MORF-20119  
MG053 MORF-20120  
MG054 MORF-20120 MORF-20121  
MG055 MORF-19836  
MG056 MORF-20122  
MG057 MORF-20123  
MG058 MORF-20124  
MG059 MORF-20124 MORF-20125  
MG060 MORF-20126  
MG061 MORF-19838  
MG062 MORF-19839 MORF-20127 MORF-20128  
MG063 MORF-19840 MORF-20128  
MG064 MORF-19841 MORF-19842  
MG065 MORF-19843 MORF-20129  
MG066 MORF-19844 MORF-20130  
MG067 MORF-19845  
MG068 MORF-20131  
MG069 MORF-19847 MORF-20135



5 MG070 MORF-20136  
MG071 MORF-19848 MORF-19849 MORF-19850  
MORF-19851 MORF-20137  
MG072 MORF-19852 MORF-19853 MORF-19854  
MORF-20138  
10 MG073 MORF-20139  
MG074 MORF-19855  
MG075 MORF-19856 MORF-19857  
MG076 MORF-19858  
15 MG077 MORF-20140  
MG078 MORF-19859 MORF-20141  
MG079 MORF-20142  
20 MG080 MORF-20143  
MG081 MORF-20144  
MG082 MORF-20145  
MG083 MORF-20146  
25 MG084 MORF-20147  
MG085 MORF-20147 MORF-20148  
MG086 MORF-19860 MORF-19861  
30 MG087 MORF-20149  
MG088 MORF-20150  
MG089 MORF-20151 MORF-20152  
MG090 MORF-19862  
35 MG091 MORF-20153  
MG092 MORF-20154  
MG093 MORF-20155  
40 MG094 MORF-20156  
MG095 MORF-19863  
MG096 MORF-20157  
MG097 MORF-20158  
45 MG098 MORF-20159  
MG099 MORF-19864 MORF-20160  
MG100 MORF-19865 MORF-20161  
50 MG101 MORF-19866  
MG102 MORF-20162  
MG103 MORF-19867 MORF-19868

EP 0 756 006 A2

MG104 MORF-20163  
MG105 MORF-19869  
MG106 MORF-20164 MORF-20165  
MG107 MORF-20164 MORF-20165  
MG108 MORF-20166  
MG109 MORF-20167  
MG110 MORF-20168  
MG111 MORF-20169  
MG112 MORF-20170  
MG113 MORF-19870 MORF-20171 MORF-20172  
MG114 MORF-20171 MORF-20172  
MG116 MORF-19871  
MG117 MORF-19872  
MG118 MORF-20173  
MG119 MORF-19873 MORF-20174  
MG120 MORF-19874  
MG121 MORF-19875 MORF-20175  
MG122 MORF-20176  
MG123 MORF-19876  
MG124 MORF-20177  
MG125 MORF-19877  
MG126 MORF-20178  
MG127 MORF-20179  
MG128 MORF-20180  
MG129 MORF-20181  
MG130 MORF-20182  
MG132 MORF-20183  
MG133 MORF-19878  
MG134 MORF-20184  
MG135 MORF-20185  
MG136 MORF-20186 MORF-20187  
MG137 MORF-20186 MORF-20187  
MG138 MORF-20188  
MG139 MORF-19879  
MG140 MORF-19884  
MG141 MORF-19885 MORF-20192

5

10

15

20

25

30

35

40

45

50

55

# EP 0 756 006 A2

	MG142 MORF-19886 MORF-20193
	MG143 MORF-20194
5	MG144 MORF-19887
	MG145 MORF-20195
	MG146 MORF-20196
10	MG147 MORF-19888 MORF-19889
	MG148 MORF-19890
	MG149 MORF-19891
	MG150 MORF-19893 MORF-20197
15	MG151 MORF-19893 MORF-20198
	MG152 MORF-19895 MORF-20199
	MG153 MORF-19894
20	MG154 MORF-19896 MORF-20200
	MG156 MORF-19897
	MG157 MORF-20201
	MG158 MORF-20202
25	MG159 MORF-19898
	MG161 MORF-19900 MORF-20203
	MG162 MORF-19899 MORF-19900
	MG163 MORF-20204
30	MG165 MORF-20205
	MG166 MORF-19901 MORF-20206
	MG167 MORF-19901 MORF-20207
35	MG168 MORF-19902 MORF-20208
	MG169 MORF-20209
	MG170 MORF-20210
	MG171 MORF-20211
40	MG172 MORF-20212
	MG175 MORF-20213
	MG176 MORF-20214
45	MG177 MORF-19903 MORF-20215
	MG178 MORF-20216
	MG179 MORF-19904 MORF-20217
	MG180 MORF-20218
50	MG181 MORF-19905
	MG182 MORF-20219

EP 0 756 006 A2

MG183 MORF-20219  
MG184 MORF-20220  
MG185 MORF-20221  
MG186 MORF-19907  
MG187 MORF-19908 MORF-19909 MORF-20225  
MG188 MORF-20226 MORF-20227  
MG189 MORF-20226 MORF-20227  
MG190 MORF-20228  
MG191 MORF-19910 MORF-19911 MORF-20229  
MG192 MORF-19911 MORF-19912 MORF-20230  
MG194 MORF-19913 MORF-20234  
MG195 MORF-20235  
MG196 MORF-20236  
MG199 MORF-19914  
MG200 MORF-19915 MORF-20237  
MG201 MORF-19916 MORF-20239  
MG202 MORF-19917  
MG203 MORF-19918 MORF-19919 MORF-20240  
MG204 MORF-20241 MORF-20242  
MG205 MORF-20243  
MG206 MORF-20244  
MG207 MORF-19920  
MG208 MORF-19921  
MG209 MORF-20245  
MG210 MORF-20246  
MG211 MORF-19922  
MG212 MORF-19924 MORF-20247 MORF-20248  
MG213 MORF-20248  
MG214 MORF-20249  
MG215 MORF-20250  
MG216 MORF-20251  
MG217 MORF-20252  
MG218 MORF-19926 MORF-19927 MORF-20253  
MG219 MORF-19928 MORF-19930 MORF-20253  
MG220 MORF-19931  
MG221 MORF-20255

	MG222 MORF-20256
	MG223 MORF-19932
5	MG224 MORF-20257
	MG225 MORF-20258
	MG226 MORF-20259
10	MG227 MORF-20260
	MG228 MORF-19933
	MG229 MORF-19934 MORF-20261
	MG230 MORF-19935
15	MG231 MORF-20262
	MG232 MORF-20263
	MG234 MORF-20264
20	MG235 MORF-19936 MORF-20265
	MG236 MORF-19937
	MG237 MORF-19938
	MG238 MORF-19939 MORF-20266
25	MG239 MORF-20267
	MG240 MORF-20268
	MG241 MORF-19940 MORF-19941 MORF-19942
30	MG242 MORF-19943
	MG243 MORF-19945
	MG244 MORF-20269
	MG245 MORF-19946
35	MG246 MORF-19947
	MG247 MORF-20270
	MG248 MORF-19948
40	MG249 MORF-19949 MORF-20271
	MG250 MORF-20272
	MG251 MORF-19950 MORF-20273
	MG252 MORF-20274
45	MG253 MORF-20275
	MG254 MORF-20276
	MG255 MORF-19951 MORF-19952
	MG256 MORF-19953
50	MG258 MORF-19954 MORF-20277
	MG259 MORF-20278

EP 0 756 006 A2

MG260 MORF-19955 MORF-19956 MORF-20279

MG261 MORF-19958 MORF-20282

MG262 MORF-20283

MG263 MORF-20285

MG264 MORF-20286 MORF-20287

MG265 MORF-20286 MORF-20287

MG266 MORF-20288

MG267 MORF-19959 MORF-19960

MG268 MORF-20290

MG269 MORF-20291

MG270 MORF-20292

MG271 MORF-20293

MG272 MORF-19961 MORF-19962 MORF-20294

MG273 MORF-20295

MG274 MORF-20296

MG275 MORF-20297

MG276 MORF-20298

MG277 MORF-19963 MORF-20299

MG278 MORF-19964 MORF-20300

MG279 MORF-19965

MG280 MORF-19966 MORF-20301

MG281 MORF-19967 MORF-19968

MG282 MORF-20302

MG283 MORF-20303

MG284 MORF-19969 MORF-19970 MORF-19971

MG285 MORF-19969 MORF-19970 MORF-19971

MG286 MORF-19972

MG288 MORF-20306

MG289 MORF-20307

MG290 MORF-20308

MG291 MORF-20309

MG292 MORF-20310

MG293 MORF-20311

MG294 MORF-19974 MORF-20312

MG295 MORF-20313

MG296 MORF-19975

	MG297 MORF-20314
	MG298 MORF-19976 MORF-20315
5	MG299 MORF-20316
	MG300 MORF-20317
	MG301 MORF-19977 MORF-20318
10	MG302 MORF-19978
	MG303 MORF-20319
	MG304 MORF-20320
	MG305 MORF-19979 MORF-20321
15	MG306 MORF-19980
	MG307 MORF-19981 MORF-19982
	MG308 MORF-20323
20	MG309 MORF-19983 MORF-19984
	MG310 MORF-20324
	MG311 MORF-20325
	MG312 MORF-20326
25	MG314 MORF-19985 MORF-19986
	MG315 MORF-19987 MORF-19988 MORF-20327
	MG316 MORF-19988 MORF-20327
30	MG317 MORF-20328 MORF-20329
	MG318 MORF-19989 MORF-19990
	MG319 MORF-20330
	MG320 MORF-19991
35	MG321 MORF-19992
	MG322 MORF-19993 MORF-20331
	MG323 MORF-19994 MORF-20332
40	MG324 MORF-19995 MORF-20333
	MG326 MORF-20334
	MG327 MORF-20335
	MG328 MORF-19996 MORF-20336
45	MG329 MORF-19997 MORF-20337
	MG330 MORF-20338 MORF-20339
	MG331 MORF-20339
50	MG332 MORF-20340
	MG333 MORF-19998
	MG334 MORF-20341

EP 0 756 006 A2

MG336 MORF-20343 MORF-20344  
MG337 MORF-19999  
MG338 MORF-20000  
MG339 MORF-20001 MORF-20345  
MG340 MORF-20006 MORF-20348  
MG341 MORF-20349  
MG342 MORF-20350  
MG343 MORF-20007  
MG344 MORF-20008  
MG345 MORF-20351  
MG346 MORF-20352  
MG348 MORF-20009  
MG349 MORF-20010  
MG350 MORF-20011  
MG351 MORF-20353  
MG352 MORF-20354  
MG353 MORF-20355  
MG354 MORF-20013 MORF-20014  
MG355 MORF-20015 MORF-20016 MORF-20356  
MG356 MORF-20357  
MG357 MORF-20358  
MG358 MORF-20017 MORF-20018 MORF-20019  
MORF-20359  
MG359 MORF-20019 MORF-20359 MORF-20360  
MG360 MORF-20361  
MG361 MORF-20362  
MG362 MORF-20363  
MG364 MORF-20364  
MG365 MORF-20020 MORF-20365  
MG366 MORF-20021  
MG367 MORF-20366  
MG368 MORF-20022 MORF-20366 MORF-20367  
MG369 MORF-20022 MORF-20023  
MG370 MORF-20368  
MG371 MORF-20368 MORF-20369  
MG372 MORF-20370



	MG373 MORF-20024
	MG374 MORF-20025
5	MG375 MORF-20371
	MG376 MORF-20026
	MG377 MORF-20027
10	MG378 MORF-20372
	MG379 MORF-20373
	MG380 MORF-20374
	MG381 MORF-20028
15	MG382 MORF-20375
	MG383 MORF-20376
	MG384 MORF-20029 MORF-20377
20	MG385 MORF-20031 MORF-20378
	MG386 MORF-20032 MORF-20379 MORF-20381
	MG387 MORF-20382
	MG388 MORF-20383
25	MG389 MORF-20033
	MG390 MORF-20034 MORF-20384
	MG391 MORF-20034 MORF-20035 MORF-20385
30	MG392 MORF-20036 MORF-20037 MORF-20386
	MG393 MORF-20038
	MG394 MORF-20387
	MG395 MORF-20039
35	MG396 MORF-20388
	MG397 MORF-20040 MORF-20041
	MG398 MORF-20042
40	MG399 MORF-20389
	MG400 MORF-20390
	MG401 MORF-20043 MORF-20391
	MG402 MORF-20392
45	MG403 MORF-20393
	MG404 MORF-20394
	MG405 MORF-20395 MORF-20396
50	MG406 MORF-20395 MORF-20396
	MG407 MORF-20044 MORF-20397
	MG408 MORF-20398

EP 0 756 006 A2

5 MG409 MORF-20045  
MG410 MORF-20046 MORF-20399  
MG411 MORF-20400  
MG412 MORF-20047  
MG413 MORF-20401  
10 MG414 MORF-20048  
MG415 MORF-20049  
MG416 MORF-20050 MORF-20051  
MG417 MORF-20402  
15 MG418 MORF-20052  
MG419 MORF-20053  
MG420 MORF-20403  
MG421 MORF-20404  
20 MG422 MORF-20054 MORF-20055  
MG423 MORF-20056  
MG425 MORF-20406  
25 MG427 MORF-20057  
MG428 MORF-20058  
MG429 MORF-20059 MORF-20407  
MG430 MORF-20408  
30 MG431 MORF-20409  
MG432 MORF-20410  
MG433 MORF-20411  
35 MG435 MORF-20060 MORF-20412  
MG436 MORF-20060 MORF-20412  
MG437 MORF-20413  
MG438 MORF-20414  
40 MG439 MORF-20061  
MG440 MORF-20062  
MG441 MORF-20063  
45 MG442 MORF-20415  
MG443 MORF-20064  
MG444 MORF-20065 MORF-20416  
MG445 MORF-20417  
50 MG447 MORF-20418  
MG448 MORF-20419 MORF-20420

EP 0 756 006 A2

MG449 MORF-20419 MORF-20420

MG450 MORF-20066

5

MG451 MORF-20421

MG452 MORF-20067

MG453 MORF-20422

10

MG454 MORF-20423 MORF-20424

MG455 MORF-20423 MORF-20424

MG456 MORF-20068

MG457 MORF-20069 MORF-20425

15

MG458 MORF-20426

MG459 MORF-20070

MG460 MORF-20427

20

MG461 MORF-20428

MG462 MORF-20429

MG463 MORF-20430

MG464 MORF-20431

25

MG467 MORF-20432

MG468 MORF-20283

MG469 MORF-20434

30

MG470 MORF-20071 MORF-20435

35

40

45

50

55

Table 2

	UID	end5	end3	gene_len
5	MG016	19253	19756	504
	MG017	19825	20352	528
	MG027	30092	30544	453
10	MG028	30547	31149	603
	MG064	74066	77683	3618
	MG076	102870	102457	414
	MG105	133569	134168	600
	MG117	143310	143951	642
15	MG147	186138	187262	1125
	MG185	211445	213547	2103
	MG186	216017	216766	750
	MG199	237094	236594	501
20	MG202	239826	240191	366
	MG207	247523	247906	384
	MG211	250997	251437	441
	MG223	268011	269243	1233
25	MG230	276166	276624	459
	MG236	280663	281082	420
	MG241	286884	288743	1860
	MG243	290976	291323	348
	MG246	293936	294778	843
30	MG256	306819	307586	768
	MG267	325157	324813	345
	MG279	341181	340528	654
	MG284	346853	347248	396
35	MG286	348260	348847	588
	MG296	364414	364028	387
	MG306	377974	376796	1179
	MG321	402922	400121	2802
	MG331	415622	414987	636
40	MG333	416716	416339	378
	MG349	446576	447787	1212
	MG350	447790	448722	933
	MG354	451197	451607	411
45	MG366	462619	464619	2001
	MG372	471234	470080	1155
	MG373	472066	471224	843
	MG376	474892	474581	312
	MG377	475479	474901	579
50	MG381	479570	480223	654
	MG397	502420	500723	1698

	MG415	520238	519929	310
	MG419	523215	522355	861
5	MG427	533270	533692	423
	MG428	533806	534318	513
	MG436	542092	541739	354
	MG439	545378	544563	816
10	MG440	546154	545381	774
	MG449	553295	552864	432
	MG450	554269	553559	711
	MG452	555665	556447	783
15	MG468	318330	319202	873

20

*The Nucleotide Sequence of the Mycoplasma genitalium Genome*

25

1 TAAGTTATTATTTAGTTAATACTTTTAACAATATTATTAAGGTATTTAAA

51 AAATACTATTATAGTATTTAACATAGTTAAATACCTTCCTTAATACTGTT

101 AAATTATATTCAATCAATACATATATAATATTATTTAAAATACTTGATAAG

151 TATTATTTAGATATTAGACAAATACTAATTTTATATTGCTTTAATACTTA

30

201 ATAAATACTACTTATGTATTAAGTAAATATTACTGTAATACTAATAACAA

251 TATTATTACAATATGCTAGATAATATTGCTAGTATCAATAATTACTAAT

301 ATAGTATTAGGAAAATACCATAATAATATTTCTACATAATACTAAGTTAA

35

351 TACTATGTGTAGaATAATAAAATAATCAGATTAAAAAAATTTTATTTATCT

401 GAAACATATTTAATCAATTGAACTGATTATTTTCAGCAGTAATAATTACA

451 TATGTACATAGTACATATGTAAAATATCATTAATTTCTGTTATATATAAT

40

501 AGTATCTATTTTAGAGAGTATTAATTATTACTATAATTAAGCATTTATGC

551 TTAATTATAAGCTTTTTATGAACAAAATTATAGACATTTTAGTTCCTTATA

601 ATAAATAATAGATATTTAAAGAAAATAAAAAAATAGAAATAAATATCATAA

651 CCCTTGATAACCCAGAAATTAATACTTAATCAAAAATGAAAATATTAATT

45

701 AATAAAAGTGAATTGAATAAAATTTGGGAAAAAATGAATAACGTTATTA

751 TTCCAATAACAAAATAAAACCACATCATTCATATTTTTTAATAGAGgCA

801 AAAGaAAAAGAAATAAACTTTTATGCTAACAATGAATACTTTTCTGTCAA

50

851 ATGTAATTTAAATaAAAAATTTGATATTTCTGAACAAGGCTCCTTAATTG

901 TTAAAGGAAAAATTTTTAACGATCTTATTAATGGCATAAAAGAAGAGATT

951 ATTACTATTCAAGAAAAAGATCAAACACTTTTGGTAAAAACaAAAAAAAC

55

1001 AAGTATTAATTTAAACACAATTAATGTGAATGAATTTCCAAGAATAAGGT

1051 TTAATGAAAAAACGATTTAAGTGAATTTAATCAATTCAAAATAAATTAT

1101 TCACTTTTAGTAAAAGGCATTAAAAAATTTTCACTCAGTTTCAAATAA  
1151 TCGTGAAATATCTTCTAAATTTAATGGAGTAAATTTCAATGGATCCAATG  
1201 GAAAAGAAATATTTTTAGAAAGCTTCTGACACTTATAAACTATCTGTTTTT  
1251 GAGATAAAGCAAGAAACAGAACCATTGATTTCATTTTGGAGAGTAATTT  
1301 ACTTAGTTTCATTAATTCCTTTAATCCTGAAGAAGATAAATCTATTGTTT  
1351 TTTATTACAGAAAAGATAATAAAGATAGCTTTAGTACAGAAATGTTGATT  
1401 TCAATGGATAACTTTATGATTAGTTACACATCGGTTAATGAAAAATTTCC  
1451 AGAGGTAACTACTTTTTTGAATTTGAACCTGAACTAAAATAGTTGTTT  
1501 AAAAAATGAATTAAGATGCACTTCAAAGAATTCAAACCTTGGCTCAA  
1551 AATGAAAGAACTTTTTTATGCGATATGCAAATTAACAGTTCTGAATTAAA  
1601 AATAAGAGCTATTGTTAATAATATCGGAAATTCCTTGAGGAAATTTCTT  
1651 GTCTTAAATTTGAAGGTTATAAACTTAATATTTCTTTTAACCCAAGTTCT  
1701 CTATTAGATCACATAGAGTCTTTTGAATCAAATGAAATAAATTTTGATTT  
1751 CCAAGGAAATAGTAAGTATTTTTTGATAACCTCTAAAAGTGAACCTGAAC  
1801 TTAAGCAAATATTGGTTCCTTCAAGATAATGAATCTTTACGATCTTTTAG  
1851 AACTACCACTACAGCATCAATAAAAGAAATAAAATTGCTTATAAAAGA  
1901 TTAGCAAAGCGTTATCACCTGATGTAAATAAATTAGGTTGCAAACTTT  
1951 TGTGAAATTAATAATGCTTATTCAATATTAAGTGATCCTAACCAAAGG  
2001 AAAAAATATGATTCAATGCTGAAAGTTAATGATTTTCAAATCGCATCAA  
2051 AATTTAGATATTAGTGTTAGATGACATGAAAAATTCATGGAAGAACTCGA  
2101 ACTTCGTAAGACCTGAGAATTTGATTTTTTTTCATCTGATGAAGATTTCT  
2151 TTTATTCTCCATTTACAAAAACAAATATGCTTCCTTTTGTAGATAAAGAT  
2201 GTTCTTTTAGCTTTTTTTCAGCTTTACAGCAAGGGCAAATAGATCATCA  
2251 ATTGGAATAATCTTTATTGAAAAGAAGAGATGTAAAAGAAGCTTGTCAAC  
2301 AGAATAAAAAATTTTATTGAAGTTATAAAAGAGCAATATAACTATTTTGGT  
2351 TGAATTGAAGCTAAGCGTTATTTCAATATTAATGTTGAACTTGAGCTCAC  
2401 ACAGAGAGAGATAAGAGATAGAGATGTTGTTAACCTACCTTTAAAAATTA  
2451 AAGTTATTAATAATGATTTTCCAAATCAACTCTGATATGAAATTTATAAA  
2501 AACTATTCATTTGCTTATCTTGAGATATAAAAAATGGTGAAATTGCTGA  
2551 ATTTTTCAATAAAGGTAATAGAGCTTTAGGATGAAAAGGTGACTTAATTG  
2601 TCAGAAATGAAAGTAGTTAATAAAGTAAACAAAAGACTGCGTATTTTTTCA  
2651 AGCTTTTTTGTGAGAACGATAAATCTAAATTATGGTTCCTTGTCCAAACGA  
2701 TAAACAAAGTAATCCTAATAAGGGCGTTTTTAATAATAAACTCAGCACT  
2751 TTATTGATTAAAAAACCTTTCATTTTAAATGTGTTATAATTATTTGTTAT  
2801 GCCATAAATTTAGTTTGTGGCAAAAGCTTCTGTACTGTTTATTTAATGGA  
2851 AGAAAATAACAAAGCAAATATCTATGACTCTAGTAGCATTAAAGGTCCTTG

2901 AAGGACTTGAGGCTGTTAGAAAACGCCCTGGAATGTACATTGGTTCTACT  
2951 GGCGAAGAAGGTTTGCATCACATGATCTGAGAGATAGTAGACAACTCAAT  
3001 TGATGAAGCAATGGGAGGTTTGGCAGTTTGTGAAGCTTACCCCTGAAG  
3051 ATAATTTGTACCCTGTAGAGGATGATGGAAGAGGGATACCTGTTGAT  
3101 ATCCATCCTAAGACTAATCGTTCTACAGTTGAAACAGTTTACAGTTCT  
3151 ACACGCTGGCGGTAAATTTGATAACGATAGCTATAAAGTGTGAGGTGGTT  
3201 TACACGGTGTGGTGCATCAGTTGTTAATGCGCTTAGTTCTTCTTTTAA  
3251 GTTTGAGTTTTTCGTCAAATAAAAAGTATTTCTCAGCTTTAGCGATGG  
3301 AGGAAAGGTAATTGGAGATTTGGTCCAAGAAGGTAAGTCTGAAAAAGAGC  
3351 ATGGAACAATTGTTGAGTTGTTCTCTGTAATGGAAAAGAGT  
3401 GATTACAAACAACTGTAATTGTAAGCAGACTCCAGCAATTAGCTTTTTT  
3451 AAACAAGGGAATAAGAATTGACTTTGTTGATAATCGTAAACAAACCCAC  
3501 AGTCTTTTCTTGAAAAATATGATGGGGGATTGGTTGAATATATCCACCAC  
3551 CTAAACAACGAAAAAGAACCACTTTTAAATGAAGTTATTGCTGATGAAAA  
3601 AACTGAACTGTAAAGCTGTTAATCGTGATGAAACTACACAGTAAAGG  
3651 TTGAAGTTGCTTTTCAATATAACAAACATACAACCAATCAATTTTCAGT  
3701 TTTTGTAAACAACATTAATACTACAGAAGGTGGAACCCATGTGGAAGGTTT  
3751 TCGTAATGCACCTTGTTAAGATCATTAAATCGCTTTGCTGTTGAAAAATAAT  
3801 TCCTAAAAGATAGTGATGAAAAGATTAAACCGTGATGATGTTTGTGAAGGA  
3851 TTAAGTCTATTATTTCCATTAAACACCCAAACCCACAATATGAAGGACA  
3901 AACTAAAAAGAAGTTAGGTAATACTGAGGTAAGACCTTAGTTAATAGTG  
3951 TTGTTAGTGAAATCTTTGAACGCTTCATGTTAGAAAACCCACAAGAAGCA  
4001 AACGCTATCATCAGAAAAACACTTTTAGCTCAAGAAGCGAGAAGAAGAAG  
4051 TCAAGAGGCTAGGGAGTTAACTCGTCGTAAATCACCTTTGATAGTGGTT  
4101 CATTACCAGGTAAATTAGCTGATTGTACAACCAGAGATCCTTCGATTAGT  
4151 GAACTTTACATTGTTGAGGGTGATAGTGCTGGTGGCACTGCTAAAACAGG  
4201 AAGAGATCGTTATTTTCAAGCTATCTTACCCTTAAGAGGAAAGATTTTAA  
4251 ACGTTGAAAAATCTAACTTTGAACAAATCTTTAATAATGCAGAAATTTCT  
4301 GCATTAGTGATGGCAATAGGCTGTGGGATTAAACCTGATTTTGAACCTGA  
4351 AAACTTAGATATAGCAAGATTGTGATCATGACAGATGCTGATGTTGATG  
4401 GTGCACACATAAGAACACTTCTCTTAACCTTCTTTTTTCGCTTTATGTAT  
4451 CCTTTGGTTGAACAAGGCAATATTTTATTGCTCAACCCCCACTTTATAA  
4501 AGTGTCATATCCCATAAAGGATTTATACATGCACACTGATGTTCAACTTG  
4551 AACAGTGAAAAAGTCAAAACCTAACGTAAAGTTTGGGTTACAAAGATAT  
4601 AAAGGACTTGGAGAAATGGATGCATTGCAGCTGTGAGAAACAACATGGA  
4651 TCCTAAGGTTAGAACATTGTTAAAAGTTACTGTTGAAGATGCTTCTATTG

4701 CTGATAAAGCTTTTTCTACTGTTGATGGGTGATGAAGTCCCCCAAGAAGA  
4751 GAATTTATTGAAAAAATGCTCGTAGTGTTAAAAACATTGATATTTAATT  
5 4801 TGGTTAGTATAAATGGCAAAGCAACAAGATCAAGTAGATAAGATTCGTGA  
4851 AAACCTAGACAATTCAACTGTCAAAAGTATTTTCATTAGCAAATGAACTTG  
4901 AGCGTTCATTCATGGAATATGCTATGTCAGTTATTGTTGCTCGTGCTTTA  
10 4951 CCTGATGCTAGAGATGGACTTAAACCAGTTCATCGTCGTGTTCTTTATGG  
5001 TGCTTATATTGGTGGCATGCACCATGATCGTCCTTTTAAAAAGTCTGCGA  
5051 GGATTGTTGGTGATGTAATGAGTAAATCCACCCTCATGGTGATATGGCA  
5101 ATATATGACACCATGTCAAGAATGGCTCAAGACTTTTCATTAAGATACCT  
15 5151 TTTAATTGATGGTCATGGTAATTTTGGTTCTATAGATGGTGATAGACCTG  
5201 CTGCACAACGTTATACAGAAGCAAGATTATCTAAACTTGCAGCAGAACTT  
5251 TTAAAAGATATTGATAAAGATACAGTTGACTTTATTGCTAATTATGATGG  
5301 TGAGGAAAAAGAACCAACTGTTCTACCAGCAGCTTCCCTAACTTACTTG  
20 5351 CAAATGGTTCTAGTGGGATTGCAGTTGGAATGTCAACATCTATTCCTTCC  
5401 CATAATCTCTCTGAATTAATTGCGGGTTAATCATGTTAATTGATAATCC  
5451 TCAATGCACTTTTCAAGAATTATTAAGTGAATTAAGGACCTGATTTTC  
25 5501 CAACAGGAGCTAACATTATCTACACAAAAGGAATTGAAAGCTACTTTGAA  
5551 ACAGGTAAAGGCAATGTAGTAATTCGTTCTAAAGTTGAGATAGAACAATT  
5601 GCAAACAAGAAGTGCATTAGTTGTAAGTGAATTCCTTACATGGTTAACA  
5651 AAACCTACCTTAATTGAAAAGATTGTAGAACTTGTTAAAGCTGAAGAGATT  
30 5701 TCAGGAATTGCTGATATCCGTGATGAATCCTCTCGAGAAGGAATAAGGTT  
5751 AGTGATTGAAGTAAACGCGACACTGTACCTGAAGTTTATTAAATCAAC  
5801 TTTTTAAATCAACAAGATTACAAGTACGCTTCCCTGTTAATATGCTTGCT  
35 5851 TTAGTTAAAGGAGCTCCTGTACTTCTCAACATGAAACAAGCTTTGGAAGT  
5901 ATATCTTGATCATCAAATTGATGTTCTTGTTAGAAAAACAAAGTTTGTGC  
5951 TTAATAAACAAACAAGAACGTTATCACATTTTAAGCGGACTTTTAATTGCT  
40 6001 GCTTTAAATATTGATGAGGTTGTTGCAATTATTAAAAATCAGCAAATAA  
6051 CCAGGAAGCAATTAATACATTAAATACAAAGTTTAAGCTTGATGAAATTC  
6101 AAGCTAAAGCAGTTCTTGACATGCGTTTAAGGAGCTTAAGCGTACTTGAA  
6151 GTTAACAACTTCAAACCTGAACAAAAGAGTTAAAAGATTCAATTGAATT  
45 6201 TTGTAAGAAAGTGTTAGCTGATCAAAAATTACAGCTAAAAATAATCAAAG  
6251 AGGAATTGCAAAAAATCAATGATCAGTTTGGTGATGAAAGAAGAAGTGAA  
6301 ATTCTCTATGATATCTCTGAGGAAATTGATGATGAATCATTGATAAAAGT  
6351 TGAGAATGTAGTGATAACTATGTCTACAAATGGTTATCTAAAAAGGATTG  
50 6401 GAGTTGATGCTTATAATCTTCAACATCGTGGTGGAGTTGGGGTTAAAGGG  
6451 CTAACACTTATGTTGATGATAGTATTAGTCAATTATTGGTCTGTTCAAC



6501 TCACTCTGACTTATTATTTTTTACTGATAAGGGTAAGGTTTATAGAATTA  
6551 GAGCTCATCAAATTCCTATGGTTTTAGAACAAATAAAGGTATTCCCGCT  
6601 GTTAACTTAATCAAAATTGAAAAGGATGAAAGAATTTGTTCAATTGTTATC  
6651 TGTTAATAACTATGATGATGGTTATTTCTTTTTCTGTACTAAAAATGGAA  
6701 TTGTTAAAAGAACGAGCTTGAATGAATTCATCAACATCTTAAGTAATGGT  
6751 AAGCGGGCTATATCTTTTGATGATAATGACACTTTGTATTCAAGTAATTA  
6801 AACCCACGGAAATGATGAGATTTTTATTGGTTCTACCAATGGATTTGTTG  
6851 TTCGCTTCCATGAAAATCAACTCAGAGTTCTTTCAAGAACAGCAAGAGGT  
6901 GTATTTGGTATCAGTTTAAATAAAGGAGAATTTGTTAATGGACTATCAAC  
6951 TTCAAGCAACGGTAGCTTACTTTTATCAGTCGGTCAAAATGGAATAGGTA  
7001 AATTAACGAGCATAGATAAATATAGACTCACAAAACGTAATGCTAAGGGA  
7051 GTTAAACTCTAAGGGTTACTGATAGAACAGGCCCTGTTGTTACAACAAC  
7101 CACTGTTTTTGGTAATGAGGATCTTTAATGATTTCTCTGCTGGTAAAA  
7151 TTGTGCGTACCAGTTTACAAGAACTTTCAGAACAAAGGTAAAAACACTTCT  
7201 GGTGTTAAGTTAATTAGATTAAAAGATAATGAACGTTTAGAAAGAGTAAC  
7251 TATCTTTAAAGAAGAGTTAGAAGACAAAGAAATGCAACTAGAAGATGTTG  
7301 GATCCAAACAAATTACGCAATAACTATGATTTCTTTAAAAAGAACTGTT  
7351 AGAAAGAAATGTAAATGAGCAATTATTAATCAGTTTATTCAAACGATA  
7401 AACTAATGCGCAAAACTTGCAACAACCTGAACTTGCTAACCAAAAACAA  
7451 AGCTTGTTGGCAAAACAAGTTGCTAAGCAAAAAGATAATAAAAAGCTATT  
7501 AGCTGAATCAAAAGAACTTAAGCAGAAGATTGAAAACCTTAAATAATGCTT  
7551 ATAAAGATTACAAAACATTAGTCAAGATTACTTCTAAATTTTCCTAAT  
7601 ATTGCTCATGAATCAGTTCTGTTGGTAAAAATGAATCAGCAAACTTAGA  
7651 ACTTCTTAAAGAAGGGAGAAAACCAGTTTTTGATTTCAAACCTTTACCAC  
7701 ATCGAGAGTTATGTGAAAAGTTAAATTTAGTTGCTTTTGATAAAGCTACT  
7751 AAGATTAGTGGAACCTAGGTTTGTGTCATATACAGATAAAGCAGCTAAACT  
7801 ACTTAGAGCGATAACTAATCTAATGATTGACCTTAATAAAAGCAAGTATC  
7851 AAGAATGAAACCTGCCAGTTGTTATTAATGAATTAAGTTTAAGATCAACC  
7901 GGACAACTACCTAAGTTTAAAGATGATGTTTTTAACTAGAAAACACCCG  
7951 TTATTATCTTTCTCCAACCTTAGAGGTACAACCTATCAATTTACATGCTA  
8001 ATGAAATTTTAAATGAAGAAGATTTACCTAAATACTACACTGCAACAGGT  
8051 ATTAACTTTCGTCAAGAAGCGGGTAGTGCTGGTAAACAAACCAAGGAAC  
8101 TATTAGATTGCATCAGTTTCAAAAACTGAGTTAGTTAAGTTTGTAAAC  
8151 CTGAAAATGCTATCAATGAATTGGAAGCAATGGTTAGAGATGCTGAACAA  
8201 ATCTTAAAGGCACCTAAGTTACCTTTTAGAAGGTTATTGTTATGTACTGG  
8251 TGATATGGGCTTTAGTGCTGAAAAAACATATGATCTTGAAGTTTGAATGG

8301 CAGCTAGCAATGAATATCGTGAAGTTTCTTCTTGTTTCATCTTGTGGTGAT  
8351 TTTCAAGCAAGAAGAGCTATGATTCTGTTACAAAGATATTAACAACGGTAA  
5 8401 AAACAGTTATGTTGCTACTTTAAATGGAACAGCATTATCTATTGATAGAA  
8451 TTTTTGCTGCAATTCTAGAAAATTTTCAAACAAAAGATGGCAAAATCTT  
8501 ATCCCACAAGCATTAAAAAATACCTTGATTTTGACACAATCAAGTAATT  
8551 TATGAATAAAGGTGTTTTTGTGTTATTGAAGGAGTTGATGGAGCGGGCA  
10 8601 AAACGCTTTAATTGAAGGTTTTAAAAAATTTATCCAATAAGTTTTTG  
8651 AACTATCAACTTACTTATACTAGAGAACCTGGTGGTACTTTGTTAGCTGA  
8701 AAAAATTCGTCAACTTCTTTTAAATGAAACAATGGAACCTCTAACTGAAG  
15 8751 CTTATTTGTTTGCCGAGCTAGAACTGAACATATCAGTAAGCTAATTAAA  
8801 CCAGCAATTGAAAAAGAACAACCTAGTTATTTTCAAGTAGATTGTTTTCTC  
8851 TAGTTTTGCATACCAAGGATTAAGCAAAAAATAGGCATTGATACAGTAA  
8901 AACAGATTAATCATCATGCGTTAAGAAATATGATGCCAACTTTACCTTT  
20 8951 ATTTTGATTGCAATTTTAAAGAAGCATTACAAAGGATGCAAAGCGTGG  
9001 TAATGATAATCTTCTTGATGAATTTATTAAAGGAAAGAATGATTTTGATA  
9051 CAGTTCGTTCTTATTATTTAAGCTTAGTTGATAAAAAAATGTTTCTTG  
25 9101 ATTAATGGTGATAATAAACAAGAACACCTAGAGAAATTTATTGAATTGTT  
9151 AACAAGATGCTTACAACAACCCACGCATTACTAATCATTCAAAGAAAAGG  
9201 TAGTTTCTTAAACCTTTTCTTGATAATTATCTTACTAGTATTGTTTG  
9251 AAAACAAAATGGTTGCAAAAAGTGATAAACTGTTTGGAATTTCTCAAT  
30 9301 AATAAATACAACAGCTTATATTGATTTGATCAAATTAATCCTTTCAAAG  
9351 AGAAATGCCCTTCAGTTAGCAAGAATTTTAAACCGTGAAAGAACAAAGTG  
9401 TAAACAATAAAAATATTTATCTAATTGAAGAAATTGAAAAATTAAGCAGT  
35 9451 AATTCTATAAATAGTTTATTGAGACTAGTTGAAGATAGTCCGATAAATAG  
9501 TTATGGTATTTTTACAACATAAAATGAAAGTTTAAATCTTTCCACTTTTT  
9551 TAAGTAGAGTACAGAAAGTAGTTTTAAAAAAGCTAGTAAAGTTCCTTTT  
9601 AAAGTAAGCAAAAATGATCAAGAAATTATTACAAGTTTTTTACTGTAGA  
40 9651 TGAACAAATTGAAGCAATTGAAAATGGAAGTTTTAACCGTTTCAAATTA  
9701 TCTTAGATGCATGTTTAAACAAAAAACAGGTACAGAACAAATTTATCAT  
9751 GCTTGACAAATTTTTAGAGATTTTTCTAATAGTGAAATTGCTCAGTTAAT  
45 9801 TACTCTAATAATTAATAAACTGAAAATATAGATAAAAAATCAATTTTGT  
9851 TTAATTGTTTAAAGTTTTGCCATATAATCCTCCAAAATCCACTTTGTTT  
9901 GCTAATTTAGTTAGTTGATAGTTATGAAAAGCGAAATTAATTTTTTGCA  
9951 CTAGCAACTGCACCTTTTAATAGTGATTACATATTATTAGGTTTTCTGG  
50 10001 TCCTGATGTTTATGAGATTTTAAACAAGATAACTAATAAAAAATAACAA  
10051 GAAAAGGGATGCAAAATTCACGCACATGGATAGTTGATGAAAACAATAAG

10101 CGAATTGATGATGTGCTATTATTTAAATTTGTCTCTCCAAATCTTATAC  
10151 AGGAGAAGATTTAATTGAAATTTCTTGTCTCATGGTAACATGTTGATCGTTA  
10201 ATGAAATTTGCGCACTTCTTTTAAAAAAGGAGGTGTTTATGCCAAACCT  
10251 GGTGAATTTACCCAAAGGAGTTTTTTTAAATGGAAAAATGAGTTTACAACA  
10301 AGCTAGTGCTGTAAATAAATTGATTTTATCTCCTAACTTATTAGTTAAAG  
10351 ATATAGTCTTAAATAATTTAGCGGGTGAAATGGATCAACAATTAGAACAA  
10401 ATAGCTCAACAAGTTAATCAATTAGTAATGCAAAATGGAAGTAAACATTGA  
10451 TTATCCAGAATATCTTGATGAACAAGTAGAACTATCAACTTTAAATAATA  
10501 AAGTTAAATTGATTATTGAAAAGCTTAAAAGAATTATTGAAAATAGTAAA  
10551 CAACTCAAAAAAAGCTTACGATCCTTTTAAATTTGCCATTATAGGCGAAAC  
10601 TAATGTAGGTAAATCTTCTTTACTCAACGCTTTATTAAATCAAGATAAAG  
10651 CGATAGTTTCAAATATTAAAGGTAGTACACGCGATGTTGTTGAAGGGGAT  
10701 TTCAATTTAAATGGTTATTTAATCAAGATCTTAGATACTGCAGGTATCCG  
10751 TAAACATAAAAGTGGGCTTGAAAAAGCAGGAATTAAGAAAGCTTTGAAT  
10801 CTATAAAGCAAGCTAATTTGGTTATTTATCTTTTAGATGCAACACATCCA  
10851 AAGAAAGATCTTGAATTAATTAGTTTTTTTAAAGAAAAATAAAAGGATTT  
10901 TTTTGTCTTCTATAACAAAAAGATTTAATTACAAATAAGTTTGAAATA  
10951 GTATTTCTGCAAAAGCAAAAGATATTAAAGAATTAGTTGATTTATTAAGT  
11001 AAATATATTAACGAGTTTTTATAAAAAAATAGATCAAAAAATCTATCTGAT  
11051 TGAAAATTGACAGCAAATTTTAATTGAAAAAATTAAAGAACAATTAGAAC  
11101 AGTTTTTTAAAGCAACAAAAAATATTTATTTTTTCGATGTTTTAGTTACC  
11151 CATCTAAGAGAAGCTCAACAAGATATTCTTAACTACTAGGTAAGGATGT  
11201 AGGTTTTGATTTAGTTAATGAAATTTTTAATAATTTTTGTTTAGGAAAAAT  
11251 AATGGAATACTTTGATGCACATTGTCATTTAAATTGTGAACCTTTACTGA  
11301 GTGAAATTGAAAAAGCATCGCTAATTTCAAATTAATTAATTTAAAGCA  
11351 AATGTTGTAGGTACAGATTTGGATAATTCTAAAATTGCTGTTGAATTAGC  
11401 TAAAAAATATCCTGATCTTTTAAAGCAACCATAGGTATCCATCCAAATG  
11451 ATGTTTCATTTAGTTGATTTTAAAAAGACAAAAAACAACCTTAATGAACTA  
11501 TTAATAAATAACAGAAATTTTATAAGTTGTATTGGTGAATATGGTTTTGA  
11551 TTATCACTACACAACAGAATTTATTGAATTGCAAAACAAATCTTTGAGA  
11601 TGCAATTTGAAATAGCTGAACTAATAAATTGGTTCACATGCTTCATATT  
11651 CGTGATGCTCATGAAAAAATTTATGAAATATTAACAAGATTAAAGCCAAC  
11701 TCAACCTGTGATTTTTCATTGTTTCAGTCAAGATATAAATATTGCTAAAA  
11751 AGCTACTATCATTAAGATTTAAATATTGACATCTTCTTTTCTATCCCA  
11801 GGGATAGTTACTTTTAAGAATGCTCAAGCATTACATGAAGCTTTAAAGAT  
11851 TATTCCTAGTGAATTACTTTTAAAGTGAACTGACTCACCGTGATTAACCC

11901 CTTCTCCTTTTCGAGGCCAAAGTTAACTGACCTGAATATGTAGTTCATACT  
11951 GTTAGCACTGTTGCTGAAATAAAAAAATAGAAATTGCTGAAATGAAGCG  
12001 AATTATTGTTAAAAATGCAAAAAAATTATTTTGACATTAAAAGTTAAATA  
12051 AAGCAATTTATTTAACAAATGGATGTTAGAACTGAAAGATTAAACGAATT  
12101 GTTTTTTGTTTATCATAAAACTTAAAAAATCAATCTAAATCTAAATATA  
12151 GCAGAGCAGTTAATTACTTAAAAAGGCGTGGATTCAATTTACAAGATTTT  
12201 TTAAAAGTTGGGGGTGGTGTGGTTATTTACAAAATAAAGAATGATTAAA  
12251 TTTACCTTTTATACAGTTTGTGATGGTAATTTAATTGGTTTTCTAAACAGAA  
12301 AAGTTAGTTATAAAAAGGAATTTTATATACACCTTTTAATAAACCTCCT  
12351 TCAAAGAGCGAAGCTTTTGTAGGACTCAGAGAATTAGTTATTAAAGACAA  
12401 TAGCATATATCTTGTGAAGGTGATTTTGACTGGTTAGCTTTTCGCAAAG  
12451 CAGGTATATTAAATCTCTTCCTCTTGTGGTTTGACTATTTCAAATCAA  
12501 CAAGTTCAATGATTAAAACAAAAAAGATTAAAAAGATTTTATCTGTTT  
12551 TGATAATGATTTAGCTGGAAAGAATGGAGCAAAAAATTTAAAGAATATC  
12601 TAACTAAGCAAGGATTTATAACAAAAGTTATAGAAATTAAAGCTGCCGCA  
12651 AAAGACTGAAATGATTTGTTTTTATTAAACAACCTCAAATTGATCAGCGGT  
12701 TTTAACTAATCAACTTCTTTTTTAAAGAATTTTTTAAATTTACTAATAATT  
12751 GTTCTGATAATTATTTTAGTGATATTAAATCTGGACAAAGCTGAACTAA  
12801 AGCTCTCGCACCAGCAGCATCTTCAATTTCAATTAACAATAACCTATTAT  
12851 ATCTATTTAAAAAGAAGTCAATAGCATAATAACCTTCCCTTAGGCGTTTA  
12901 GCTATTTCTTTATTTTCTTTTAGTAAATCACTTTAATTTAAACAAGGA  
12951 AACTTCAGCACCTTGTGAAAAGTTAGCTTTAAATTGATTAGCATTAGAAA  
13001 TTTTTTTAATAACTTTAATTATTTTTCCAAACAAAATATAAGCACGATAT  
13051 TCAACTGTGCCAATTGATAAAAAAGGTTGAACAATTCATTCTGTTGCATT  
13101 TTCAATGTTTAAATGTTTGATCTCGTCAGCACTATTAATAAATGTACAT  
13151 CTTTTCCACCGTGTGAATTACGTTTCTTAACGATGACAGGAAATGATTTG  
13201 ATTGTTTCTTTACTAAGAAGAGAAGAAATTGACAGTTAGAAATCTATTTTG  
13251 TTTTAATCATTTATATGTTTCGTATTTATCGTTTGCTATAAAAAACAACAT  
13301 TAAAAGGATTAACATAAAAAAGTATTTATTTGATTATTGGTTTTTAAAAAA  
13351 TCTACTTTTCTTGAACGATTTAAAAATCAATTCAGCTTCATTAATTTTAGC  
13401 TTCGAAATTAATGTCTTTATTTCAAGTAATAAGACTTCAGCATTTAGTT  
13451 TTTTCTTTTGTAATTCCTTGATTAGACTTAAAGCAAATGTTGATTTTTT  
13501 TCAAAATCATCCTTGTTGTCATAAACAACTAATGCTTTTCTGTTTTTTAA  
13551 TTTAATTTTCCCATTAATCTAAATTGCTTTTAAAGCTCAATTGCAAGA  
13601 TTAGTATTTAAATACATTGAGCTTCTTGTTAATTGCACATTAGGATTTAC  
13651 TTCACAAAAGATCAATGATCTGTCTTGATCAAACAAAAATCAATACCGC

13701 AATAAAAAAGTTGCATTACTTTACTAATTTTAACTGCTAAATTTTCTTGT  
13751 TCCTTATTCAAAAAAAGCGTTCTGCCTTTGCCCTTTATTGAGATTAGA  
13801 ACGAAAATCACTATTATTAGTTGTATGTAAAGCACCTATAACTTTATTGT  
13851 TCACAACAATAACTCTTACCGATTACCTTTAGAGCAAGTAATGTATTTT  
13901 TGCACAATTGCTTGTTGATTAAAAGACATTAAAGTTTTTCTTAATTTTTG  
13951 TTCATCTAAACACAAAAAACATAATCACCAAAGAACCAAAACACTTT  
14001 TAACAATAACAGGAACTCCATACTTTGTTTTATTGATTAATAAAAACA  
14051 TCGAGCATTACTGGATTTCACCTCCCTGTCAAAATTTTGAGGTCCTAAAG  
14101 TGTTTTAATCTGCTTTATGAATGGATATTGTGCAATGATAGCGTGACTAA  
14151 GTCCTTTATTATCTGCATTGTTAATTCCAATTGAACGTTAATTACTTCA  
14201 AAACCATTGCTTTCTAGTCATCTAGCTAAAGCAATATTTTTATCCATAAA  
14251 AAGAATTTTGTGGATATGAAGGGTAAATTTGCTTTTGCTTTAGTTGTAT  
14301 TAATATCAAACTAGTAAAGAATTTTAGTTCTATATCTAACTCTTCACTA  
14351 GCATTTTTTAAAAGTTGAGTTTGATTAAATTTAGAGCTAATTGGATTAAA  
14401 TGCTGGATTGTAAACAACGTTTATTTTTTTCATGCAATATTCAAAGATT  
14451 TTTATTATTGCTAAAACGTAAAGGGCCAACACCGCCAGGCGTTTTAGT  
14501 TCATCATCTAGCTTTTTTTTCAATGCCTTCAGGATTTATATCACCACAAA  
14551 GTTTATTTTGCTTGTTTCTTGAAACACCTATATCAAATAAAATAACTCCT  
14601 TTTTTAAAGTTTTTAGCTTGAAAAAATGAGATTTTCCAATAGCAGTAAA  
14651 AACTATATCAGCACTTTTAATCAATTCAAATGTATTGGAGTATCTTTAT  
14701 CGCATGCTTGAACCTTTATAACCACTAGTTTTTAAAAATTCATAAATAGGT  
14751 TTGCCACCAGTTATTCCCAAACCTACCACAACAATTTTTTGATTATTAAA  
14801 TTCAAGGTTAAATAGTTCTTTTAGTGTTATTATAGCTTCAACTATACAAG  
14851 GTTTAATTTTCAGCCAAATGATTAGTTGTAAACCATCAACATCTTTTAAA  
14901 GGATTAATTGCTTCTAGTAGTGAGTTTTTATCTAAGTGTTGGATAAACTGG  
14951 CAATTGCAAAATGATACCAGTAACATTTACATCATGATTTAAACTAATTA  
15001 TTTTTTCTATTAACTCTGCTTGAGTTATTTGATTAGATAGTTTAATTAAT  
15051 TCACTTTTGTCTCTACAGTGTTACAAGCAATAAGTTTTTGTTTAATAAA  
15101 ACTGTCTGATGAATCATCATCATTAGCTTGAATAATCACTAACTTACATT  
15151 TTGATCAATCAAAATCTTGTAAGTTTCTAAGATTGATTGCGCTTTTAGT  
15201 TTTCCATCAAATGACATCTTATTTTGCCTAATATAAAACAAAACGTCTAA  
15251 CTTCTTATTTATGCAAAGGTAAGTTAGACGTTGGAATTCTTTAATGGTGG  
15301 AGATGAAGGGTCTCAAACCTCAACCTCCTGAGTGCAAATCAGGTGCTCT  
15351 ATCAGTTGAGCTACATCCCCATTATTGGTGGAAGTAAATGGACTTGAACC  
15401 ATCGACCTCACCTTATCAGGGGTGTGCTCTAACCAACTGAGCTATACTT  
15451 CCAAGCATAATCCTAAGGGTATTTAACTAATTATTATAACAATTTTAATT

15501 TAACCAAAATACCCCTCGAATTTTAAACAGTTTTTATAATCAAAACAGCTA  
15551 ATTTTATGGGGCTTGTTTTAAAAGAATTTAACAATAAAATAAGAACAGCA  
5 15601 TTAATTCTCGCTCCTTTTTTCACTTTCGCTCAGATAGTGATTGATTTAAT  
15651 CATTCCTTCTTTTTTAGCAAGTGCTATTTTCAGTTGTGTTTTCAATTGATA  
15701 AATTA AACAGGATGAGTCAGGCGGAAAGACAATTTTCAGTTGATTTTATT  
15751 GGTGGGGCTAATATTAATTTTGCTAATGTAGAGAAGCGCAAATAGTTTT  
10 15801 AGCAACCACAGTTATTTTACTTGCAATTATGTGGACTTTTTTTTGGTCTAA  
15851 TATCTATTTATGTGCAAGTTATGTTTCAGCAAACACTTCTTTTCTATTA  
15901 AGAAAAAGATCTTGCAAAATTAATGCGAATCACAACCCCATCACATGA  
15951 CCATTATGGTTCTTCTACTTTATTAGTTAGATTAACAAATGATGTTTATT  
16001 TGATGGAGGTAATTGCTTTTTGATTTTTTAAGGCTAATTATTCGTGCTCCG  
16051 CTTTGTGTTATAGGTGGATTAGTGTTTCAGTAACACAAATCAAGATAT  
16101 GTCAATATCTTTACTAATTACTTTTCCTTTGATTCTTTTGGTAATTGGTA  
20 16151 TTCTAAACCGTAAATCTATTCCTTTATTTAAAGAAAATCAAAAATCAGTT  
16201 GATAAGATAAATGAAAGAGTAGAAGAAGATGTTTCAGGTTATAAAGTAAT  
16251 TCAATCTTTTAATCTTCATTCCTTTACAAATAACAAATTTAAGATTGCAA  
25 16301 ATGAAGGATGAAAAAGAATAGTACAAGTTCTTTATTTATAAACTCACTT  
16351 AACATTCCATTTACCTTTTTTTTAAAGCAGTTTAACTATTATTATTGCTCT  
16401 ACTATTAGTTTTTTCAATTAGATAGTAGTGTTTCAGTTGACCCATTACCGC  
16451 AGGATGCAGCTATTAGACCTAATATCTTTGCTTTTTTCCAATATAACTTT  
30 16501 TACATTGTTTTAGGGTTTATCTTAACCTCTTTAACAATGGTGAACTTTAA  
16551 TCGTTCTAGAGTTGCACTAGGCAGAAATTAAAGATATTTTATCTCAGCCTG  
16601 AAATAAAAATATTACAAATAAAGATCAAAAAGAATTATTACCTACCTTG  
35 16651 GAGTTTAGAAATATCTCTTTTGGTCTTGGCAATAAGAACAATAACAATTT  
16701 TTTACAAAATCTTAGTTTTAAATTTGAAGCATATAAAACATATGGTATTG  
16751 TTGGGCCTACAGGCTCTGGAAAATCTTTAATTGCTAACATTATCGGTGGT  
16801 TTATATGAGCCTAATGAGGGTGAAATCTCATTGGTGGGGAGAAAATTCA  
40 16851 ATCTATTGACAGTTTATATCTATCAGAAATGATAGGAATTGTTTTCCAAC  
16901 AAAACATCCTTTTTTAAAGGAACAATTTCTTCTAATATAAAAAATTGGTATT  
16951 GAAACTAGAAGTGATTGAAAGAATCAATCTGATTTACAAAAGAATGAAGC  
45 17001 GATGAAAAACGCAGCTAAAATAGCTTGCGCTGACACCTTTATTGAAAAGT  
17051 TTTCTGATAGTTATGATCACAATGTTGAACAGTTAGGTAAAACTTATCT  
17101 GGTGGACAAAAACAAAGAGTTGCTATTGCAAGAACTTTAATTACAAAACC  
17151 AAGAATTTTAGTTTTTGATGATAGTATGAGTGCTCTTGATGCTCTAACTG  
50 17201 AAAAAAAGTAAGAGAAAATATTGAAAATGATTTAAAGCTAACTACCAAA  
17251 ATCATTATTAGTCAAAACATTAATTCAATTAAACACGCAGATAAAATTTT

17301 GGTAATTGATAATGGCAGAATTGTTGGTTTTGATAGTGATCAAAAGCTAA  
17351 TGAAAAATTGTTCACTTTATCAAAAGATGAAAGAATCTCAAAAAGATTG  
17401 GGAGGTGATTTTGATGCAGTTAACTAGTGTAACCAAGTTCTTGAAAGA  
17451 TTTTAAAGAGATTAATTACTTCAATGGAAGGAAGTTGAAGTTATAAATTA  
17501 CTTTATGTTTTTTTTGTGTATAGTTCTTGGTATTTTATATGGAATTGCTAA  
17551 CCCTATCTTATTAGCACAAAGGTCTTGGTTTTATTTTCTATTACTAGTA  
17601 GTAATGGTCGTGCTGTTGACTCAATATATTCATTAATTTACCCAACAAAT  
17651 TTAAATGTATTCATTAGGCTCACAATTGTGAGCGTAACTGTTTTTGTAGC  
17701 TTATGCATTAATCTTTGTATTTAATGTAGCGCAAACTATGTAGGGATTA  
17751 AACTTTACCAACAAACATGTGCTACTTTGCGTTGAAAGGCATATTTAAAA  
17801 ATGCAGAGTATGTCAACCAGCTTTTTTGATACGCAAAATAATGGTGATCT  
17851 TATGAGTAGGTTAACTAATGATATGTATAACATTGATAACCTATTCACTC  
17901 AAGCTGGTGGACAAGCTATTCAAAGTTTGTTTAATATTTTAACAACCTCA  
17951 GTATTAATATTTTTATTAAGCCCAGTTATTGCACTTATTTCACTTTCAAT  
18001 TTTAGCTACATTAATTACTTTTTCTTTTGCCTTTCTAAAGAAATCAAAAA  
18051 CTTCATATAGTCAAGTACAAAATAATTTGGGTGATATGTCTGGTTATATT  
18101 GAAGAGGTTTTAACTAATCATAAGGTTGTTTCATGTCTTGAAGTTGCAAGA  
18151 GATAATGATTAAGGATTTTGATCAATACAACAAATCAATGATCAAACCAA  
18201 CTGTAAGAGGGAATACATATTCGATCTTTCTTTTTCTTGGTTTGGTTTT  
18251 ATATCAAATATTACTTATCTGGTTTCTATATCAATTGCTACTGCTTTTAG  
18301 TGTTAATTCTATTCCTTCATTTGGAATTAGTGTTATTAATATTCAATCA  
18351 TGTTGTCTTACATTGCTTCTTTAAGGCAAATAACTTTAGCATTAGATCAA  
18401 ATCTTTACCCTTTGAAACTTAGTTCAATTAGGGGTGTTAGTGCAGAAAG  
18451 AGTATTTAAGGTATTAGATCTTAATGTAGAGAAAGATACTGCTACTATTG  
18501 ACAAATTACCTGATATTAAAGGTAATATAAGGTTTGAAAATGTAGCATT  
18551 GGTTACAATAAAGATAAACCTACTTTAACAGGAATTAACCTTTAGTGTTAA  
18601 ACATGGAGATGTAGTTGCAATAGTAGGTCCTACAGGAGCTGGTAAATCAA  
18651 CTATTATTAATCTATTGATGAAATCTATAAACCTTTTGAAGGAAAGATT  
18701 TATATGGATAACTTTGAAATTAGTGATGTAACAAAAAGCATGAAGAGA  
18751 AAAGATTTCTATAGTATTACAAGATTCATTCTTATTTAGCGGCACAATTA  
18801 AAGAAAATATTCGTTTAGGCAGACAGGATGCTACTGATGATGAGATTATC  
18851 GCTGCATGTAAACTGCTAATGCTCATGATTTTCATCATGCGTTTACCAA  
18901 AGGATATGACACTTATATTTCCAATAAAGCAGATTATCTTTCTGTTGGTG  
18951 AAAGGCAATTATTAACAATTGCCAGAGCAGTAATCCGTAATGCTCCAGTT  
19001 TTGCTCTTAGATGAAGCAACTAGTTCAGTTGATGTCCATTGAGAAAAATT  
19051 AATTCAAGAATCAATAGGAAGGTTAATGAAAAATAAACTTCTTTTATAA

19101 TTTCTCATCGTCTTTCAATTATTCGTGATGCAACATTAATAATGGTTATT  
19151 AATGATGGTAAAGTACTTGAAATGGGTAATCATGATCAGCTGATGAAACA  
19201 AAATGGATTTTATGCACGTTTAAAAACAATCTTCGGTTCGTTAATAAATTC  
19251 TAATGACTGTTGCTGAAATTAAAAAAGTGCATTAAATAATCAGGTATTT  
19301 AATGAAGCAAAAGCGCTTTTAGAAAAAGGTAATGTTATTTTTCCAAAAA  
19351 ATTCTTAAAGCGAAAGAAGATCATTATTGAAGTATTAGATGGTAAGGTTT  
19401 TTAAGGTTCAAATTAATTTAAAAACCGCTGCTGCACACTGGATTGTAGT  
19451 TGCTCTAATGATAAGCAAAATTGCGTTCATATAATTGCAGCGCTTTTGAA  
19501 ATATAATGaTCTAAAAAATCAAGATAACAAAGAATTTGACCTTAATAAAG  
19551 CCGATAAATTAGAGTGCAAAGAAGTTGAAATTcTAATTGaAAATGTTAGC  
19601 TTAGCAATTGTTAATGGCAGCTGaAAATTAAAGATAGGTTTTGTAAATTAA  
19651 TATTGATAAAGTTCAAACtAAAtACAACtGCTTTACGTTTTTATTGTTGTG  
19701 ATAATAAGATGTTTATTTTCTACATACTGAAGATGAACACTTTTCAGGA  
19751 TTGCTTTAGATAAAATTAATAGTGTGAAAGACaAACATTATTAATTTTT  
19801 GATCAGCTAAATAAAACAAAGCAAATGCAATATGAAAATAACAGTTTGCT  
19851 TTTTAATTTAGATCAATTCCTAAGCCTAGTTAAGGAAGTTAAAAACCTT  
19901 CATTATTCTTATTAAATGAGGATAAACTGACAATATCTTTTCTTAAGA  
19951 AGTCAACATAAAATCAATGGATTAAGCCACGTTTGTGGTTTTTTAAATAA  
20001 TAAGGTTTTTGATTTTGTATCCTACAATGAAAAAACTAAGCAAATTGTTT  
20051 TACGCTTAGCTTATCTTAATAAGTTCACTGATTTTAAATTTCCATACAAC  
20101 ATTAACATCTATAAACTTGCTTTTGGAGAAACATTATTTTCCATTTTTT  
20151 AATCCATTTAAAAATGAATGGTTTTTAAAAACATCTTTTTTCAAAGTGATG  
20201 TTGTTATTGTTAAGGAAAGTGAATATCTACCTAAGATGTTTTTGACTATT  
20251 GAATTTAATACACAAAAAACAAGTTTATAACTGATGCTTTTTTTAAATA  
20301 TAAGAATAAAAAATAGCAATACTTTAACAACtGTTTACCCCATCGCTATA  
20351 CTTAGCTCAAAAAACTAATACATCAAACtTCAACCGTTTACTTTTTTATG  
20401 AACAAGCACTACAAAGTTTTATGAAGAATTATTTCAAATAGATTATTTA  
20451 AGAAGATTTGAAACATTCCCATTAAAGATAAGAATCAAATTGCGCTTTT  
20501 TAAAACTGTTTTTGATGATTACAAAACCATTGATTTAGCAGAATTGAAAC  
20551 TTACAAGTAATCTCTTAAATTACAAACAGTTACATTTTTTCAATAAGTGAT  
20601 ATTAAAGCTTTAAAAATTGAAGATAGACAACTAAAAATTGAATTTAAAGC  
20651 TGGCGGGATAGATCTAAAGTTAATTAAGTGTTTTAAGTAACTACTATA  
20701 AGGGTAATGCTATTTGTATTGGTGAAGATGGTTGATATGATTTGAACGAT  
20751 GAAAAATGCTAAAGCACTAATTTCAATTTGGAGTCAAATTGACTTAAGAAA  
20801 TGCTACTTGTGATGCTAATAACAATTTGCTTCTTGCTAAATACCACTTGT  
20851 TTGAAGTTGTAGATACTATTAGTAAATACACTGATGTAACtAATTTATTA



20901 GATGAAAAACAGCCTTACAATTAAAAATAGCTAGTGAAAAATCAATTTC  
20951 TCTTTCGTTAGATAATAACCAAATTAATAACTTACGCAAATATCAAAAAAG  
21001 AAGGAGTTAAATGGATAAGGGCATTAGAAGATAATCAGTTTGGTGGAATT  
21051 TTAGCAGATGAAATGGGGTTAGGTAAAACCTGCTCAAGTGATCTTTGCAAT  
21101 GCTGGATAGTTATCAATCAACAAAATCACTTTTACCTAGTTTAATTATCG  
21151 TTCCAGCATCCTTACTCTTAAATTGAAAAAGTGAGTTCCAAAAGTTTGCA  
21201 CCTCATGTGAAAAATAGTTACTGCTAATGGCAATTTTAAAGAACGCTCGCA  
21251 GGTATATGAATCATTAAAAAATCAGATTTTGTTAATGAGTTTAAATGTCT  
21301 TAAGAAGTGATATTAATGAATATCTCAAAAAAGTTCCATTATGTAGTA  
21351 ATTGATGAAGCACAAGGAATCAAAAATGAAAATTCTACTGTAACAAAAGC  
21401 CGCTAAAAAATTAAGGTAATTTTGTCTTAGCACTTACCGGTACTCCTA  
21451 TTGAAATCGTTTGCTTGATCTTTGATCTTGTTTTGATTTTGTTTTACCA  
21501 AATTTCTTGGTAATAAAAAACAGTTTTCAGATCAATTTGAAAAAGAAAA  
21551 AAATGATGAAAGCTTTCAAAAATTAATGAAAAAACGAGTCCTTTTATTT  
21601 TAAGAAGGACTAAAAATAAGTTTTAAAGAAGTACCTAAAAAATTATT  
21651 ACTGATATCTATGTTGAACCTTAGTGAAGAACATCAAAAAGTATGATAA  
21701 ACAAAAAACAGATGGTTTGAAGGAGATTAAAGAAAGTGATGCTAAAAATG  
21751 CTTTAAATATCCTTAGTTTAAATCTTGAAATTAAGGCATATTTGTAGCTTA  
21801 GTTAAAGACAATGATGTTAATGATTTTGAAGATAATTCCAAAGCTAATGC  
21851 AGCTTTAAACATTATTTATGAAGCACTTGAAAATAAACGCAAAGTTATTT  
21901 TGTTTTACTCAATTTTTAGATGTAATTGATTGTTTTAAGCAAAGTTAAAA  
21951 AATCAAAAGATTGATCACCTGGTATTTGATGGTAGAAAACTGTGAAGAA  
22001 TAGAAACACTATTATCCAGAAGTTCAATAGTGCTAAAGAACCTTGTTGTA  
22051 TGCTAGCTTCTTTAAAAGCTGGTGGAGTTGGTATTAAGTAACTGCTGCT  
22101 GAAGTTGTTATTCTTTTGTGATGTGATGAAACAGTGCTGTTGAAATCA  
22151 AGCAACTGATAGAGCACATCGTATTGGTCAAAGTAAAACCTGTACAAGTTT  
22201 ATAGAATTATTGCTAAAAATACTATTGAAGAGCGAGTTTGTCAAGTTCAG  
22251 AATCAGAAACAAGAACTTGTTAAAAAAACCTTGGTTGAGGATGTAAATTT  
22301 CTTTAAATCTCTTTCACATGAAGAACTCTTAAAGCTTTTGAATAAAGCA  
22351 AGAATTATAATTAACACTCTAAGGATGCAAGTGATAAATGGCTGCTGGTA  
22401 AAAGGGATTATTATGAAGTTCTAGGGATATCTAAAAACGCTAGTTCTCAA  
22451 GACATAAAAAGAGCTTTTAGAAAGCTTGCAATGCAATATCACCCCGATCG  
22501 TCATAAAGCAGAAAATGAACTACTCAAAAACAAAATGAGGAAAAGTTTA  
22551 AAGAGGTTAATGAAGCATATGAAGTTCTAAGTGATGAAGAAAAACGTAAG  
22601 CTTTATGACCAGTTTGGTCATGAAGGGTTAAATGCTTCTGGTTTTTCATGA  
22651 AGCAGGGTTTAAATCCTTTTGACATCTTTAATAGTGTTTTTGGTGAGGGAT

22701 TTTCCTTTGGAATGGATGGTGATTACCATTTGATTTTCATTTTAAATCGT  
22751 TCTAAAAACGTCAACAACAAATTGTTGTTCCCTATAACCTTGATATTGC  
5 22801 TTTAGTAATTGAAATTAACCTTTTTGAAATGACTAATGGTTGCAACAAAA  
22851 CCATCAAATATGAAAGAAAAGTTTCATGTCATAGTTGTAATGGTTTTGGC  
22901 GCTGAAGGCGGGGAAAGTGGATTGGATCTTTGTAAGGATTGTAATGGCAA  
10 22951 TGGTTTTGTTATTAAAAACCAACGTTCTATCTTTGGAACCATTCAATCCC  
23001 AAGTCTTGTGTTCAACTTGCAATGGACAAGGAAAAACAAATTAAAGTTAAG  
23051 TGCAAACTTGTCGTTCTAACAAATACACTGTTACCAATCAAATTAAAGA  
23101 GATTAAATATTCCAGCAGGAATGTATAGTGGTGAAGCTTTAGTTGATGAAA  
15 23151 GTGGTGGTAATGAATTTAAAGGTCACTATGGAAAATTAATCATTCAAGTG  
23201 AATGTATTGGCAAGTAAGATTTTCAAACGTAGTGATAATAATGTTATTGC  
23251 CAATGTTTTAGTAGATCCAATGGTTGCTATAGTTGGTGGGGTAATTGAAC  
23301 TACCTACTCTTGAAGGGATTAAAGAATTTAATATTAGACCAGGCACTAAG  
20 23351 AGTGGCGAACAGATTGTTATTCTAACGGTGGGATTAAATTCTCAAAGAG  
23401 TTTTAAAGAAAAGCTGGGGACTTAATCATTATTATTAGTTATGCACGTC  
23451 CTTGTGAATACACTAECTTAGAATTGAAAAAATTACGTGAGTTTATCAAA  
25 23501 CCTAATCAAGAGGTTAAACAATTTTAAATACTTTAAAAAATGAATACAA  
23551 AACTTAATGTAAAGGTTATCTAAATGTTGGTGATAACCATCAACTTTAT  
23601 TACTGAACACAAGGAAATCCTAATGGTAAACCGGTTTTGTATATCCATGG  
23651 CGGACCTGGTTCTGGTACTGATGAAGGATGTTTAAAGTATTTTGATCTTG  
30 23701 AAACAACCTGGATTATTTTATTAGATCAAAGAGGTTGTGGTAAGAGTAAG  
23751 ACTAATGATATCTTTTATGAAAATAACACTGATAAATTAGTTAGTGATTT  
23801 TGAAATTTTACGTCAAAAATTAAACATTAAAACTGAACACTCTTTGGTG  
35 23851 GTAGTTGGGGTTCTGCACTTGCTTTAGTTTATGCAATTAACACCCACAA  
23901 GTAGTTGATAAGATCTTTTAAAGAGCACTTTTTTATAGCTAGAGAAAAAGA  
23951 CTGATCTGAAGCTTTAATGGGATTAGGAAAAATGTTTTATCCTTATGAAC  
24001 ACCAACGCTTTATGGATAGTATTCCTAAAGCTTATCAGAACAGTTATGAA  
40 24051 CAAATTGTAACTACTGTTATGATCAATTTCAAATGGTGATGAATCAAC  
24101 CAAAGAAAACTTGCTAAAGCTTGGGTGGATTGAGAATCAACATTACTTT  
24151 CACCTATTAAACAAAATTCATTCAACAGCaACAGACTTTAAATTAGTTGAA  
45 24201 AAACCTAGCTTTATTGGAATGTCACTATGCAGTTAATAAAAGTTTTTTGGA  
24251 TGAAAACCTTCATTCTAGATAACATTAGTGTTCTTAAAAATAAAAGTATTT  
24301 ATTTGGCTCATGGTAGATTTGATCTGATCTGTCTTTATATCAACCATTA  
24351 GCATTAAAAACAAGCATTCCCTGAATTACAACCTTTATGTAACCAATAATGC  
50 24401 TGGTCATAGTGGTAGTGCTAATAATTTAGCAACTATAAAACACCTTT  
24451 TAAAACTTACCTTTAATGAAGCGTTGTTATATTACAACCCCTATCTACT

24501 ACGCATCAGGTAAGCCACACATAGGTCATGCTTTTACCACTATTTTGGCG  
24551 GATGTAATTAAGCGTTTTAAATCCAAAACGGATATGAGGCTTTTTTGCT  
24601 TGTTGGCAGTGATGAACATGGCAATAAAATAGAAAGTAAAGCTAAAAGTT  
24651 TAAATTTAGATCCTAAAACATTGTGTGATATTAACGCTCAAGCTTTTAAG  
24701 TTAATGTGAAAGACCCTTAATATTAGTTTTGATCACTTTATTAGAACAAC  
24751 TGATGAAATCCATAAACAAGTTCAAAAAACATTTCAAGATTTATATG  
24801 ACAAAAACTAATTTATCAAAGTGAATGAAAAGGGGCATATTGTGTTGAG  
24851 TGTGAACAAAATTACTTTACTTTTAATAAACAACAATGTTATGTGAAAT  
24901 AGGTCATAATCTCAGTCTTGTCCAAGAACCTTGCTGATTTATTTCTTTT  
24951 CTTCTACTAAAAATTGAATTGAAACAACGATAGGAAAAAATCAACTTAAC  
25001 ATTATTCCTAAATCACGTGCTTCTGAATTAAAAAATAACTTTATAAACAA  
25051 TGGTTTAAACGATTTAGCATTAAACAAGAAAAATGTTACTTGAGGAATAA  
25101 AAGTTCCTTTTGATCCAAATCAAACAATCTATGTTTGGTTTGATGCATTG  
25151 TTTTCTTATATCACCAATTTAGGATTTAGAAATGGTGATCCTAATTTTAT  
25201 AAAGTGATGAAATAATGACAATAAAGAAAGAGAAGTTATCCATCTTATAT  
25251 CACGTGAAATCACCAGATTTCACTGCATCTATTGACCGATTTTCTACAC  
25301 TTACTTGATATTAAGTTACCAACCCAATTTTTATCACATGGCTGGATAGT  
25351 TGATGGTGAAGGGAGAAAGATGTCAAAATCTTTAAACAACGTTATCTCTC  
25401 CAGAACAATTAATTGATCAATTTGGTGTGATGGTACAAGATATTGTTTA  
25451 TTAAAAGAGATGCGTTTAGATAAAGATAATCGTTGTAGTGTTAGCATCTT  
25501 AAAAGAGATTTATAATGCTGATCTTGCCAATAGTTTTGGAAACCATGTTT  
25551 CACGTACTTTTGGCATGATTAAGAAAGTATCTAACCGGCAAATTAGAATAC  
25601 CAAATTATTACTGATAATGCACTTCAAAAAATAATGATTTTAATAGATGA  
25651 ATCAATCGTTCAATTTGATCATTACTTTAACAGTTATGAATTTTATAGAG  
25701 CGATTAATCTACTTTTAAAAATTGTTTTTGAATTAAGTAAATTAATTGAT  
25751 GATTTCAAACCATGAGAATTGTTTAAAAATCAGGAATTCTCACTTTTAAA  
25801 ACAACTACTTTTTACTTGTGTTAGGTGTGTGCAGGTATGCTATGTGTTGT  
25851 TAACACCTATCTTAGTAAATACTGCTTCAAAAGTTTTTCATTTATTTAAT  
25901 TTCGCTGATGATGCCTGTAGAAAAGATCAATTAAGAGATGCAACTTTATT  
25951 AAAAAAATTTATTATCTCTAATTCAATGGAAGTTTTATTTAAAGAGTAG  
26001 ATTAAGAAAAGTAGTATTAGAATTTTATTGATTTATGCAATTAGAGTACC  
26051 TCAATCTTATTTCTCAAGCTAAAGTTATTGCAGAAAAACAATTTAAAGCT  
26101 AACCCTTTTTCTTTTGAACAATTTGAAAAGAAGTAGTTAAACATTTCAA  
26151 GATTTCAAACAAGATGAACCAAGCTTAATTGGTCGTTTTTATCAAGATT  
26201 TTCTTGAGGATCCTAACTTTGTCTATTTAGGTGATAGAAAATGAAACTT  
26251 CGTGATTTTATGAAGTTTGATGAATGGAACAAGATATCACAATCTATGTT

26301 TGTTACAAAGGAGATTTTTGAAGAAGGTTATGAAGATCTTTCCAATAAAA  
26351 AAGTAGAACCTGAGGAAGGAGTTGGTGATTTTATTATGGGAAATGATGGT  
5 26401 GATGACAATGAACTGGCAGTGAAATAGTACAAGGTTTAATTAATGATT  
26451 ATTCAGTGAGGAAAATCAATAGTAGATATGCTTGTTAACTTTAAATTGAT  
26501 GCTTCAAAAAGCAAAGCTAGGTAAATATGCAATCCCTCACATTAACATCA  
10 26551 ATAATATGAATGGGCCAAAGCTGTTTAAACAGCAGCAAATCAAGCTAAT  
26601 AGCCCAATTATTGTTTCAGTATCTGAAGGTGCTTTAAAGTACATGTCTGG  
26651 TTATAGTGTGTTATCCCGCTTGTTAAGGGTTTAATTGAATCACTAAGTG  
26701 TTAAAGTACCAGTGACATTACATTTAGATCATGGTAGTTATGATGCATGT  
15 26751 ATCCAAGCATTACAGGCTGGATTTAGTTCAGTAATGTTTGATGGTTCACA  
26801 TTTACCATTGAAGAAAATTTCAATAAATCTAAAAAGTTAATAGAGATAG  
26851 CACAAAAAACAAATGCTTCTGTTGAAGTTGAGTTGGTACTATTGGTGGA  
26901 GAAGAAGATGGTGTTATAGGACAAGGTGAGTTAGCTAATGTTGATGAATG  
20 26951 TAAACAAATCGCTAGTTTAAACAGATGCTTTAGCAGCAGGAATTGGTA  
27001 ATATCCATGGTATCTATCCTAAGAATTGAAAAGGATTAACTTTCTTTG  
27051 ATTGAACAATATCAAAAATTACTAAGTTACCCCTTAGTTTACATGGTGG  
25 27101 CTCTGGAATCTTAGAAAATGATGTTAAAAAGCAATTAGTTTAGGGATT  
27151 GCAAACTAAATATTAATACTGAGTGTCAATTAGCATTTGCACATGAAAT  
27201 AGAAAATACATTGAATCAAATAAAGACTTGGATCTTAACAAAAAGGTTA  
27251 TGATCCTAGAAAACTTTTAAAGAACCTACTCAAGCAATTGTTGATACTT  
30 27301 GCTTGGAAGAGATTGATTTGTGTGGTTCTAGAAATAAAGCATAGATGTTA  
27351 AGTGCAGGGATAGTTGGTTTACCTAATGTTGGTAAGTCACTTTATTTAG  
27401 TGCTATTACTAATTTGCAAGTTGAAATAGCAAATATCCTTTTGCAACTA  
35 27451 TAGAACCTAATACTGGCATTGTTAATGTTAGTGATGAGAGATTAGATAAA  
27501 TTAGCTAGCTTAATTAATCCTGAAAAGATAGTTTATACAACCTTTCGTTT  
27551 TGTTGATATAGCAGGTCTTGTTAAAGGCGCCAGTCAAGGTCAAGGATTGG  
27601 GTAATCAATCTTAGCAAACATCCGTGAAGTGGATTAAATTTGTCATGTT  
40 27651 GTAAGATGTTTTCAAGATAAAAAAATTGTTTCATGTTAACAATACAATAGA  
27701 TCCTGTTTTGATTTTGAAATTATTGTTAATGAACTAATCCAAGCTGATT  
27751 TTGAATTAATAACAAACAGAATCGGCAAGCTTAAAGAAAAGCTGAATCA  
45 27801 GGTGATAAAATCGCTAAAGAAGAGTTTGTATTACTTGAAATTGTTTTAAA  
27851 TGGATTAAAAACAAGGTCAAATGCCCATTGAGACTCTAAGTGAAAGTGAAT  
27901 TGAAAACAATTAATCACTTAATCTATTAACAGCTAAACCTATTCTAATA  
27951 GTAGCCAATGTATCTGAGAATGACTTATTAAACCTTGATAATAATGAAGC  
50 28001 TTTAAAAAATTGAATGCTTTTCTTGATCAAAAAAGATTCCCAAGGCAA  
28051 TCACAGTTGTTCTTTAATTGAAAAAGAATTAAGCGGTTTGAAATTAGAA

28101 CAACGTCAATACTTTTTGGATGAACTTGGCTTAAAAAATTATTCAGGTTT  
28151 AAACCGAGTAATTCAAGCTGCATATCAAACCTTTAAACCTTTGGTCTTTTT  
28201 TTACTTTTGGTAAAAAAGAAGTTAGAGCATGAACATTTAAAAAGGGTTGA  
28251 AATGCTCCTCAGTGTGCTGGGCAAATTCATTCTGATTTTGAAAAAGGATT  
28301 TATTAAAGTTGAAGTAATTAGTTGAGATCAATTGTTTGCAATGAAATCTT  
28351 TACAAGAAGCTAAAAAACAAGGTTTGATAAGATTGGAAGGCAAAATTAC  
28401 TTAATAAAAGATGGTGATGTTTGTAACCTTTAAATTTAACGTCACCTAAAA  
28451 ATTAATCTATTTTCAAATGAGTTTTTTCAACATTTATTAATTAATAAAT  
28501 AATGCTTTTTAAAGTTGAATCTTAATTCATTTTTCAATACTTTTTTAGGC  
28551 TTCCTATTCTTTAATTAAATTAATACGCTTTTCTAAAAGTAAAAGTTAAG  
28601 AAAAGTACTTTTATTCAAACAAAAACGTTTTTATAATTTTAGAGATAGTT  
28651 GTGCCAAGTAAGTATTTATTACCGTTATAATCCAACATACAATTGTTG  
28701 TCAATACATAAAAAAGGCATTAGATTCATTGCTTTTACAGAATGAATATT  
28751 TTTTAAAAACACAAGTACTAATAGTTAACGATGGTTCACTAGACAATACT  
28801 AAGGAAGTTGTTAGTGACTATTTAATAAAGTACTCCAATATTAGTTATTT  
28851 TGAAAAAACTAATGGTAATTGGGGTAGTGTTATTAATGTTAAAAAA  
28901 ATAAATTAGCCTTAGGTCAATATATTACTGTTTTAGATAGCGATGATTAT  
28951 TTTTTAAAGATAGTTTTTAAAAAAGTGGCTCGTTTCTTTGGCCATGACAT  
29001 GATCATTGGCGCTTTTTATTGTTATATTAATGAAAATAAACTCGTTTTT  
29051 TAAAACCTTATTTCCGTAAGACTGGTGTTATTAAAGAACATACCAAATTA  
29101 AGAACCCCCCATTCCTCAACCTATTGCTAAATTTTACAGTAATAAACTTTT  
29151 CTATGAACTACATGATCTTAAGGAAAAGTTATCTTCCAGGATTGTTTAA  
29201 TGTATCACGATGCTATTAACAGAGTTGAAAGTGTTTTTTATTTGCGAGAG  
29251 CCTTTAGCAGTTTGGTTTTCTACAAGACCTGGCAATTCTACAACAACCTC  
29301 TTGAGAAAATCCAAATAAATTTAATGCTTGGTGTGAAATTCTCCAAAAAA  
29351 TGAATTTGTATGGAGCTGGGATAGTAATCTACATCTATACTATGCTACCT  
29401 GGATTTCTAAAACAACTAAAGAAAAAACAATAACTGAATTTGAACCA  
29451 TAAACCAGCTTACACTTGATTACCTAAACCTTTAGCGTTTATTTTTGGTG  
29501 GTTTAATGGCATTTAAAACCAGAAAATACATTAAATATCCTAAGTAATTT  
29551 ATGGCAGAAATGATAGAAGCAAAAAATCTTCGTAATGGGCAAACCATCTT  
29601 CGGTCCTAACAAAGAGATTTTATTAGTACTGGAAAATACATTTAACAAAA  
29651 CCGCAATGCGCCAGGGAATTGTTAAACTAAAGTTAAAAACTTAAGAACT  
29701 GGGGCTATTGTTTGGCTTGAATTTACTGGTGACAAATTAGAACAAGTAAT  
29751 TATTGATAAGAAAAAATGAATTTCTTATACAAAGATGGTAATAACTTTG  
29801 TTTTTATGGATCAAAAAGACTACAGTCAGATTGAGATTAATGAAAAAAA  
29851 TTAGAGTGGGAAAAAATTTCACTACTGAAGAAATTGAAGTTACTGTTAT

29901 TACTTATCAAGATGAAATTCTAGGAGTTAATTTACCTGATTAGTTCCTA  
29951 TTGAAGTTGAGTTTGCTGAAGATGCTATTCAGGGCAATACTGCTAACATG  
30001 GCAAGAAAAAAGCACGCCTTGTAAGTGGTTATGAACTTGATGTACCCCA  
30051 ATTTATTAATACTGGTGATAAGATTGTAATTGCCACTGTTGATGGCAATT  
30101 ACCGTGAAAGGTTTAACAAATAAATTAAGTAAACCCAAAGACGAATTGC  
30151 TGTAGTGGAATTTATCTTTTCTCTCCTCTTTTCTTACCTAAAGAAGCTG  
30201 AAGTTATTCAAGCAGATTTTTTAGAGTATGATACTAAAGAACGACAACTA  
30251 AATGAATGACAAAACTAATTGTTAAAGCATTAGTGAAAATATCTTCTC  
30301 TTTTCAAAAGAAAATTGAAGAACAACAATTGAAAAATCAATTAGAAATTC  
30351 AAATAAATACAATAAATATCAGGAAAAAGATTGATCTTTTAACTACT  
30401 GCAGTTGTTTTATGTGCACTTAGTGAACAAAAGGCACATAATACTGATAA  
30451 ACCACTTTTAATTAGTGAGGCATTGTTGATTATGGATCATTATCACAAG  
30501 GTGCTGAAAAAACAACACTCATGCTTTATTAGATAAGCTCTTGTAATGA  
30551 AACGTAAGTGAAGACAACACTATAATGTTTTTTTAGCTAATCTAGTTTTA  
30601 GTATTTGGCTTTGCTTTAAATATTTTGGTTGCAAAACAATCTTTAAATAA  
30651 CACAACGCCCCAGTTCAGGTTTTTGTGTGTAACCTTTTCTTGCGCTTG  
30701 TCATAGGTGCTGTTCTCTATTTTTTTTGATGTTAAGTGGTTTTTAATTGAC  
30751 TATCCATACAAGAAATTTCACTTTCAAAAAAATGAGCAATTGTTTATTT  
30801 ATCAGGGGTATTGTATTTTTTTTAAATGTTTTAATTGGAGTAGTTTTAC  
30851 TTGTTGTAATGGTTAATTACATTACTAACCATAATTCTTGAAAGGGAATAT  
30901 GAAAGATTATTTACAAATTCATTACCTTATTTATGATCAACAACAGGAAC  
30951 TAGTATTGTTTTAAGTCTTATTAGTATAGGAATGAGTAAACTGCACATT  
31001 TTTTTATTGATATAGAGATTTTGAAAGCCAAAAAGGAGAACCCTGAT  
31051 CCTAATAAACTGATAATAGAGCAGTTGTTATTAATCTTGATGAGAATAA  
31101 AAAGAATGAAAAAGaACAGTCCCCTCCTTCTGCAGAAATGACTAGTCTTT  
31151 AATTTCACTACCAAATAACCTTTTATGaACAAGCTCATTTAAAGTGTTAT  
31201 CTTTTAAAAAAGTGCACACAATAACTGTTGCAAATCCAAAGCACAACCA  
31251 GCACTTCTTGCTGTTATTAATTTATTTGCTACTGTTACTTTTGCTGTTGA  
31301 TCTGTTTTTCAGACATAACTAAATTTGGGTTTGGAAAAGAAGAATAGATCT  
31351 CATCTTTAGTGATAATACCATGTTTAAATAGAACATTGCGTGTGTCAAA  
31401 ATAGCAAAAAGATAAAGGTTATTTACTTTGAAATAATTAATTGTTTTAAG  
31451 CAGTTTTTCATCTTTATCTAAGTGTGTTGTAGCTCCTATTCCACCGGGAA  
31501 TATAAACTGCATCAAATCTGATAAGTTAATGGTGTGACAATATTGTGA  
31551 ACTTCAACAACACCATTACTAGCAGTTATCTTTTTTAATGAATGGTGATA  
31601 ACATGTTGTTTGTATTGTTTTAATGAACTAAATACAACCATTACATTAG  
31651 TATATTCAACATCATTCATCTCTGGATAGACAATAACAAGTATCTTTTTTC

31701 ATTTTATTTAGTACCAAATAAACGGTCCCCAGCATCACCAAGACCAGGGA  
31751 TTATGTATCTATTGTCAATTTAACTTTTCATCAATTGCTGCAAGAAATATA  
31801 TCAACATGAGGATGCATTTTTtCTACTTTATTAATTCCTTCAGGTGCTGC  
31851 TACTATAGCAATAACACTAATTTTGATAGGTTTATCTTCTTTAATAGATT  
31901 TAATAGCAGTTAACAATGTAGTTCAGTAGCAAGCATAGGATCAAGAATA  
31951 ATAACATGTGAATCAGAGATGTTTTTCAGGCATCTTTTTATAGTATGAAAT  
32001 TACACTGGTTGTTTGGGTTTGACGATAGATTCTTAAATGACCAACTCTGA  
32051 TTTTATCTGAATAGCGAACAATAGCATCAATCATTCCAAGTCCAGCACGC  
32101 ATAATAGGTACAAGAACAATGTCATTTTTTAATTTGTAGCCCTTTGTTTT  
32151 AGCAAAGGGAGTTTCAACTTCAACTGTTGCTAGTGGTAGCTGTTTAGTTG  
32201 CTTCAAAAAGAGTAATGAAGTGATTTGATTCAAGGCCATGCGAAACTGG  
32251 GAGGTTGTTGTATTTTTATCACGCAGTTTTGTCAATTCATTCAAGATTAA  
32301 AGCATGTTGAACTTTTTTTATCACGTTAGTTATCTTTAAATAAGTTTAA  
32351 CTAAAAATTAGTTGAAAAGTTTATGATCATCTTGATGTTCAAATTCATCA  
32401 AACAGTTGTAATTGTTCCATCGTTTCAACGTGTTTTTTAGTAATTTTGGT  
32451 TCTTTTTTTGAAATCATTTAAGGAAGCAAATGGTTTTTCATTTCTTGCTT  
32501 CTACAATTGAAGAAGCTACCGCTTCTCCCATTCCTGGAATAGTGATGAAA  
32551 GGCGCAATTAAAACACCATTATGTTCAACAAACATCCTTGCAATTAGAGTT  
32601 TTGAATAGAGATTTGTTGCAACTTTATATTGCGTGCCATCATTTCTAAAT  
32651 AAACCTCATAACTTGTTAAAAGCTCCGCTTCTTTGGTTTAACTTTTTTT  
32701 ATTCTGTAAAGCTTATTAAGTTCATCTAAACGGTTTTTAATAAATTCATA  
32751 CCCTTTTTCAAACCATTAATATCATGTTCCCTTTAGTTTGAACTTAATA  
32801 AACAAGCATAGTAACCTCAAAGGGTGATAAAGCTTAAATCAAGCAATTCTT  
32851 CAAGCCATTAAAACATAAGCTGCAGCATGTGCCTTAGGGAATAGATAATT  
32901 AATTTTTAAACAAGCATTAAATCCAATATTGTTCAACACCACAGTTTTGCA  
32951 TCAGGCTAACTTCTTTAGCATTTACTTTAATACCTTTTTCTTACTTTTTCC  
33001 ATGATTTCAAAGCATCTTTTGCTTGCAATCCCTTTATTAATTAGATAAAG  
33051 CATGATGTCATCTCTACAAGCAATTACATCTCTTAAAGTTAACCTATTGC  
33101 TTTTAATTAGTTTTTGTGCATTATCTGCTCACACGTTTTTACCATGGCTT  
33151 AATCCTGAAACTCTAATTAAGTCAGCAAAGTCTTTAGGTTTTGTCTGTTT  
33201 TAAAATTTTTCTAACAAATTTAGTCCCAAATTCAGGGATACCAACCGCTC  
33251 CTGTAACCTCATCAACAATGCCTGGTTTTAGGTTTAAATGGTTTGTGAA  
33301 GAAAACATCGAAATTAAGTTCTTATCAAAGTGAGGGATATTTGGGGATT  
33351 TATCTTAGTTAGATCAGCTAAGTGCTTTAACATTGTTGGATCATCTTGAC  
33401 CTAAGATATCAAGTTTTTAATATGGCATCACCTAATGCATCATATTCAAAA  
33451 TGGGTGGTCTTTCATTCACCTTCAACATCATCTGCTGGAAAACCACAGGG

33501 AGTAAATTCATAAACAGAATGATCACTAGGAAAGATCATAATCCCCCTG  
33551 GATGTTGCCCTGTTGTTCTCTTAATTCCTATAAGCTTTTGTTTAAATCTT  
5 33601 TCAATTTTCAGCAGTAGTTGCAAGATCAACACGTTTAATGATTTCAAAATA  
33651 GTTTCTAGCATAACCATAAGCAGTTTTTTTCAGCAACTGTTGCAATTGTTT  
33701 CTGCCCTGAAGGTGTTATTAACCTCCAAATAATTTTCTGACATAATCATGG  
33751 GCTTTAGCTTGATATTCGCTAGAAAAATTAAGATCGATATCAGGAATTTT  
10 33801 ATCACCAGAAAAACCCATAAAAGTAGCAAAAGGAATGTTATGACCATCAC  
33851 CTTTGAAACTTGCTTTTTTCATGGCATTTAGGACAATCACGAATCATCAAA  
33901 TCATATCCATCATCAACACTGTCACTAAGTTCAAAGTAATGACATTGTTT  
15 33951 ACAAAGATAATGAGCAGCTAATGGATTGATTTCTGATATACCAATTAAAT  
34001 TAGCAATTAAAGAAGAGCCTATAGAACCACGTGGACCTACAAAATAACCA  
34051 TCTTTAACAGATTGTTCTACTAATAGATGGGAAATTCAAAGACAATTCC  
34101 AAAACCATTACTAATGATTGCATTTAGTTCTTTTTCAATTCTTTCCTTAA  
20 34151 TAAGTTTAGGTAAATTTTTACCATACCTTTTTTCAGCTTGTTTTCAAGTT  
34201 TTATCAATTAATTTTTGGTTAGAATCTTGCATCACTGGTGGATAAAGCTT  
34251 GTTTTTAGTTGGTACTAATTCATTTAAGTCAAGTAGCTTCACTATCTTAT  
25 34301 TAGTGTTTTCAACGACTAATTTATAGGCAATATCTTCTCTAAAAAACTC  
34351 ATCTTTTTTAGCATCTCATCAGTGGTGTGAAGAAATACTTCAGGAACGGT  
34401 TTGTTCTTTTTCTTTATTGTTAAAGTGTCTATGTCATTTCCACCTAAGC  
34451 CCTTAGCACAACTATTGCCTTATAATATTCATTTTCCAAGGATGGATA  
30 34501 AAGTAAGCATCAGATGCAACAGCAACTAATTTCTTAAGTTTTGTTGCTGT  
34551 TTTGATACTAGTTTGATTGCATCATTAATAAGTTCTTTTTTCAGTCCCT  
34601 CACGTAGTGTATAACCAAGGTAAGCATTGGGTTGTGAAATAAGCACAAAG  
34651 TCAACTTTTTCAATTGCTTTTTCAAGTTCATTAATTGGTTTTGTTAATGC  
35 34701 AGCTTTAAAGATGTCACCCCTGAACAGGGTTTTCTGTTAATAAAAAAGATT  
34751 TTCTAAATTTAGCTAAGCTGCTAGCTAAAATAATGGTCTGTTAGCATTA  
34801 TGATCTGTTAATGCAATTGATAACATCTCATATAGGTTTTGAAAGCCCCG  
40 34851 TTGGTTTTTTACATAAACGATTGCTGTGTTTGAAATACCCTTTTCATCA  
34901 GATCAATTTGACACTTTTTATTAGGTTTTGATCTATCTCTGTTAAGGTA  
34951 TTAATACCCATTCTTTTAACTGCTTTTTAAAGTAAAAGAAAACTTTTTT  
45 35001 TAAAGCTTCTGTATCATATTGACACGGTGTAAATCTTTCATCATCAAAT  
35051 CAAGTTTTTAGTTTGAACAAATATTGCTTAAAGTATGGGATGAAAACAAG  
35101 GGATTCAATGCTCATGATAAACATAAGGTATCAATCAGTGGGTTTGTTAA  
35151 TGGTTTGATGTTGTATTTTTCAAATTGAGTTTGCAAAAAGGGTAAATCAA  
50 35201 AATTAATACCATTATGAGCTACCATAACACAATCATCTAGATAATTTCTT  
35251 ATCTTTTCTAAACCTTGCTGTTGATCAATACCGCCTTCAAGCATCTCATC



35301 AGTTATTTTGGTGATTTTCAGTGATTGTTTTTGGGATAGGTTTGTCAATTT  
35351 TTAAAAAGAATTGCTGATGATCTATCTCGCTGTTATTCTTAATTTTGCGT  
35401 GCTGAAAACCTCAATAACATCATCATACCTACCATGTAATCCAGTGGTTTT  
35451 AATATCAAAAATAACAAAGGTGGCATCACTTAACTTAGTGTTATCTGGGT  
35501 TGTGAACAATTTTGATGTGATCATCAGTTAAGTTGAATTCCAAACCATAG  
35551 ATAGCTTTTAAATCATATTTTTTTAGCCACTTCATAAAACTTGGGATAAAT  
35601 ATGGATATTATCTTTATCTGTAACAGTTATTGCTTTTCAACCTCTTTCTT  
35651 TAGCAAACCTGTGCATATTCTTCAATGTCAATTGATACCATCAAAGCAGTC  
35701 ATTTTAGTATGAAAACTAACTCCACTCGCTTTTGTTTTGATAAATCTAA  
35751 CCTTTTATAGTTATTAGGTATTTCAACAGGATTTATCTCTCTAACAATTC  
35801 CATATAAGATTTGAGTATTAGGGTCACGTTCTACTTGGATATGGGCTTTT  
35851 ATCCAATTGCCAATAGTAATTCCTTCAATCTTTTTTTTCATCAGTATAGGA  
35901 TCATTTCAAAATTAACGATCCACCTAATTGAAAATCAGTTACATAGATAT  
35951 TAAGTGTTTTTTTACCAGTTAACTTTTCATGGGTTTTTAATTCAAAGATT  
36001 TGCCCAATAATCTTGACATCATCGATCTGTTGGTTAATCTTGTGGATAGG  
36051 GATAAATCTGTGCAAATACCTTTGTTTCAAACCTGCTTATCATATTGAG  
36101 AAACAGTTACAGCTTTTACTTTTAATTTAGATTCATTTTTATCAATAGGA  
36151 TAAAGTGCAATGAAGTTAAAGTTTTTAAAACCAGCATTATTCATCCAAAA  
36201 AATGAAAGATTTACTTTTTTTGAACTAATCATTCAAGTTAATTCTTTGGTTT  
36251 GACATTGTGCTTTTAATTCGTCATTTTCATAACTAAGAAAATTGGGATTA  
36301 CTTAACTCTTGTTCAATGAGAATTTTGATTTCTTATCTTTTGAAAAGAA  
36351 ACTGTGAAAATAGTCTTTAATAATAGCTATCGTTACAGAAGAAAACTAT  
36401 TTTTGTATTTAAAGAATGGCTCATTCTCCTTAAAGGTAATGGTAAGTTTA  
36451 AAAGATTCATTATCAGCTTTTAAATCCCTCATTTAATTCATTAAATCCTTC  
36501 ATATAAGCATTTCAAATATCAATAGTTAAAGGGCGACTAATAGTTATTG  
36551 CAAATAGAAAAACCTTCTCTTCAATATATTTATTAAAGTAAATTGATTCA  
36601 ATCCTTTCAATTAAGCTGTTAAGCTCATTGTGGTCAAGGATATTGTTATC  
36651 TATCAAAAAATTGGAGAGTGCAAGAACCTTTTTATCTTTTTCATTCTCAA  
36701 GATTAAATACCATAAGCGTTTATTAAAAAATCAAATAAAAGATCGAAA  
36751 TTTATCAATAATTATTTTTAGTTTTAGCCACTTTTTTCGTAAAAAATAA  
36801 AAAAAAAGCAGTTTTTGCTATTTTAGACTAAAAGTGGTTATATACCAAA  
36851 ATTTAAACCTTCTTTTGGTTAGTTCTTACTAACAGTTTTAAATGTTACAC  
36901 AAGTTTTTCAAAGTGTGAATTTAAAAACTTCAAATAGTTGTTTATTCTGT  
36951 ATCTAATTAACCTTTAATCTTTCAATAATGAAAACAATTCATAAACTATT  
37001 TTTAGGTCTTTGTTTACCCGCAACATTAGGTCCTTTACTTGGAATTGTTG  
37051 TTACAAATACTGACCAAAGTATTAAGTTTACAAGCAAATCAAATTCGATT

37101 AATAAGAATAACCAAAATAAAGAGTTGGCTCTACTTAGAGATAATTTGAT  
37151 GAACGAAGCGAAAGTTGATGAACCACTTTCCTTTGAAAAACGGTTTGAAA  
5 37201 ACTTTAAAAATAAGTATAGTGATATACATAGCTTAAATAACAGTGTTTTT  
37251 TCACTTCATGACGTTTATGACTTATTAGGTGGATTAAACAATCATTGAC  
37301 AACATTTTTTGATGAAGTGATTGCCCAACAACAAAAGATCAAGGATGCAG  
37351 ATAAGATCTTTCCAAGTACTAAAGATAATCCACCTAAAGAAGAAAATCCT  
10 37401 AATGTTTTAGATACACTAGCTAACTACCAAGGAGCAGGATTTTTCCCTAG  
37451 TTTAGGTAAAAATGGTTTTAATTTACCTGAAGCAGTGTTCCAAAATTTCA  
37501 CTGATTTTAGGATTAATGACTACAAGATTAAAAATTTAATGTTGATCTT  
15 37551 GTTAGTGAAAATGACATTATTAAACATGATAAAGTTCGTTATGCTTTTGA  
37601 AGTTAAGTCAATATTGCTTTAGTTTTATCTATTAATAAGTCAAATGTTG  
37651 ATTTTGACTTTGATTTTCATTTTAAAGACTGATAATTTCTCAGACATTGAA  
37701 AACTTTAAATGAAATTTTCAACAGAAAACCTGCTTTACAATTTGTTTTTA  
20 37751 TACCAAGATCAATGTACATAAGTTAAGTTTCAATGGTAGTGATTCCACTT  
37801 ACATTGCCAATATCTTGTTACAAGATCAGTTCAACCTATTAGAAATTGAT  
37851 TTAAATAAATCTATTTATGCATTAGATCTTGAAAATGCTAAAGAACGCTT  
25 37901 TGATAAGGAATTTGTTCAACCTCTTTATCAAAAACGACGTGAAGCAAAGC  
37951 TTGCTTGAGAAGAAGAACAGAGACGCATTGCTGAAGAACAACGTAGACAA  
38001 GAAGAGGAGAGAGCTAGAATCTTAAAAGAGTTAAAAGAAAAGCTGAGAA  
38051 AGATAAAAGAGTTAAAGAAGCACAAAACAACCTTCAAAAAGCACTTGGTA  
30 38101 ACTTAGATACTTTCTTTAACTTCTTTAGCAGTGGTCAAGATAGAGTTTTA  
38151 CTTGGTTTTGATCCAAATAAATACAATGTGCAAACTCGTGAAGGTTTGTT  
38201 TAAAGCATTACAAATTTCTATTCTAACTTCAAACTTGAACATTCTATA  
38251 TCTCCTTGTTGGGGTGAAAAGAAGGTAGTGTTAACTGTTGAAAAACCT  
35 38301 ATCTGAAATGCCTTGAGAGATGATAAAGCATTTCAATATGCTTTTGTTTT  
38351 AGGTCCAAATACTTCTGAACAACAACCTTGGTAGAGTAACCTACCTGGTT  
38401 ATGGTTATGAAGGAATTAGAATGAGTGATTGGTTGAGGTGAGCATTGGGT  
40 38451 TACTATACTAGTTTCACTTTAAGTCCACCTAAAAATGTTGAAGCTAATCT  
38501 TATAGGTGATGCTAATGATAAAAAACACATTTGAATCTCACCTCATACTT  
38551 TCAAAATAAACAGAGAGTATGGTGATGGTGAAAGATTCAAAGGTAAAGCA  
45 38601 TATCGTTTTAACTATCAATAAGTTTTGAACTAGAAGGTCATTTAACTGC  
38651 CCACTGATGAACAATTGCCTTTAGAGGTAGTATTCCTGGAAGCTGAAGTG  
38701 GTAAGTTAAGAGTTACCCATGAGTTTGATGGTGATGTGCCTTACTATAGA  
38751 TTACATACAACTCCACCACAATATCGTTTAACTGATGATATGAAATTATT  
50 38801 GTTTGTTCCGCACAGTATCCAAAGGGTAACTGCAGTTGGTAATGAAAGCA  
38851 TTAATGGTCTTCTCAGATCACAAAACCTTCATAACTTGAACGTCAATCA

38901 TATGAAGCGACTGCTCCTATTGATTTAATATCATATATGCTTTATGCAAT  
38951 TAGTGATAAAAAACACCTCAAAAATAAGTTTTATATCATTAACGTTTAA  
39001 ATAAATATTATTGCTAAGATTACTTTAACTTGTTAGCAAACTTTAATCA  
39051 TTTTTTAGCTAAATTAAACAACCAGTTAATTAGTAAACAGTTCCAGAATT  
39101 AAAATCAAATATTAGTTAGTTTTTATTTTGTATTTTCAAATTCTACTCA  
39151 ATTAGGATGATGGTTTCTTGCTGAATTGATAGGAACATTTATCCTAATTA  
39201 TCTTTGGTAATGGTGCAGTTGCCCAAGTTAATTTAAAGAAGATGGCTACA  
39251 AGTGAAACAAAAGCCAAGTTTTTAACAGTTGCACTTACTTGAGGAATAGG  
39301 TGTTTTATTGGTGTTTTAACTGCTAATGCTATCTTTAAGGGTAGTGGTC  
39351 ATTTAAACCTGCTATATCATTTATTTATGCAATTAATGGCAGTATCAAA  
39401 TCACCTACTGCATTAATATGACCTGGTTTTGTAAATGGGATTTTAGCTCA  
39451 ATTCTTAGGTGCAATGATAGCTCAAACAACACTTAACTTTTATTTTGAA  
39501 AACAACTATCATCAACCGATCCACAAACAGTTCTAGCAATGCATTGTACA  
39551 AGTCCTAGTGTATTTAACATTACTAGGAATTTTCTAACTGAATTTATTGC  
39601 AACTTTAATATTGATAGGTGGAGTTGTTGCTGCTAGTCACTTTCTTCATA  
39651 ACAACCCAACTCTGTTCCCTCCTGGATTTATGGGGCTTTGATTGGTTGCT  
39701 GGGATTATTATTGCTTTTGGTGGCGCTACAGGCTCCGCAATTAATCCTGC  
39751 AAGGGATTTGGGAAGTAAATTTGTGTTTCAATTAACCCAATTAATAATA  
39801 AGGATGCGAATTGAAAGTACAGCTGAATTCAGTAATTGCTCCTTTATCT  
39851 GCAGGATTAGTTTTATCAATAATTATTGGGTTTTCCCTGCACCTGTTCT  
39901 TTAAAGTTTTTGGTTTTAACAGTAACGTGCTTTTATAGTTAAAAATGAGTG  
39951 GTGCAGTTTGCACTAGCTTCATAAGCTTCTGCATCACCAATTAAGACAA  
40001 GGTTATCATTAGTATTTTTATTTACTAGTCTTTGGGTTCTGTTGTGCTAAA  
40051 CTACCACAAACATTGCAAATAGCATCAAGTTTATTAACATACATCAGCTAT  
40101 TGCTAAAAGTTGGGGAATACAACCAAAGGCTCAGCTCTAAAATCAGTAT  
40151 CAAGCCCAGAAATAATTACATTTGTTTCTATCTCATTGAGAGTTGTAACA  
40201 ACTTCTATAATCTCATTTGAAAAGAATTGTGCTTCATCAATGGCAACAAT  
40251 TTGATAGTTTTTATCAACTAAGTGATCATAGATCTCAAAGGAGAATTAA  
40301 TAGTTATTGCTTGATCATATTCACCGTTGCGTGATTTGACAATATTAGTT  
40351 TGTCTAGTATCAATTATTGGTTTGAAGATAACAACCTGAAATTTTGCTAT  
40401 CTTTCACCGTTTTATTTTGTGAAGTAATTTCTCTGTTTTTCCAGAAAACA  
40451 TTGGGCCACAAATAACTTCAGTTCAGCCCTTTTTGGTTTGAAAAGATGGT  
40501 TGATATTTACCCATATAATTTGAAATTATAATTAATGACACATGAACTT  
40551 CTTGCAAAAACCAAGGGGAGTTAAAGATTGGTTTGGTGATGAATTAGTTT  
40601 ATTTTAATTGGATTGTTAAAAAATAAGATCTTTAGCATTTAATTGGGGT  
40651 TTTAGTGAAGTTAAACTCCGTTGTTTGAATGCACAACTTTTTCAAAG

40701 ATCTAATGCTAATGCTGATATTGTTCAAAAAGAACTATACCAGTTTTTTG  
40751 ATAAATCTCAAAGAGAATTAGCTTTAAGACCTGAAGCTACTACACCAATA  
5 40801 GTAAGACTTGCTTGTGAAAACAAATTAATGCAAGAAGCAAATTTTCCCTT  
40851 AAAGTTATTTTGCATTGGTTCAATGTATCGTTATGAACGTCCACAAAACA  
40901 ATAGGTTTCGTGAACATTGGCAATTTAGTTGCGAAGTATTGGTTTTTCC  
40951 AACCTGTTTATCTTTTTAGATACACTTTTGTGTTGCTAACTCTTGCTTGA  
10 41001 AGCACTTGGAATTACTGGATATGTGCTTAAATTAATAATCTTGCTAACT  
41051 TTGAAACACTTAGTAAGTGAAATAAAGCCCTAAAAGATTATTTAACTCCA  
41101 TATAAATTAGAACTAACTGAGCTTTCTCAAAAAAGATTAGAAAAAATCC  
41151 TTTGAGAATTTTAGATGACAAGATAGATCAAAAAAATCATTGTGTTAAAA  
15 41201 ATGCTCCTAAATTAAGTATTTTTAGATGCAAGTGCAAAACAAGATTCA  
41251 GAATTGTTAAAAACACAACATAAAAAACACAATATTAGTTTTGAATGAAC  
41301 AGACAATCTAGTTAGAGGATTGGATTACTATACTGGATTTGTGTTTGAAT  
20 41351 ATGTAAAAAATCAAGACACAATTTTAGCAGGTGGAGTTTATGATAACTTA  
41401 GTTGAAGAATTAAGTAGTAATCCAACCTCCCGCATTAGGTTTTGCTGTGG  
41451 AATTGAACGGTTAATTAAGTGTGTTAGAAATTGATAAAAAAGCATTATTT  
25 41501 TGAATACTAAACCAAAGCAGATGTTAGTAATTTGCTTATTTGAAGAAGCG  
41551 CTTGAAGAATTGGTTTGACTAGCTAAATTATGAAGGGAATATAACCAAGT  
41601 AACTATTTATCCTAAGGTTATTAAAGTTGATAATGGGATTAGATTAGCAA  
41651 ATCGCTTGGGTTATACTTTTATTGGCATTGTTGGAAAACTGATTTTGAC  
30 41701 AAAAAAGCTATTACAATCAAAAACCTTAGTATCTAAACAACAGACCATTTA  
41751 CACTTGAAATGAACCTTGAGAACGAAATGTGTTTTAACCAACGAATTTTA  
41801 ATTGGCTCAATTTCACTGAACAACCTCAATAAAACAATAGTTATTATTGG  
35 41851 GTGAATTAAACGGATTAAAAAGTTAGGTGAAATTAACCTTATTATCGTTG  
41901 GTGATAAATCAGGAACCTATCCAAGTAACCTGCAAAGATAAAGAACAGATT  
41951 CAACAACCTTACAAGAGAAGACATAGTTATTGTTAAAGCCAAATTACAACG  
42001 CTTAGATAGTGTTAGATTTGAACTGATAAATCCAACCTATTAACTTTTTT  
40 42051 CAAAGTCAAAAACCTCCTCCTTAATTATTGAAGATGAACTGATGCTTTA  
42101 GAAGAAGTTAGGTTAAATACCGTTACCTTGATCTGAGAAGACGTTTGAT  
42151 GCAAAAACGATTGTTATTGCGTCATCAATTTATATTAGCAATTCGTAACCT  
42201 GATTTAACCAGCAGGGTTTTATTGAAATAGAAACACCTACCTTATCCAAA  
45 42251 TCAACTCCTGAGGGAGCACAAAGACTTTTGTTCCTGCAAGAATTAGAAA  
42301 AGATTGTTTTTATGCTTTAGTTCAAAGTCCACAAATCTATAAGCAGCTCT  
42351 TAATGATTGCAGGAGTTGAAAAATATTTTCAAATTGCAAGGGTCTATCGT  
50 42401 GATGAAGATAGCAGAAAAGATCGTCAACCAGAACACACACAAATTGATTT  
42451 CGAGATCTCTTTTTGTAACCAAAAAATGATTATGAATCTAGTTGAAAAAC

42501 TCTTTTTTAGTGTTTTCTTAGATGTTTTTCAAATCAAAATAAAAAGACT  
42551 TTTCTGTTTTTAAATTTTCAGAACTTTTTGAAAGATTGAGTAGCGATAA  
42601 ACCAGATTACGTTATGGTTTTGAAATAAAAGATTCACCTCGCTTTTTC  
42651 AAGATCATCAGAATCAGTTCCTAAATTAATTGAAGCAAAAGGCATTATT  
42701 GGTGGTATTGAACTTACTAATATTGAGTTAAGTACAGACAAAATTAAAGC  
42751 ATTAAGAAAAATTGCTAAGGACCATGATGTGAGTTTAGAAGTTCATAATA  
42801 AAAATAATTCAACATTA AAAACTTCAATTAATGTGATGAAAAAACT  
42851 CTTCTGTTAGTAGCAAATAAATCTAAAAAGAAGGCATGAAGTCTTTAGG  
42901 AGCAATTAGAAATGAGTTGAAATACCACTTGGATATTGTCAAACCTAACC  
42951 AATACAGCTTTTGTGAGTTGTTGATTTCCCTCTCTATGATTTTGATGAG  
43001 AAAACAAATCAGTGAATATCAAATCACAACATCTTTCAAACCTAAACA  
43051 AGAATGAATTGATAATTTTGAATCAAATAAAAACGAAGCATTAGCGAAC  
43101 AGTTTGATCTGTTTTAAATGGTTTTGAAATTGGTAGTGGTTCAATAAGA  
43151 ATTAATGATCCAATTGTTCAAAAAAGACTAATGAATTCTTTGAACATTGA  
43201 CCCAAATAAGTTTGCTTTTCTTCTAGAAGCTTATCAATATGGTGCTCCTG  
43251 TTCATGGTGAATGGGACTAGGTATTGATCGTTTAATGATGATTCTTAAT  
43301 CAACTGATAACATCAGAGAAGTAATCGCTTTTCCTAAGAATAATCATGG  
43351 TATTGAAGTCCATACAAACGCTCCTGATAAAATTGACAAAGAGGAGGTTA  
43401 AATGATGGATAAAAAGAACTAGTGAAATAGAGTTTCACTTAAAGAATCTTT  
43451 TGGCTTGATGCATATAAACTTTCACACCGTTTAATGTATCCACAAGAT  
43501 ACACAAAACCTTTATAGTATGTTAACTGCAAGAGGTGTTTATGGTGATT  
43551 TAAGGAGTTTGTGTTGAAACCATGATTTTGCTAAAGAGATCCTTTTGAATG  
43601 TATTTAATGGTTTTGTAAACAGTGTAATTGAAGTTAAAAAAAACAAATTG  
43651 CTAGCTGCAGCATTGACAGATAAATTAGTTAGTGTTTTTAATGATCATGA  
43701 ATTGGCTAATGAATTCACACAACACATCTGTCAATTAGCTAGTTTCTTAG  
43751 AGAAAAATAAAAAAATGCCGTTAGTTGCAAAGATCCATGAAAGTGATCAA  
43801 TCATTACCATTTAGAACTCCTTTAATAACTATAGAAGGAGTTGAAAAATAT  
43851 TCCAAACAACCTTTGTATGGTTAGTTAATTACTTTGAACTGTACTTCTAG  
43901 AAAACATTTGGTTGTTTCAAACCTGCTTCTACAGTTGCTAAAAGAATTAAA  
43951 TCTTTACTTGAAAAATATGCTAAAGAAACCGCAGATGAAACAAGTTTTAT  
44001 TAATTTTCAATGCCACGACTTTAGTATGCGGGGCATGAGTAGTTTGCAA  
44051 GTGCTTTGTATGTTGCTAGAGCACACTTGCAATACTTTACTGGAAGTGAC  
44101 ACGATCTTAGGTGGGGATAATTCTCGTTCAATTTTAGCTTCTGAACATTC  
44151 AGTGATGTGCGCAGATGGTAGTAAACATGAATTGAAAACTTTTCAACGTT  
44201 TATTGGAAAAGTTTAAAGATAAAAAACTTTCTTTAGTGATTGATTCTTAT  
44251 GACATGTGAAATGTCCTTGATAACATTATTCCAAGGTTAAAAACTTAAT

44301 CTTAATGCGTGGTGCTACGCTTTATTTGCGTGCTGATTCTGGTAATTATC  
44351 AAACCTCTTATTTGCAATCCTAATTACAAAAAGCAAGATAAAAGTACATGA  
5 44401 GCAATGATCGATTACTTAGATCATCATTTTAGTTCAACTATAAATAAAAA  
44451 AGGTTATAAGGTTTTAAACAAGAAAATTGGCATTATTTATGGTGATGGA  
44501 TCACCTATCAAAAGATAGAATGGATCTTAAATTGTTTAAAAAACCATGGT  
10 44551 TATTGTtCTTCAAACATTATTTTTGGAGTTGGTAGTAGCACTTATCAAAA  
44601 TTTAAACCGTGATACTTTAGGTTTTGTATACAAATTGACTGCTATTAAAA  
44651 GAAATAATAGATGGATAGGCGTTAAAAAACTCCCATAACTGATCTATCT  
44701 AAAAGTTCAAAAGGCGGTAGATATAAAACAAAGCGATTAATTACAGTTTA  
15 44751 TTAATCAATTTCTTTCCATTTTAAAGCACGTTCAACTGCTTTATGTCAAC  
44801 TGTTAATTTTGGTTTTTCTTATGTTTGGGTCCATAGTGCTTTTGAACTTT  
44851 TTATCAAGAGTAGTGAGTTTTTCAAGTTGATGAATGTCTTTTCAAAATCC  
44901 ACAAGCAAAGTCCAGCTAAAAAACAAACCAACTGCAGTGGTTTCTTTAT  
20 44951 TTTTAGGGATAGAAACAATTACATCTGCAATATCAGCTTGAAACTGCATT  
45001 AAATAGTTTGATTTAACAATCCCCCATCAGCTTTAATGCTAGTAATCTT  
45051 ATAGCCTAGATCACTTGCCATTGCATTTAATAAATCATTAGTTTGAAAAG  
25 45101 CAATTGACTCTAAGCTAGCTTTTACTATGTGCTCTCTTTTAGTGCTTGCT  
45151 TCAATTCCCTAAGATAATACCCCTAGCACTAGCATCTCATCAAGGAGCTCC  
45201 AAGTCCACTGAAAGCTGGTACAAAAACTAGGTTTTGTTCATTTTCTTTTG  
45251 CAAGTTCTGCATAAAAATCACTTTTCTTTTCTGAATAGATAATTTTAAAT  
30 45301 GCATCCCTTAACCATTTTATAGCCGCACCCGCTACAAACACACTACCTTC  
45351 CAATGCATATACAGGTGGATGATTTTCTAGTTGCCATGCTACTGTTGTGA  
45401 GCAGATTGTGCTTTGAGAGTGTGGTTTTATCACCAATGTTTCATGAGTACA  
35 45451 AAACATCCAGTACCATAGGTATTTTTTACCATTCCAGGTTCCAGTACAGAG  
45501 TTGACCAAACAAAGCTGCTTGCTGGTCTCCTAAAAGTCTCTAATTGGTA  
45551 CAATACCTTTAGCATTACTAGATCAGTGATTAGTTTCAATATCACCAAAG  
45601 TAAGCATTGGAACCTCAGAACTTTAGGTAAGATTGAAACTGGTACTTCAAA  
40 45651 TAAATCACATAACTCTTTGGATCACTCCATTTTGACAATGTCAAATAAAA  
45701 GAGTTCTTGAAGCATTTGAAACATCTGTAACATGCATTTTCCATTAGTT  
45751 AGTTTTTCAGATTAATCAGCTATCAATGGTGCCAAATAACAACCTTTTTTG  
45 45801 CTCCATTAGTTTCTTTGCTAAAGGAACATTTTTTAAGATTCAAGCTATCT  
45851 TAGTAGCACTAAAAATAGGGGTTAATAGGTAATCCAGTTTTTTGTTTTACT  
45901 TTGGTTTGGATTAACTTATCCTCATTGAATTTTTGACATAGTGCTGCAGT  
45951 TCTTTGATCCTGTCAAACGATGGCATTATAAACAGGCAAACCATTTTCTT  
50 46001 TATTTCAATAAACTATTGTTTCTCTTTGATTGGTAATACCAACTGCAATC  
46051 ACTTCATGAGATTGATTGTGCTTTATTTTTAGCACTTTGCATGGTAGC

46101 TAGTTGGGCTGATCAAATTTCTAGTGGATCTTGTTCAACTCAACCACTAT  
46151 TAGGAAAAAAGTGTTAAATTCGTTTTGTGCTATTGCTATTTGGTTAAGA  
5 46201 TTGTGATCAAAAACAATTGATCGACAAGAACTAGTACCTTCATCTAAGGC  
46251 AATAATGTATTGTTTTTTTAGATCCATGATAAGTTGTAATTAGGATTTCA  
46301 ATTTATCTTCTTTTTTAACTTTAAATTAAGGAGTTCAACTGCTCTCTTAG  
10 46351 CAATAGCAGGACTTGATGTTAAACCAGGGGATTTTCATGCCACCAAGGATG  
46401 ATAAAGTTAGGATTGCTTTTTGCTGTTCTAATAACAAAGTCATTTGTTTC  
46451 AATATCAATAGCTCTTGAACCTGCAAACTATAAATACTATTTTCAAATT  
46501 GCAATGAAGGAACCATTTTTTACCAATAGTTTAAATTTGGTTAATTGAA  
15 46551 TCTAAATCTATGGAACGAGTTTTGTTTTTTTCAATTCCTCAACTGCATT  
46601 AGGTCCACAAGGATATTACCATCTAACATCTCAGCAACAACCTACTCCCT  
46651 TACCATGGATAGTAGGTACCATAAAAATAATTGTGTTAATCTTAAGGTTG  
20 46701 TTTTGATTTTTTAAACTAGATATTGTCCTTTTCTTGTTGTTTGTAA  
46751 ATTATCAACTTGTTAGTTTCTGCTAGTCAATCTGCATAATGACCAGCTG  
46801 CATCAATTAACCTTTTTGGTTTTAAATTGTGGTGTGTTTCATTGTTAATA  
46851 AAAACTAAAAATCATCATCAGAATCTATTTCAATTTTTGTAACTTTTT  
25 46901 ATTTGAGTAGATGGCAACATTGTTTTGTAACTAGCAAGGGCTAAACACT  
46951 TGGTTGCAATTAAAGGGTCAATTAGTCAACTACCTTCAACTTTTAAACTA  
47001 GCTACTACATTTGGATTGATAAACGGTTCCTGCAATAAAGTTTGTTGTTG  
30 47051 ATCTAATATTTGAATGTTTTCAACAGGAATTGAGTTTTTAATCCCTTTT  
47101 CTTTTAACAAATTTAATTGAAGTTTTTCTTCATTGTTGAAAGCAACAATT  
47151 AAAGTAGCAATTTTTTCTTGGAAGATTAGTTTTTTAAATCAATCCTC  
47201 AATTGAGATTTTTCTCCCTAAGATGTTGTATTGTCAGTTAGCTTATTAG  
35 47251 GATTAGGATCAATTCCTGAATGGATTACACCACTGTTAGCCTGCGAAGTT  
47301 TCACAACCCAAAAAGCATTTTTTTCTAAAAGTGCAACTTTTAATTTATA  
47351 TTGGCTGAGTTCATATGCACAACTAGTACCGATGACCCCCACCCACAA  
47401 TTAAACGTCAATTGTTTGCATTAATTAATCTTCTAGTATTTAGTTAGTT  
40 47451 ATTTTGCAAAAAAGGATTAGTTTTATAGTTGTGATTTACTTTTTGGTATC  
47501 TCTATAAAAAGTAGTATCAAACATTTTTTTATCTTTTGATTTCTTTTAC  
47551 TAAAAATAATTAGCTAAAATACCGTCATATATGGGAAAGCTATTATTTGG  
45 47601 TAAGTTAGTTTTTAAAAAGAGCTTGTTTTTACTGAGTGGTATGAGCAGTT  
47651 TAGCAGTTTTTTTAACTGCATGTGGGGCTACCAAAATATTTGATTCCTCT  
47701 GTACAGCTATTAGTGTGAGATAACTTTTCCACACTTGCTGATAAATCATT  
47751 TTCACAAATGTCCTATGAAGGAATCAGGAGCTTTTTTAAAAAAGTAAGG  
50 47801 GTGTTGATTTACCTGAAGCAGATAGTTCACAATTACAAGAAGGCAATGGC  
47851 TTGTGAAAACGTCTGGTTTTACATTAAGTGATAGAATTGCTACTTTTAA

47901 TAACATCAAAAATGATGGCTCTGATGTTATTGTTGCAACAGGTTTTAAACC  
47951 AACAGAATCACTTCAAGCAATTACTTCTGATGACATTAGGTTTCAAAGT  
5 48001 GATAAAGAAAGCTTAGCTAAAACAGGTTTTATTTTTGTTGATGGAGCTAT  
48051 TGAAAAGGAGTTTTAATAAAAGAAATGGTGTTCCTCAATTTAAGTCAACTC  
48101 CTACCAATATCTCATCAGTTGCTTTTAGAAGTGATGATGGTTCTTTTTTA  
10 48151 ACTGGAGTTGCTACTGCAGTTTACTTAAATCTTAACCAAGAATATTTCTT  
48201 TGATAAAAGTGGTTGGTCAACTAATAGTAGTAATAATAACGAACTAACTG  
48251 TAAGTGGTTTTGTAGGTATTGCTCTACCTTCAACGCTTCTTTTCTAAAT  
48301 GGTTTTCGACTAGGTATTGCTTATTTTAATGAAGTGATTTATAAACATTT  
15 48351 AAGCGATGCACAAGATTCTCTGCACAAGTGACCCTTCTAAACAACTG  
48401 TTTTAAACAACCTTCAAGTTGCAAATGGTGAAAAAGGATTAAAAAGATT  
48451 AAATGGATTTACCAAAACAAGGAAGTGATGGAGAACTATAAACATTCA  
48501 AGATCACCAATCAGGTTCTTTTTCAGATACTGAACCTAGAGCAATAACAA  
20 48551 TAGCTAATAATTTAATTGATAAAGGAGTTAATGCTATCATTCCTATTGCT  
48601 GGACCACAAACGAATTTAGTGGTTACTCAAATTGCTAGAAGACAAGCCCA  
48651 TACTGCAGTTATTGGCGTTGATAGTGCACAGGAATTGCTAGATATTAATA  
25 48701 TTGATGCTCCAAATAAAGATAAGTTAAAAATGGGGAATAAAAAGATTATT  
48751 CCCTTCTCTTCTATTAAGGCTTTGGATGTTGCTGTTGAAAGTATCTTATC  
48801 AACATTAGAAAAAGGTTCCAGCCAAAATGGTTATCAAGGCTTTGGATATA  
48851 ACAACATAGGTACAGTGAAAAACAACCTCTGTTGGGGTTAGTGAAGCAGGT  
30 48901 TATGAATTTTTAATAGATCCTGTTTTTTGAAAAAATACTAGTTCAATGCA  
48951 AGCTATGTCTTTATCAGCAAGTCTAAAAGCTAATGCAGCATCTTCATCAG  
49001 ATAATAAGAAAAAATTATCAGAAGTTGCTACTAAGAAAAATGAAAACGGT  
35 49051 TCGACAAAAAATGGTAGTAATGACATCATTGACAAATATGCCAACTCTT  
49101 AACAAAATCTAGTTCTTCAACTAGTATGAGAAACGGTAGTTCAGATAGCA  
49151 ATCAACAGAATTTTAAACAACAGATAATGATGGTGATTGAACTATTGTT  
49201 GGTGATGAATTAGGTAAATATAAGTCTAGTGAAGTGCCTATTTTTACAGG  
40 49251 TAGTTCTTCATACCCAACTTTTCAAAGTGAAGCACAAAATGTTTTAGATG  
49301 GTGGAGCGAATGTTGCTTCAACACAAGGCTTTAAATGAAGCTTTAAACAA  
49351 ATTTAGAATTTTGATTACTTAAAGATATGAAAAAATTTCAAGCAGTTATT  
45 49401 AAAGACCCAGTGGGAATTACGCACGTCCTGCTTCTATCCTTGCAAGTGA  
49451 GGCTAGTAAGTTTAAATCTGAACCTAAACTGGTAGCTCCAAGTGGTGTG  
49501 AAGGTAATATTAAATCAATTATTAACCTAATGTCTTTAGGAATTAGACAT  
50 49551 AATGACAACATTACTATCAAAGCAGATGGAGCTGATGAAGAAGAAGCTTT  
49601 AGCAGCTATTAAAGCTTGTCTTGAAAAAATAAAGTTATCTAACTTAGCA  
49651 TATTTTAATCAATTAAATCTGTTTATTTTTTAATAGTAAAAACACAATTT



49701 AACCTTGTTTCTATTTAACAAAATTGGTTTGAAAAAGGCTATCAATTTTG  
49751 CTGTAAAAAATTAAGATATTTTTATCAAAAATTAGCATAAAAAATTGTT  
49801 ATACTAATTAACGTTTTTTTATTGAAAATTAAGTATTTAAATTGAACGaAC  
49851 ATTCCTTAATTGAAATTGAAGGTTTGAACAAGACCTTTGATGATGGTTAT  
49901 GTTTCTATAAGAGACATTAGCCTAAATATTA AAAAAGGCGAATTTATTAC  
49951 TATTTTAGGCCCTTCTGGTTGTGGTAAAACTACCCTGTTGAGGTTATTAG  
50001 CTGGATTGAAGATCCTACTTATGGCAAGATCAAAGTTAATGGTATTGAC  
50051 ATTAAAGACATGGCAATCCATAAGCGTCCTTTTGCACAGTTTTTCAAGA  
50101 CTATGCTTTATTTTCCCATCTAACTGTTTATAAAAAACATTGCTTATGGTC  
50151 TGAAGGTAATGTGAACAAAGTTAGATGAAATTCCAAAACCTGTAAGTGAT  
50201 TATCAAAAGCAACTTGCTCTTAAGCATTAAAGCTAGAAAGAAAAATAGA  
50251 GCAGTTACAAAAAACAATTCTAATGCTCAAAGAATAAAGAAATTAAAGG  
50301 AAAAATTACAAAAACTTTTAGAAATTAACAAACAAAAAGTTATTGAGTTT  
50351 GAAATAAAGAAAACTACGTAGAGAAGATATTTACAAGAATTAGAGCA  
50401 ATTAACAAAAGAATGGGATCTACTTTCTCAAAGAACTAAAAGAAGTTG  
50451 AACAACAAAAACAAGCAATTGATAAAAGTTTTGAAAAAGTAGAGAATAAA  
50501 TACAAAAAAGATCCTTGGTTTTTTCAACACAGTGAAATACGTTTAAAAACA  
50551 ATATCAGAAGAAAAAACTGAGTTGAAAGCTGATATTAAAGCAACAAAGA  
50601 ACAAAGAACAAATCCAAAAATTAATAAGAACTTCAAACCTTAAAAACA  
50651 AAATACGCTAATAAAAAAGCAATTGACAAAGAGTATGACAAATTAGTTGT  
50701 AGCTTACAATAAGAAAGACTATTGAACTTCTTATTGAGAAACATACACAC  
50751 TTCAACAAAAAGAAGCTTTTGAAAAACGTTATCTTTCAAGAAAACTAACT  
50801 AAAGCTGAACAAAATAAAAAAGTTAGTGATGTTATTGAAATGGTTGGTTT  
50851 AAAAGGTAAAGAAGATCGTTTGCCTGATGAATTATCAGGGGGAATGAAAC  
50901 AAAGAGTTGCTTTAGCACGTTCTTTAGTAGTAGAACCTGAAATCTTTTA  
50951 TTAGATGAACCATTATCTGCACTTGATGCAAAGGTTAGAAAGAATTTACA  
51001 AAAAGAATTACAACAGATTCATAAAAAAAGTGGATTGACTTTTATCTTAG  
51051 TAACTCATGATCAAGAAGAGGCTTTAGTTTTATCAGATCGGATAGTGGTT  
51101 ATGAATGAGGGAAACATCTTACAAGTTGGTAATCCTGTTGATATTTATGA  
51151 CTCTCCTAAGACTGAATGAATTGCTAATTTCAATGGTCAAGCTAACATCT  
51201 TTAAAGGTACTTATTTAGGAGAAAAAAGATTCAAGTTACAGAGTGGTGAA  
51251 ATCATTCAAACCTGATGTTGATAATAACTATGTTGTAGGTAAGCAATATAA  
51301 GATCTTAATTCGTCCTGAAGACTTTGATCTTGTTCTTGAAAATAAAGGTT  
51351 TTTTAAATGTTTCGTGTTATTGATAAAAACTACAAAGGATTGCTTTGAAAG  
51401 ATAACCACACAATTAAAGATAACACTATTGTTGATTTGGAGAGTGTTAA  
51451 TGAAGTTGATGTAAATAAGACCTTTGGTGTTTTATTTGATCCTATAGATG

51501 TTCATTTAATGGAAGTTTAAACAAGATGCACATTAAGAAATACTGACT  
51551 TCTGCTCCCCCTTCTTTTTATTAATGACAATCTTCTTTATTATTCCAATGG  
51601 CATGGATTATTGTTAGTGGATTACAAAGTGAAGATGGGGCTAGTATTAGT  
51651 CAAAAATATGAACCACTTGTAGTGGCTTAGGTTTTTTAACAGTTTCTG  
51701 AACCAGTTTGTGGATCTCAATAGTGAAGTGAATTTGTTGCATTGTTGTTTT  
51751 CTTTTCTTTTTGTACTTTCTCTCCCAATCAAAAAACAAAATTTTTTAA  
51801 GCGTTTGTATTTC AATTGCAACAGTTCCTATTTGAAGTAGTTTCTTAT  
51851 TAAGTTAATTGGATTGAAAACCTACTTGATTATTAAATTGGACTTTCTT  
51901 TAAACAGAGTTGGTGATAACAACCTAACTTTTGGTTCAGGATATACCTTA  
51951 CTGGAACAATTTATCTGTTTACTCCTTTTATGTTTTTACCACCTTTATAA  
52001 CCACTTCTGTGTTTTACCTAAAACTTGTTGTTAGCTAGTCAAGATTGG  
52051 GTTATAACTGGATTACAGCTTTGTGAAAGTAGTAATTCCTTTTTCTAAA  
52101 ACCGCAATGTTATCAGGAATTGCTTTAACTTTTTTCCCTGCTTTAACTTC  
52151 AGTTGCAATTGCTCAGTTTTTAGATAACTCTAACCAAGCCGAAACCCCTG  
52201 GTAAC TACATATTTACCTTGGGTAATAATGGTTATGATAGTGCAATTGAA  
52251 AGAGGCAGAGCTGCTGGAGCAATTATTATTGCTGCTTTAATTACTTTTGC  
52301 AATTTACTTTACTGTGTTTTTTTTGCCTAAAATTGTCCGTATTGTTTATA  
52351 ACAAATGAAAACAACATGAAAAAGCATTTTAAGAATTTAATTAAAAACAG  
52401 TTATTTCTTTCTGTTAATAACTTTAATCTATTTACCACCTTTAATAGTTG  
52451 TACTTGTTAGTTTAAACGGTTCTTCTCAAGAGGAAATATAGTGCTTGAT  
52501 TTTGGTAATGTTTTAAATCCTAATCCTGATTCTAAATCTGCTTATTTAAG  
52551 ATTAGGTGAAACTGATTTTGCAACACCCTAATAAATTCAATCATTATAG  
52601 GTGTGATCACTGTTTTAGTGTCTGTTCTTATTGCTGTTATCAGTGCGTTT  
52651 GCGCTTTTAAGAACAAGGAATGCTTTAAAAAAGACAATCTTTGGAATTAC  
52701 TAATTTTCTTTAGCAACTCCTGATATTATTACTGCTATCTCTTTAGTGT  
52751 TGTTATTTGCTAACACTTGATTAAAGTTTAAACCAGCAGTTAGGTTTTTTT  
52801 ACCATTATTACTTCCCATATCTCTTTTTTCAAGTGCCTTATGCATTGATTTT  
52851 GATTTACCCTAAAATTCAAAAATTGAATCCTAATTTAATTCTTGCTTCTC  
52901 AAGATTTAGGCTATTGCGCTTTAAAAACTTTTTTCCATATTACTCTACCT  
52951 TATCTAATGCCAAGTATTTTTTTCAGCAGTACTAGTAGTATTGCAACTAG  
53001 TTTTGATGATTATGTAATTACCTCTTTAGTACAAGGATCAGTAAAAACTA  
53051 TAGCAACTGAACTCTATTCAATTTAGAAAAGGAATTAAGCATGGGCAATC  
53101 GCCTTTGGGTCTATTCTCATATTGATTAGTGTCTTAGGAGTCTGTTTAA  
53151 AACCTTGCAAAAGTATTTAAGGGAAAAAAGAAAGGAAATAATCAAAATAA  
53201 GACAAATGAAAAACAGTTAAATATTGCTTTTTCTCACTTTTTGTTAGTC  
53251 TCTCATCAATATTGAGTAGTTGTGGTTCAACAACATTTGTACTAGCTAAC

53301 TTTGAATCTTATATTTTCGCCCTTATTGCTAGAAAAGAGTACAAGAAAAACA  
53351 TCCCTTAACTTTCTTGACTTATCCTAGTAATGAAAACTAATTAATGGTT  
53401 TTGCTAACAACTTATTTCAGTAGCAGTAGCATCTACTTATGCAGTTAGT  
53451 GAATTGATAGAAAGGGATCTATTATCACCAATAGATTGAAGTCAGTTTAA  
53501 TCTGAAAAAAGTAGTAGTTCAAGTGATAAAGTAAATAATGCCAGTGATG  
53551 CAAAGGATTTGTTTATTGATTCAATTAAGAGATCAGTCAACAAACCAAA  
53601 GATAGTAAAAACAATGAATTACTGCATTGAGCAGTTCCTTATTTTCTTCA  
53651 AAACCTTAGTGTGTTTATCGTGGTGAAAAAATTAGTGAACCTGAACAGG  
53701 AAAATGTTTCATGAACTGATGTAATTAAGCAATTGTGAAACACAAAGAT  
53751 CGCTTTAATGACAATAGGTTAGTTTTTCATTGATGATGCTAGAACGATCTT  
53801 TTCACTTGCTAACATCGTTAATACTAACAACAATTCAGCTGATGTTAATC  
53851 CAAAGGAAGATGGAATTGGTTATTTCACTAATGTCTATGAAAGCTTTCAA  
53901 AGACTTGATTAAACAAAATCTAATTTAGATAGTATCTTTGTTAATTCTGA  
53951 TTCCAATATTGTGATCAATGAATTGGCAAGTGGTAGAAGACAAGGAGGAA  
54001 TTGTTTACAATGGTGATGCAGTGTATGCTGCATTGGGCGGTGATTTACGT  
54051 GATGAATTGAGTGAAGAACAGATTCCTGATGGGAACAACCTTCACATTGT  
54101 GCAACCCAAAATTTCCCCAGTTGCTTTAGATCTTTTGGTTATCAATAAAC  
54151 AACAATCTAATTTTCAAAAAGAAGCACATGAGATCATTTTTGATCTTGCT  
54201 TTGGATGGTGCTGATCAAACTAAAGAACAGTTAATTAATACTGATGAAGA  
54251 ATTGGGTACTGATGATGAAGACTTTTACTTAAAAGGAGCGATGCAAACT  
54301 TTAGTTATGTGAACTATGTTTCACCATTAAAAGTAATATCTGATCCAAGT  
54351 ACTGGAATAGTCAGTTCAAAAAGAATAATGCTGAAATGAAAAGTAAACA  
54401 AATGTCAACTGATCAAATGACTAGTGAAAAAGAATTTGATTATTACACTG  
54451 AAACACTTAAAGCATTATTAGAGAAAGAAGATAGTGCAGAATTAATGAA  
54501 AATGAAAAAACTAGTTGAAACCATTAAAGAAAGCTTACACTATTGAAAA  
54551 AGATAGTTCAATTCGGTGAAACCAATTGGTCGAAAAACCAATTTCTCCCT  
54601 TACAACGTAGTAATTTATCGTTATCTTGATTAGACTTTAAATTACACTGG  
54651 TGATAATATGGAACAACCGTTGTGTGTTTTAGGGATTGAAACAACCTGTG  
54701 ATGATACAGGTCTTAGTATTGTCAATTGATCAAAAAATCAAGAGTAACATT  
54751 GTTATCTCTTCTGCTAACTTACATGTAAAAACAGGAGGAGTTGTACCTGA  
54801 AATTGCAGCACGATGCCACGAACAAAATCTCTTTAAAGCAATAAGAGATT  
54851 TAAATTTTGAGATAAGAGATTTATCTCACATTGCTTATGCATGTAATCCT  
54901 GGGTTAGCAGGATGTTTACATGTGGGAGCCACTTTTGCTAGAAGCTTAAG  
54951 TTTCTTATTAGACAAACCATTGTTACCCATCAACCATCTTTATGCGCATA  
55001 TCTTTTCTTGTTAATTGATCAAGATTTAAATAAGCTGCAATTACCAGCA  
55051 TTAGGCCTTGTAATTTTCAGGTGGACATACTGCCATTTATCTAGTTAAATC

55101 ATTTTATGAACTTGAAC TAATTGCTGAACTAGTGATGATGCAATTGGTG  
55151 AAGTTTATGACAAGATAGGCAGAGCAATGGGCTTTGATTATCCTGCTGGT  
55201 AGTAAAATTGATAGTCTTTTAAATAAAGAATTAGTTAAACCTCACTATTT  
55251 CTTTAAACCTTCTACTAAGTGAAC TAAGTTTTCTATTCTGGTTTAAAT  
55301 CTCAGTGTTTAAACAAGATTAAACAAATAAGTGCTAATAAAACCCGAATT  
55351 GATTGGAGTGAATTAGCATCCAATTTTCAAGCTACTATTATGATCATT  
55401 CATTGATCATGTTAAAAATGCAATTAAAAAATTTGCCCTAAATGTTGT  
55451 TAGTAGGAGGTGGAGTTAGTGCCAATTCTTATCTATCTAACAGAATTAGT  
55501 ACATTAAATTTACCCTTTTAAATTGCTGATAGCAAATACACCAGTGATAA  
55551 TGGAGCAATGATTGGTTTTTATGCATCACTTTTAAATTAATGGCGATAAGA  
55601 ATTAAAAGTACAAGAGTTGGTAGATTGTTTCTGAATCAGTGGGATTAGG  
55651 TCATCCTGATAAAATTTGTGATCAGATTGCAGATAGTATCTTAGACCAAT  
55701 GTTTACTACAGAGTAAACTAGTCATGTAGCATGTGAAGTCTTTGCTTCT  
55751 AAAACCTTATTTTAAAGGTGGTGAGATTTCAACAAGTGGCTATGTTGA  
55801 TGTTGTTCAAAC TGCTTGAAGAATTTAAGAAATTTAGGTTACAACGAGA  
55851 CTGATTTCAAGTTTTTTAAGCTGTATCAACAACCAATCACTAGAAATTAAT  
55901 CAAGCAGTTTTAAAAAATAATGAGATTAATGCAGGAGATCAAGGCATTAC  
55951 TGTTGGTTATGCAGTGAATGAAACAAAGCAACTAATGCCTTTAGGAGTTT  
56001 TACTAGCACACTCGTTTTTAAACAAGCAGAAAACTAACAAAACATTT  
56051 GATTTTTTAAAAAATGATATGAAAAGTCAAGTGGTTTTAACTACAGTTT  
56101 AAACCAAGTTGAATGTGAAGAAGTTTACTATCAATTCAACACACTAATG  
56151 CTATTAGTTTAACAGAATTGAGAAAAGTGATTGAAAATAATGTAATTCTA  
56201 CCTGTTTTAAACCAATATGGTTTTCAAGATAAAAAGCCAACCTGTTTAGT  
56251 GAATCCTGGTGGTTCTTTTGTGTTTAGGTGGACCTATGGCAGATACTGGAC  
56301 TAACTGGTAGAAAAATCATTGTTGACACCTATGGTCCATATGCTCACCAT  
56351 GGTGGTGGTAGCTTTAGTGGCAAAGATCCTAGTAAGGTGGATAGAACAGG  
56401 TGCTTATTTTGCACGTTTTATCGCAAAACATATTGTAAGTTTAGGCTGGG  
56451 CCAGTGAGTGTGAAGTCAGTATTAGCTGAGTCTTTTCAAACCCAATCCA  
56501 CAATCTATTACTGTAAAGTGTGTTTAACTAACATACAGTATGATGAAGT  
56551 GTTAATTAATAGAGTTGTAAATAACTATTTCAACTGATCGATTACTAAAA  
56601 TTATTGACAAGCTAAAATTACTTGATTTTGTGTAAGTATTCTGATTATGCA  
56651 GTTTATGGaCATTTTGGTAATGATCTTTCACCATGAGAACAGCCCACTGA  
56701 ATTGGATAAAATTAGAATGCTTAATCAAAAATTTCCATTAGATCCTAATAA  
56751 AAAAAAGGAACAACAAGGCGTAGTAAAACCAATCTACCGTTGTTAAAG  
56801 AAAAGAAAAACAGCCATTTAAAAAACCAATTGGAGTGAATTTAAGCTG  
56851 TTCACTTTTTTAAAAAGCACACTTATTTTGCTTGGTTGTATTAGCTTT

5

10

15

20

25

30

35

40

45

50

55

56901 TCTTATCTTGATTATTTTACTTAGCAGCTTATTTGCTATTCCACTTAGCC  
56951 AAATACCTTCAAGTACTGTTTAAAAGAATTGTCCAAATCCACCAAACGGG  
57001 TTA CTACCTGTTTTTAATAGTTTACCCATTTCTGTTGCTTTTAGTTGCAT  
57051 CTTATTTTCATTCCTTCATCAGTTTGTTTAACTCATCCATTTTCTCCCTG  
57101 AACCTTTTATGATGCGCTGTTTCTATTAGGATCAGGATTAATTAATTTG  
57151 GGATGTCTCCTTTCTTCTCTAGTCATAGAGTTAATTAAACCTTTTCATAG  
57201 TTCAATTTTGTTTTCAATTAATTCAGCATTTTCTTCTGATACAGAAAAGT  
57251 TAGCAGGCAACATTTTTATCAGTGaACTGACACTTCCCATTTTGTGCATT  
57301 TGTTGCATGTAGATCAAAAGATCTTCTAAATCCATTTTCCCAAAACAT  
57351 CTTGCTGATGTTTTAGTTAAATCTTTTTTATCAAAAACCTGTTTCAGCTT  
57401 TTTCAACTAACTCATTACATCACCCAAACCTAAGATCCGATTGGCTATC  
57451 CTTTCAGGATGAAATTGTTCCAATCCATCTAATTTTTCAGAAACACCAAT  
57501 TAATTTAATGGGTACTTGTAAGTGAAGCTAATGAAAGTGCAGCTCCTG  
57551 CTCTAGCATCACTGTCTAATTTACTGATAATAAATCCAGTTAGTTTTAA  
57601 CGTTTGTGGAACGTTTGAGCAACATTGATAATTTCTGACCGCTTAATCC  
57651 ATCTACTACCATGATAATTTTCATCAGGATTTAATTCATTTTAACTTA  
57701 CCAATTCATCCATTAATGTTTCATTTGTTTGTAAATCTACCAGCGGTATCA  
57751 CAAATGATTGTTTGACATTTTGCAGTTTTAAAGCACTGAGTGCTGCTTT  
57801 TGTTGTTTTAGCAACTGGTTGAGTGCCTTGTTGCAAAAAATACGCTGTTAG  
57851 TTTGTTGTGAAAGCGTTTCAAGTTGTTCAATGGCAGCGGGTCTGTAGATG  
57901 TCCAAGCCTACTAACATTGTTTTTGTCTGTATTTCTTTCAAGTCAATA  
57951 AGCTAGTTTGCCACAAGTTGTTGTTTACCTGATCCTTGTAACCAACCA  
58001 TCATTATTTTTAAAGGTCTTTTTTCATTTAGTTCTTGTTGGGTGGCTT  
58051 AAGATATTAATTAGTTCTGTTTTGATTGTTTTTAATAGAGACTTTTGCAA  
58101 ATCTTGACCAGGTTCAATGGTTTGTCTACTGTTTTATCTCTAATTGCTT  
58151 TGATGAAATTTTAAACAACAAGCAGGTTAACATCAGCATCAAGCAATGCA  
58201 ATTCTAATCTCTTTTAGAACTAACTCTACATCTTCTCAGTGATCGTTTG  
58251 AGCGTTAATTTTTTTTTGTCATCGTGCATACGATGCTTGATAACATTG  
58301 CTTTGAACATGATTTTAAATTATTTATTATTAAATAATGTTTTAATAAAA  
58351 CAATATTGCAATATGACCCACATATAAGTGCTAAGAAAGATGACATTAG  
58401 CAAAGTTGTTTTTAATGCCAGGTGATCCATTGAGAGCTAAATGGATAGCTG  
58451 AGCAATTCTTAGATCAAGCTAAATTAGTCAATGAAGTGAGGGGAATGTTT  
58501 GCTTATACTGGGCAGTATAAATCTAAAACAGTTACAGTAATGGGCCATGG  
58551 AATGGGGATCCCTTCTATTGGAATTTATTCATATGAGTTGATGAATTTT  
58601 ATGAGGTTGAACTATCATTAGAATCGGAAGTTGTGGTGCTTTAGCACCG  
58651 CAATTAATAATTAAGATCTTGTTATTGCTTCAAAGCATGAAGTGAGTC

58701 TATTTATGCTAAAGACATGGGTGTTGAAATTCAGAAGATAAGATCTTAT  
58751 TTGCAACAAGTTCCTTTAGTGGAATTAGCAAAAGAACTGCGATTAGAAGC  
58801 AAGCTTGATTTTCATGAAGGATTAGTATTTTGTGAGGATGCTTTTTATCA  
58851 AACTAGAAAAGATGTAATTAGTCTTGCTAAAGAAAAAATAGTTTAGCAG  
58901 TTGAAATGGAAGCACATGCACTTTATGCTAATGCAATCCTGTTGAAGAAA  
58951 AAAGCACTTACACTCTTAACAGTATCTGATTCTCTAGTAACTCATGAAGC  
59001 ACTTAGTTCTGAATTAAGACAAAAGTCATTTAAGCAAATGGCTTTATTAG  
59051 CACTTGAAATGACTCAAAAATAATCTAATCTATGAAATTAGAATACAAC  
59101 CGGATTATTGATAGCACCTTAGTCAAAGCTGATACGCTTCCCCATGAAAT  
59151 AGATACTTTATGTGCTGATGCTCATAAATACCAGTTTTTTCAGTGTGTG  
59201 TTAATCCTAGTTATGTTAGTTATGCTAAAAACATCTTGAAAAATACTGCA  
59251 GTTCAACTCTGTTGTGTTGTTGGTTTTCCCTTAGGACAAACAACCCAAAA  
59301 ACAGAAGGTATATGAAGCTAAGATTGCTATTAAAGAGGGAGCGGATGAAA  
59351 TTGATATGGTAATGAATATTGCTGAGTTTAAAAACGTTGTGCTTGTGTT  
59401 ATTACTGAAATTAGAGCTGTAAAAAAGTGTGTGGCAAGCGTAAATTAAA  
59451 AGTAATTATTGAAACTGCACTTTTAACAAATGATGAAATCAAAGATGCAG  
59501 TTAATGTTTGCAATTGATGGCAATGCAGATTATGTTAAACTTCCACTGGT  
59551 TTTTCTTTCCGTGGTGCATCTTTAGAAGATGTTTCAAGATTATGAATAATGC  
59601 TGCAGCAAATTTAATTAATAAATCAAAGCTTCAGGTGGGATTAAAAACAGCAA  
59651 AGCAATTTATAGATTTATTTCAAGCTGGAGCTAGTAGAATTGGAACCTTCA  
59701 AATGCGGTCCAAATAATGCAAGAATTAAAAAAATGAACCATGAATATCA  
59751 TTAATTTAATTAATAAAAAACAACGCGGAAAAGCTTTAAATTTAGCTGAA  
59801 ATCAATTGGTTTGTTAATGCTGTTTTAAACAAAACCATGCTGATTATCA  
59851 AATTACTGCATTTTGTGATGGCTATTTGGTTTAAAGGGATGAACCCAAATG  
59901 AACTTTTTTTTATTAACAAAAGCAATGGTGGATACTGGTGAAATTATTAAG  
59951 TTTAATCACCATGGCAAGATTAGTGTGATAAACATTCAACTGGTGGTAT  
60001 TGGTGATAAGGTTTCTTTAGCATTGGTTTCTATCTTAACTAGTTTAGGAT  
60051 TTAGTGTTGCTAAATTATCAGGAAGAGGCCTTGGTTATACTGGTGGAACA  
60101 ATTGATAAATTAGAAGCAGTTGGAGTTAAACAGAATTAACGACCAACA  
60151 AGCACAAGCATGTTTAGATAAAAAATGATTGTTTTATCATCGGACAAAGTA  
60201 AGGACATCGCACCAGTTGATAAAGTACTTTATGGTTTAAGAGATATTACT  
60251 GGAACAGTTGATAGTTTGCCTTTAATTGCATCTAGTATTATGTCTAAAAA  
60301 GCTAGCAGTTATGAACGAGTATATTTTCATTGATCTTAAATATGGAAAAG  
60351 GTGCCTTTTGTAAACTAAGAAAATTGCTAACGAACTTGCAAACTGATG  
60401 CAAAGTATTGCTAAAAGTTTTAAAGAAAGCTGTCTGTTAAATTAAGTGA  
60451 TATGAATCAAGTACTTGGTAAAGCTGTTGGCAATGTAATTGAAGTTAATG

60501 AAGCTGTAACTTTCTAAAACAAGATTTAGATCAAGTAGGACAAGATTTT  
60551 ATTGATTTAATGCAACAATTGTTATTAACATTCTACTTGAAACAAAACA  
60601 AGCAAAAACCAAAACAAAAGGCTATTGAACTTTATCAGGATGTTTTAACTA  
60651 GTAAAAAAGCATGAAATCGCTTTTTATCTTTTATTGAATCTCAAGGAGGA  
60701 AATGTTGAATTATTTACTCAAAAAGAAGGTTTTTTTAAACCTAAGTATAA  
60751 GGCATCTATAAAAGCTGAAAAAGTGGTATACTACATTTTACTGATCCAA  
60801 TTGATTTAGCTAAAATTGGGATTAATCTAGGGGCAGGTAGGATGAAGAAA  
60851 ACAGATCAAATTGATCCAATGGCAGGGTTATTTTAAATGAAAAAAGATAA  
60901 TGAGTCTGTGGCAGTTGGAGACACTGTATTAAACCTGTATAGTTCCTAGTC  
60951 CTATTAGCAATGAATATATCTCTGCTGCTCAAAAAACAATAATTATTAAT  
61001 AAATAAAAATTCCTATGAAGGTGAATTTAGAGTGGATAATTAAACAGTTA  
61051 CAAATGATAGTTAAAAGAGCATATACTCCCTTTTCTAACTTTAAAGTTGC  
61101 ATGTATGATTATTGCTAACAACCAAACTTTTTTTGGAGTTAACATTGAAA  
61151 ATTCTTCCTTTCCAGTAACTTTGTGTGCTGAAAGAAGCGCCATTGCTAGC  
61201 ATGGTTACAAGTGGTCATAGGAAAATTGATTATGTTTTTGTCTTACTCAA  
61251 TACTAAAAATAAGAGTAACTCACCTGTGGAATGTGCAGACAAAACCTTAC  
61301 TGGAATTTTCCCATCAAAAAACAAAGCTTTTTTGTATTGATAATGATAGT  
61351 AGTTATAAACAATTTTCCATTGATGAATTATTAATGAATGGTTTTAAAAA  
61401 GAGCTAATGGATAAACTTAGATTAGAAGTTGAAAGATGGTTAAATCATCC  
61451 TAATGTTAATTGGGAGTTAAAACAACAAATTAAGGAGTTGAATGAATCAG  
61501 AAATTCAGAAGCTTTTTAGTTTGGAAAAACCTTTATTTGGCACTGCAGGT  
61551 GTAAGAAACAAAATGGCACCAGGTTATCATGGTATGAATGTTTTTCTTA  
61601 TGCCTATTTGACCCAAGGTTATGTTAAGTACATTGAATCCATCAATGAAC  
61651 CAAAGCGTCAACTACGGTTTTTAGTAGCACGTGATACAAGAAAAAATGGT  
61701 GGTTTATTTTAGAAACGGTTTGTGATGTAATTACATCTATGGGTCAATT  
61751 GGCTTATGTGTTTATGATAACCAGCCAGTTTCAACACCTCTAGTGTCCC  
61801 ATGTCATTTTAAATATGGTTTTAGTGGAGGTATTAATATCACAGCTAGC  
61851 CATAACCCTAAAGATGATAATGGTTTTAAGGTTTATGATCATACTGGTGC  
61901 ACAGCTTTTAGACACACAAACAAACCAATTGTTAAGTGATTTACCTTGTG  
61951 TTACATCTATGCTAGATTTGGAATTACAACCAATCCAAAGTTTGTCCAT  
62001 ACTCTTGACAATGAAAAGGTTTATAAAAACTATTTTCAAGAGTTGAAAAA  
62051 GGTGTTGGTTATTAACAACAACAAATTTCAAAGACATTAAGGTAGTTTTTA  
62101 GTGGGCTTAATGGGACTTCAGTTTGCTTAATGCAACGCTTTTTTAAAGTAC  
62151 CTTGGTTATAGCAATATTATCAGTGTGAGGAACAAAATTGGTTTGATGA  
62201 GAATTTTGAAAAATGCTCCTAACTTAAATCCAGAGTATAAAGATACATGGA  
62251 TATTAGCACAAAAATATGCTAAGAAAAATAATGCTAAGTTAATTATTATG

62301 GCAGACCCTGATGCTGATAGATTTGCAATTGCAGAGTTAAATAATAATCA  
62351 ATGACATTATTTTTTCAGGTAATGAAACAGGAGCAATTACTGCTTACTATA  
5 62401 AACTTAATCATAAGGTTTTTAAATCACCTTACATTGTCTCAACTTTTGTCT  
62451 TCAACTTATTTGGTAAATAAGATTGCTAAAAGATATGGCGCTTTTGTGCA  
62501 TAGAACCAATGTTGGTTTTAAGTACATTGGTCAAGCAATTAATGAGTTAT  
10 62551 CACAAACAAACGAATTAGTTGTTGGTTTTGAAGAGGCAATTGGTTTAATA  
62601 ACTAGTGATAAATTAAACCGCGAGAAAGATGCTTATCAAGCTGCTGCATT  
62651 ATTGCTTGAGATTGCTAGACATTGCAAAGAACAAAACATCACGCTTTTAG  
62701 ATTTTTATAAAAGAATTCTTTCTGAGTTTGGTGAATATTTCAATTTAACA  
15 62751 ATATCTCATCCCTTTAAAGCTACTGCTACTGATTGAAAAGAAGAGATTAA  
62801 AGCTTTATTTAATCAACTTATAAATGCTAATTTAACTGAAGTGGCTGGTT  
62851 TTAAAGTAGTTAAAGTCCATCTTGATAAAACAAACAAATATCTTAGAGTTT  
62901 GGTTTTGAAAATGGCTGGGTAAATTCGCTTTTTCAGGTAAGTGAACCTAA  
20 62951 ATTGAAATTTTACTTTGACCTAACTAATGGCACTAGAGAGGCTCTAGAAA  
63001 AGCAAGCTAAGAAAATTTATAAATCTTTGTAAATTTACTCAAACCTCAAC  
63051 AAAGCTTAAATTTTCTAAAGGTAAGTTAATTAATTGGGTTTTAGATGTTA  
25 63101 ATTCTATCTCTACAAGTCTTTGTTAACTGTACCTTGATAAAGTGCCTTT  
63151 ATCTGTCCTTGAACATGAATAGTATCAGTTAAATGTACCTCTACTAAATT  
63201 ACCAACACTAAATTCAAAGAGTTGTTCAACTTTATTGTCAAGTATCAAGAA  
63251 TTTTCATTTTGCCCAAAAAGGAACTAATACTGATGGATCAAGTTTGGTT  
30 63301 TGCTCACTTTGAATAATCGTTGCTTTTTCTTTCCATTCTTGTCTTG  
63351 ACTATTTTGTAGTTTTTTTAAAGCTTCTTTTAGTTTTTTCAGCATCAACAA  
63401 TTTCTGAATCTTCATCCTCTTTTGGTTTTTGAATGGCTTGTTTTTGTCTT  
35 63451 AAGATATATTGAAATTTTTCATCAAATTTATCACTGTCCATTTCAATAAT  
63501 GGCAGTATTTGTTAGCATAATTCGTTTGCTAGGATTGATTGATATCCCTT  
63551 TAAGCATTTGTTCTAAATTATTAGCATCTTTTTCATCTAAAGGGATAGGT  
63601 AAAGCACCCCTGCCAGAAGAACCTACTATGCCAGTGATCCCAGGGAAGTT  
40 63651 ACGAACAATTCTTCAAGCATCTTCACTATAAATCATCTTTATGTAGATGT  
63701 ATCTACCAAGGAGATTTTTTCACTAATTTTACCCTAAGATAACGGTAA  
63751 TCATCAAGAACAAACCATTTGTTAAAGTAGTGTTCTTTAAGGAACGAGG  
45 63801 AAGTTTTCTGATTTTAATGAATAAACTTCTTCATGAACCTCCCTTTCTT  
63851 TTAGAACTTTAACATCAACAATCTCATGATTAAATCCTAAAGCTTGAATT  
63901 TTAGCTTTTAGATTTTTTACAACAGCTTCATCTTTAATACTAACAGGAGC  
63951 TACATACCACTTTGGTGTTAATTCAGTCTGCATAAATTAATTTTAA  
50 64001 ATATCCCAACGTAATTAACAATTGATTGATACCAAAAAAGATTCCCTACC  
64051 ATCAGTCCACTAAGTAGCAAAATTTAAAGAAAAATTATGATAAGTTGTCT



64101 ACCTTTTACTCAAACAATTTTGTGATCTCTTTATCAACTCCAAATCATA  
64151 AATTAACAATTCGTTTTTTTAAAAGGAAGCTTGGGTTTCTTTTCCTTTGCT  
5 64201 AAACCTTTCATGCTTTTTCTTTTCTTTAGTTCTTTCCTTATCTTTACTTTT  
64251 CTTGGCTTCTGTTCTAAGTTTGAGCTGTTTATGTAACATGAATTGAAG  
64301 CATCATCATAAGCAGTTAGCTTTTCCTTCTTTTTTAAAGCTAAAAGGCAGT  
64351 TTTTTTTCATGGCTTTTTTAAAAAGAATCTAGATGCTTAGTTTTTTTGATT  
10 64401 GCACTGCTTGCACTACTTGTTGATGATAAGTCGCTGCAAAGGTTGTTTTG  
64451 TTCACCGTTTTACATAGTTACGACTTAAACAGTCTTGACAGACAAAAATA  
64501 ATCTTTTTGCGCAACTTCAGTAGCAAATTATAAATTATCTGCTTGTTTTA  
15 64551 CTAATTTAATCTTTTGATAGCAATAGAGCTGTAAAAGGCCAAAGGGTAAA  
64601 AAACAAGATCAGTGTAGAATTTTTTTGAATTTAGGTTCAATATTTTCACA  
64651 TGCAGTATTAATTGTTTTTCAAATCATTATGCTGATAACTAACTGGATGA  
64701 TCATAAAACAGATAGCAAAAACCTCTAAAACAATTAAAACCTGCTCGTAAA  
20 64751 TTAATAAAATAGGATCACTTCTAATTGCACTTAACTAGCTTTTCTAAT  
64801 TAAATCAAAGATGATACCAATCCCTACTAAAGAGATAATACAACTAAAA  
64851 AAAAGATACTAATTAACAAAAGAATCTCATTAAAGGTTATGGAGTTTTTTA  
25 64901 AATACTTTCATGGAAAAGTGTATAGAGCATACTTGATTTTAAATGCATT  
64951 TTTTAGCTAAATAATTGCATGCATCTTTTAACTTAACACCAATATCCATT  
65001 AACTTCTTTATTTTCATATACTAAGTATTGATTGGAAGATAATGTTTGGTG  
65051 ATTAATATTTTGATTATCAATAACAATTACAAATTCCTTTTAAAGTGA  
30 65101 TGTCAGGTAAAGTGTTTTCACTGGTGTTAAATCAATAATGTGATTCAATG  
65151 AACTTAGTTAATTCTCTTCTATAAAAAACGTCATTGTTTTTAAAAACATT  
65201 TTTACAGTTTCTAAAGTATTTCTAACCTATGCACTGCTTCAAAAAAAA  
35 65251 CGATAGTGCTTTTCTGATTTTGATAGGTACTTAAATAATTTTTGAGCTGA  
65301 TTTTGTGTGACTTAAAAAACCTAAAAACAAAAGTGGTGTTGTTTTTAA  
65351 ACCACTAGTGATCAATCCACACATTAATGCACTAGGACCATTAATAACTT  
65401 CGATTCTTATCTCCTTATTTTTTGATATGATCCAATTAATCATTTTCAAT  
40 65451 CCAGGATCAGATAAACTAGGATAACCTGCATCACTAACAAGACAACACTT  
65501 AAAGTTAGTTATAAATTCCTCAGCAAAAGTTAAATTCGTTTTTCTTTAA  
65551 AACTGTTGTTAATAACAACTTTTTTTGCTTGCAATCAATGTTGAGTAAA  
45 65601 TCCAGCATTTTCTTGTTACTCTACTATCTTCACAGAATAACACTTCACA  
65651 ATCTTGTAACGCTTTTTTTAGCTCTTCACTTATCTCTGAATATTACCAA  
65701 TTGGTGTAGCAACTACTTTAAGTGTTTTTCATACATCTTGAAAAGTTAGAT  
65751 TTAATAAGTTAAGTTTTTTTAAATAGTTGCTTGTTGGTTAAAATAAGGTAAA  
50 65801 TTAAGATTATGCATAAAAGTAATCGCTTTTTTCTTATCATTTAACTTTAA  
65851 GCTTAAATACTGATCTCATAATATGCTTTGATTAGCATTTTTTGTGATTG

5 65901 CAACACGATTATTTAAAGCAGCAATTAAAGCACTAGTTTCCATTTTCAGCA  
65951 ATACCAGCTTTTTTAGCGTTTTTTAACCTTGCAATTCATATCAACATAACA  
66001 GTTGTAAATAGTTTGTAGATGTTGTTCTAATTTACTTCTAATCTTTTTGC  
66051 CTTGTTGATCTGGATCTAATAACAAGATAACAGTTTGCTTTTCACTGATT  
66101 TTTTAAATTAGGTTAATAGTTTCTTTTTTAAAGCTGAACCATTGTTGT  
10 66151 AATTACATCTACATCAAAAATTTGCTGTAATTTAGCTTGGTCAGTTTAC  
66201 CCTCACAACAATTACCCCATCAATTTTATACGTGCTTTTGTATCCATT  
66251 CAATGTGACGTTTCATATATTGCAGAACTGATAAGCTGTTAGCGTAACAC  
66301 AGAACACCTCTTCATATAAAGATGCTAGATCAACTACTTCAAAGCTGCTT  
15 66351 TACAGCTTTAAACTTATATTGAGGAATAGAGTTTGATACAAACAAGAAAT  
66401 CAATTAGTTTTTGATCAAATGCTTCCATAAACTTTTGTCTGCATCATTG  
66451 TTAAACAAACCATGAGTTGCCATTACACACACTTTTTTAGCTTGTCTTT  
20 66501 TTGTAATAGCTTGGCTGCTGCAATTACTGTACCACCAGTATCTATCATGT  
66551 CATCAACTATTAAaCAGTTTTTATTTTTCACTTCACCTAAACATTAAAT  
66601 GATTCAAGCAACATTATGAGATGGTCTTCTTTATCAATAATGGCTAATGG  
66651 TAGTTCTAGTGTATTTGCAATTAACCTTGCTCTTTTAACCCCAACATAAT  
25 66701 CAGGGGAAACAACCAAGTCTTTTTTACCAAGTAGTTCTATAACTCTA  
66751 AAAAGAAAGATGTGATAAGTCTTAAAGAATCAACGGGAATATCAAAAAA  
66801 ACCTTGGGTTTGATCACTATGAATGTCAGTTAGAACAACCTGTTAGCAC  
66851 CTGCTTTTGTAAACATATCAGCAATCAATTTACTGGTAATTGGTTCTCTT  
30 66901 CCTTTTGTCTTCTATCTTGTCTTGCATATCCATAATAGGGTAGAATGGC  
66951 AGTAATACTTTTAGCACTACCTCTTTTCAATGCATCAATAGCAATTAAAA  
67001 GTTCCATTAAGCTATCGTTAACATTAGGACAGGTTGATTGAAAAATATAG  
35 67051 ATATCTTTGTTACGAACTGATTCATCAAAACGGATATAAGTTTACCATC  
67101 AGCAAAGTGTTTCGCAAACCATTTTGCCCTCTGAAATATTTAGTTTTTTGC  
67151 AGATATTTTCAACCAGTGTTTTGCTTTTAGATAAACTAAAAATAACGTGC  
40 67201 TTTTATTATCGATACTCAGCTTCAAGCTCGCGTCGGATTGTTTTCTTTT  
67251 TAATAGTTTTCAGTTTGTCAAATTTCTTTTTAGGTTTGGCCAATCAAATT  
67301 TCCACTTTAATTTTGCCATTTCTAAAGAATACTTTACTTGGGATTACAGA  
67351 TAAAGATTGTTGTTGTTTTTTATTGATAATTTGTTTAATTTATGTTTAT  
45 67401 TTAATAAAAGTTTCTTAATTCTATCTGAAGCGTGATTAAATGGACCTGCA  
67451 AAACATAAAGGTGGAATAGTGAAGTGTCTAAAAAAGCTCATTGTTTTT  
67501 AACAAAAACATAAGCTTCTTTTAAACTACCTTGACCTAAACTTAAAGCTT  
50 67551 TAACTTCACTTCTTTTAAACTATTCCAGCACAATAAGATTCCATTAAA  
67601 TGATAGTCATATTTAGCCTTAGGATTGTTAAACAAGAATTAACATTTATCA  
67651 ATGAAATTATCTGTAATTATACCTACTTACAATTGTGCATCATTTATTGA

67701 AAAAGCAATTAATTCAATTGTTAAAAATAGACCTAATGATTTGGAAATAG  
67751 AAGTTTAAATTATTGATGATGGATCAATTGACAATACTAACAAAGTTATT  
5 67801 AAGAAAATTCAAGACCATAATAATTAACTTTGCAGTATTTTACAA  
67851 AAGTAATGGTAACTGGGGTAGTGTTATTAATTATGTTAGAAACAATAAAC  
67901 TAGCAAAAGGGGAATGAGTAACAGTATTGGATAGTGATGACATTTTTTCA  
10 67951 AAAAAACAATTTCTATTTTCAAAAATATGCCCAAAACAAAGATATGA  
68001 TCGGATTATTTTTGACTACTATAAATGCTGAAAAAGTTTTTGTGAAAA  
68051 TTCCTACCTATGCAAGGTTTAGAAAAGAAATTAAAGGTGAATTGAAAAA  
68101 CAAACACCTTTTTGTATTCCCTTAGCTAAGTTTTTTAAAAATGAGGTTTT  
15 68151 CTATCAACTTCCTAACTAAGAGAAAATGTTGGTTTTCAAGACGCTATTT  
68201 ATACGATGCATGCATTACAAATTGCAAATAATGTTTTCCATGTTCTAA  
68251 GCTGGAGGATATTACTTTTTTAAAGGGTAGGTAACCTATGAGTATCCC  
20 68301 TTGACACAGTTCTAGGTTTGATATTGAAGTACAAATCTGCAAGGATCTGA  
68351 TTGAAAATAATGCGCAAGAGATCGCTTTAGTGCATTTACTTCGTTAAAA  
68401 TTTTCGTAATTTAGTTGATGATAAAAAGATTAAATTTACAGTTAAAAGAGA  
68451 CTTTTGTTTTAGTGTTTTAGTTGGTATAGTAGGTTAATTTTATCTCTGA  
25 68501 TGTATAACTTCTGATTGAAACGTTATTTCAACAGTTCTGAATAACGATTT  
68551 TTTTGCTTATTTGCAATTACAACTGTCATTCATTGAGTTTTCATTTTCT  
68601 TGTCATTTCTGAACCAATTGATCACCATCTTTAATCCAACAAGCAGGAA  
30 68651 AGAACTTAACAATTAGGTTTGCTAGTGCAATAAGTCCTAAGAAGAAAACA  
68701 ATACTTACAATTACCCCTGGTAAAATACTTGACCTTTTCCTTGAATTAA  
68751 AACAGGCGCTTGAGAGAAATACTGATTGGGTAAATGTCAAATAAGGTGTAAG  
68801 CAATATAACCAAAGCCCCAACAAAATCCAAAAGAATAGGAAGTTCATTC  
35 68851 TTCTTGTAATCTTTAAATTATATGGCAGGATTAAATTTGAACTTGATAA  
68901 ACTCCAAGCAAATGCACCACCGATAAATGAAAAGATACTAATTAAAGCAA  
68951 ACCCAGCTGCACTACCAATACCAAGTGTGCTGCAAACATGATGATTATA  
40 69001 AGCAATACCACTATGTTAGCTGTTAATAAGAAGTGCAATTCACCTCTCTT  
69051 GTCATAAATGGTTTTATTAAATGGTGAAAAACAACAAAGCCCAAAGCAT  
69101 AACCAATAACTCAAAAAATAGCAAGTGTGCTAAACCTGTTGTGTACACA  
69151 CCAGTACTTATCAAACCATTGATCCTGATGGGGAAACAGTTTGCAAGAT  
45 69201 GCTAAATCAAGCTGGAGTTAACGGATTGACTATTAGTATTAAACTATGC  
69251 CATAAACACCAATTAATTTTCATGTTGTTTTATTCTTTAAGATATCTATG  
69301 GATTTTGGTTGAGTAGTTAACTCATATTTTCTTAGTTTGCTTTTGAGG  
50 69351 AAAGATGTGATCTATCTTGCTTTCAAACCATAAAAAATAACATAAGTTAG  
69401 CAAACACAACCAAAATCATCAGTCATAATGTAAACCCAGTATTGAGAG  
69451 GCTACTTGTTGAACTTGTTCAAATAAAAACGGTGTGAAAACCTACTGCAAT

69501 CCCAATGTTAAAACCCCAAAGGTTAGCATTAGATAGGATTGATTTTTTTC  
69551 TGTTTGAAGAAAGATTAGCAATTGCTGGTTGAGTATAAACTACTAAGGTA  
5 69601 GTTCCACCAATAGCAATTGTGCTTCTAAAGATAATAACAATGCATAACC  
69651 AGTAATTGATGCAGCTGTACCAATACTATTACCATCCAAACCCCTTAATAA  
69701 GTTCAACACTTGTTCCATCTGCAAGCATCGTTTTACCATTGATCATCACC  
10 69751 GGTCCAAGTAATTGACCCACTTGTAATGCTACTTAGTGAACTTAATTG  
69801 AGTTTTTACTGAATCTGATAAAGGTCTTAATAAAGTTAATTGATTATGAC  
69851 CATTCAAAGGGTCTCCTATAATAAGAAAGGGAAAACAAACACACATGATT  
69901 CCCATCATGATTAAAACCGCATAACGATAACCAAATTTCAAAACAACAAC  
15 69951 TCCACAAAGAATAGAACCCTACTGCTCTCAATAAAGTGATAGTTCAGTTGG  
70001 TGGAAAGATGTGGCTATTTGCCCAGCATTTCAGTAAAGAAAGAACTTAAC  
70051 CAACCACTGTACTGTGGTAAAGTGGTGGTTGATTGAGTAAGTATACCAGT  
70101 TGGTTTACCACTAATTCGATCAATTACAAACCATTCAACTACAAACAATA  
20 70151 GATACCCAAAAATTACTATGATCCACAGGGTAATAAGTTTCAGATCACTT  
70201 ACTTTTTTTTGACTTTTATTTTCCACAAATTAAGACAGAATTTACATTAG  
70251 ACTAATTTTAAAGCTGTAGCTAATTGTTTTTTAGAACAACTGAATCAA  
25 70301 AGAATTTGAAATTGTCTTTTCATTGTTAACAGCATTTAACAACAAAATTGA  
70351 ATAAAAATAAAAAACAGACCCTGATGGTCTGTTGGATATTTAATGGCGGA  
70401 AGCGGTGGGATTGCAACCCACGCACCGTAGAACGATCTAACACCTTAGCA  
70451 GGGTGTCTCTTAAACCACTTGAGTACGCTCCCAGTTTGTGTGTTAAATTTA  
30 70501 TTATAAATATGCAACTAATTAGCGCTTTAGATGTTTAAAAATTTATTAAG  
70551 ACCATCCCTATTTTTTAACTGGAGCCAAAAACATTTAAAAATAAATTTT  
70601 CGTTTTTAAACAAGCAGCAAATGCATTACAAAAACAGGCTGTTATCAAT  
35 70651 GATAACAATGTTGCATTTGAAGCTTTAAAAAAGCGTGAAGAAGAGATTAC  
70701 AACTGGAATTATTACTAGTTTAGCTTTACCTCACTTACAAAGTCAAAGTG  
70751 TTATAGAACCTTTTGTGCTGTATTTAAGGTTAAAAACTTAGATTGACAA  
70801 TCATTAGATCAAAAACCAAGTTAAATTGATATTTTTAATTGGTGTCTTGT  
40 70851 TGACAAAACCAATTTGCATCTTGATTTTCATTAGTAACTTTTCCAAGTTAA  
70901 TGTTGAATGAAACATTTGCAAGTAAGGTTTAAATGTCACTAGCTATAAC  
70951 GGCTTGATTAAACTAATTGATCTTTTTTAACCAACAAAAAGTGCAAGACCA  
45 71001 ACCAGCTGTTGAAACAAAAAAGAGTATGACTTTGTTGCTGTAACAGCAT  
71051 GCCCAACTGGCATTGCCCATACTTTCATGGCTAAAGAAGCGTTGGAAGCA  
71101 TTTGCAAAAAAGCATAACTTATATGTAAAAGTTGAACTCAAGGTACAGA  
71151 TGGGATACAAAATCAACTTACAAGTGACGATATTAATAACGCTAAAGGTG  
50 71201 TTATTCTTGCTTGTGATCGTTTAATTGATTCTCTAGGTTTTATGCAAT  
71251 AAGAATGTGATTGAAGTGTCAACTACTAAAGCCATTAAAAAACCTGATGA

5

10

15

20

25

30

35

40

45

50

55

71301 GGTGTATGAATTAATTAAAAACCAAAGGGTAAACAGCTTGCAAATAGTG  
71351 CTAAACCAACTAATCAAACCCAATTAGCTGAAAGTGAAGGGGAATTCAAC  
71401 TTTAATAATTTTCACAAGCGGATTTATCGTGCCATTTTAAGTGGTGTTC  
71451 TTACATGCTACCATTTCGTTGTTTTTGGTGGGATATTAATTGCACTCTCTT  
71501 TTCTAATTGATATAAAATAACGCTAATAATGCTGGTGGTAACCTTTGGCACA  
71551 ATTAATCCTGTTGCTAACTGGTTAAATAAGCTAGGAGGAATTCCTTTAG  
71601 TTTAATTGTTCTTATCTTATCTGCATACATTGCATATGCATTGGTATCAA  
71651 GACAGGGATTATTACCTGGTTTTGTTGTTGGTTTAACTCTCTTCAGGACAA  
71701 TTTTTATTAAATATTGTTCTGACCAATGGAACAATTGAATGGTTAGCACC  
71751 ATCACAAGTATCAAGTGGCTTTTTTGGTGCTATCTTTGGAGGACTTTTGA  
71801 GTGCTTGCTTAATAATTGTTCAACAAAACCTACATCTATAAAAAATTACCT  
71851 CAATCTTTGCAGGGAATTAAAAACATCTTGTTTTATTCCTTGTTTGGTAC  
71901 TTTATTCCTGCTGGTTTTATTTTGGGTTATTAACATTCCTTTAATTTATC  
71951 TAAACTATGGATTAAGTCTGTTTTTAAATATTATGAACAGCCCTATCCTA  
72001 GCACCTTTACTTGGTTTTGTAAATTGGGTTGATGATGTGCTTTGATTTAGG  
72051 GGGGCCAATTAATAAAGCAGCTTATGTTTTTGGTGTGTTTCTTTACAAA  
72101 ATCAAATGCAGGAACAATTCGATGGCTGCAGCTATGCTATCAGGGATG  
72151 GTACCTCCTTTATCAATTGCTTTGGCAGCTTCCATTGAAAAGAGCTGCTT  
72201 TGATAAACAGGAATTACCTGCAGCTTATGCTTGTTATCTGATGGGATTGA  
72251 GTTTTATTAGTGAAGGTGCTATCCCATTTGTTGTTAAAAAACCTAAGGTG  
72301 ATGTTAACTGCTAACTTAATTGCTGGAGCAATTTGTGGAGCATTAAACAGG  
72351 AGCATTTGCCTTATCAATTCGTGCTCCTCATGGCGGTGTTTTTGTGTTTG  
72401 CACTTTTAAAACTACTTTACAAGGGATTGAAGGAGCTACATTACAAACT  
72451 GGAGTTGGCATTGGTTTGGCATTGGTTTGTAAATAATTAGTATGATAGT  
72501 TGGTAGTAGTATTATCATTGGCTATGACTTGATTGCAAAACATAACCAAA  
72551 GAAAGCAAACTCTGAATAGTTAATTACGCTTGCGCAATTGATTATTATGT  
72601 TGATTTAAACAAGCAAAAAAATAGTGTTTTAATACCTGGTGGTAAGGGGA  
72651 TTAATGTTGCTATTGTAATGAAATCACTTGGTTTTGATCCAAGTGCATT  
72701 ACTTTTTTGGGACAACCCACTAAAACTTATTTTTAGAGTTGGTAAAACC  
72751 TTATGATCTAAATATAGTTAGCTTCATTTCTGAACTAAAACAAGAATTA  
72801 ACCTTAAGTTATTAAAAGATGAAAAAACTACTGAAATTAATGATTTAAGT  
72851 CCTTTAATAACAGATGCTAATCTAACTGAATTGTTAACTTTTTTAAAGC  
72901 TAATGTTAAGAATAATGATTTGGTTATCATCAACGGAAGATTTAAATTTG  
72951 AAGCTTTAGAAAAAGTTCTAACTTGGTCTTTACATTAACAGAAAATGTG  
73001 GTTATAGATGTTGATGAAAGCAAAATGTTAACGCTTTTAAATCAGTCTAA  
73051 ACCACTAGTTATGAAACCTAACATTGATGAGTTTCAAACTATGATTAATA

73101 CTTTTTTTCACGATCAACAAAGCTTAATAGCAGCAATTAAAAAATTTTCAT  
73151 TACTGTAAGCTCTTATTATTATCTGATGGTGACAAAGGAGCTTATCTTTT  
5 73201 TGATCAGAATAAGTTATTGTTTGTAAAGTTCTATCACTCCTAAACAAGTAG  
73251 TTAGCACCACAGGAGCAGGTGATACTTTGTTGGCAGTTTTTTTAGCAAAT  
73301 TTGATTCTAAAGGTAGATTAAAAACTGCTTTGATTAAAGCAACTAACTA  
73351 TGCAAGTGCAACAATTAGTAAGTTAGGTGTTGTTGATAGTAAAGACAAAA  
10 73401 TTAGTGTTATAACCCCAAAAAGTTACTATTTATAATTAATATTTGATGGT  
73451 AAAAAGAAAGCGAAAGCCTAAGCTTAATTCGCGTAATATTTAACTATCC  
73501 AGATTGTTTTAACAATCTTTAGTATGATCTTTTTTCTTACTTTGCTATCT  
15 73551 TTAATCTTGTTTTTGTAGTTTGCAAAGTAATTAGCTACAGCTTTAGTTGA  
73601 AAACAGAAATAAAGCTGTGGAACTGTAGATAACATTGCTTTTTTTTAA  
73651 AGAACTGATTTTTAAATTTGTCTCTGACTAATTTATTAGTGTGTTAAACC  
73701 TAATTAATAATGTTATTCGTTCTTTAAAGAGTGCTAAGATTGCTTTAATA  
20 73751 GCGTTAACTTTTTTAATTTTTGTGCTGTTGGTGGTTTTGTGTTGTTAA  
73801 TAACACAGTTAATAATTTTAAACGCTGCTTTTAACTATGTCACCCCACTG  
73851 GTAAATTAAGCAATGCCATCATTAAATGAGCGTTATGACTTTGGTAAATTA  
73901 GAGTTTCAAGAACAGACCAATAATCTCAGAATAGTAGCGACAGTTTTAC  
25 73951 TTTAACTTTAACTAATGATTCAAGAACAAGTTTTATTAATAATGCCTTGA  
74001 GAACTAACCTTCTTTGTATGAAGGATTAGTAACCCAACTTTTAGCTAT  
74051 CAAAACAAAACGAAATGACTGAAAAACCAATATAGTTAATCAGTCTAA  
30 74101 AATTATTGCTGCTAACCAATCTTAACAATGCATTAAGTAAAGATAAACAGC  
74151 TCTTAGTTTCAGGTCAACTTGAAAACTAAATGCTGTTTTTCGGGAATAT  
74201 AAAGCTATTAATATTACTGACAAAAGTGTTTTTAAAAAATTGATAGTATC  
74251 AGAACCTAATGATTTGGTAAATAGCCTAGTTATTTTTGATGGTCAAATT  
35 74301 TATCTAGCTCCAAACAAAGTGATTTCAATAATTTTTTAAATCAATTTAAC  
74351 GAAATTAAATCAAAGGGTAAAGATAATTTAAGTACTACTTTAAAACTGG  
74401 GCAGTATCAGGCATTTTACAAACTCTTTTGATTATGCTCAAGCGAGTG  
40 74451 AAACAACATTAAGATCAGCTTCAAAGTTAATTTCAAATCCAGATTCA  
74501 AGTGAAACAAATCAGGTAAAAATCTCTTGATACTCCAAGTACGCTTAC  
74551 TAATATTGGGGGTCAATTAACCTTACAATGAACAGAAAATAGCCTAACAA  
45 74601 AACAGATAGTTATCTTTGATCCTAGTAGTTATGAAACAATAGTCGCTCCT  
74651 GGTAAGTGAAGTTATCAACAACAATTAGGTAAAGAAGTTATCCTGATAT  
74701 TAACAAGTGAAGATTTAAAAAACTACCACTTGAACAATTTGAAAGTG  
74751 AATTTTTAAAAATTGATCAAAAGTATAAGATCAGTATTGATAATATCGAT  
50 74801 TATTTAGTTATGGGGTTGGAATTAGTCCAGATTTTGTATTATCCTGTTTT  
74851 TAGTGCATCTTTAATTGTTCTTAACATTGAAAATGAACAACCTTTACTATG

74901 TTAACCAAACCTGGATATGAAAGAACTTTTTCTCTTTTTTAACAAATCCA  
74951 GTTGAAACAGCAATAGTAGCAAGATTGATTAATCTTGAAAGTGATCTTAA  
75001 TACTATCAACCAGTGAGCTGTTGAAAACATGTCATGACCAACAAACATTA  
75051 AAGCTGCATACAGTAGTTCTGATACCACTAATATTTGAATTTATTAGCA  
75101 GCAAGAACAGTTTTTATCCCTAATCTAATTAACACAATTAATTTAGTGGC  
75151 TTTGTTTTTAACTATTGCTATCCTAACTGTTGCTATAATTGTCAGCATTT  
75201 TAATCCTGATTAGTTATTTAAAGAAAAACACTGAGCAAATTGGCATTTTA  
75251 AAAGCAAATGGGTAAAGTGGTAAAAAGATTAACCTTAGCTTGTTAATCTT  
75301 TGGGTTAATTCCTGCTATAGTAGGTGCTATTTCTGGATATAGCTTTGGAA  
75351 TTGGATTTCAAGACGTAGCTATTCATCTATTTAGTAACTATTGATTTATA  
75401 CCAACAGCAACATCAAGTTTTTCAGTAGTAGGATTGTTGTTTTTTTCACT  
75451 GTTTGTTATCTTAATTATGAGTAGTATATCGCTTTTAGTGGGATCAATTA  
75501 TCCTAAAGAAGGATGTTGTAAAGATTTTAAAGCATGACAGTGAATTTAAA  
75551 GTTTCAAGATTAGGACTTAGTTCTAAGAAATTGTTTGCTAGGTTTGGTAT  
75601 TATGACCAGGTTTAGAGTAGCATTAGCATTAAACGCTCCTTGAAAATTAG  
75651 TTTTCTAACCTTGATGAGTTCATTTACAATGATGATTTTAAACCTTAGT  
75701 TTTGCAACTAAAGATAGCTTTGAAAATGCTCAATCAAAAATAATTTAAC  
75751 TAATCAGAACCACCAATATGAATTTGAACTCGCTTCAGCAACAACACAAA  
75801 GTGGTTTATTGAAGTGACAGTTATTTGCAGAACTAGGTACAACCTGATAAA  
75851 AGAAGTGAAAGTAGTGTAAGCTTGCAAATAAAAGGATGGATATTAGTAA  
75901 TGTTGATGCATCTAAAGATTGAAAGAACCAACAAGTAATTAATTTTAA  
75951 GCGATGCTAGTGGCTTTAGTAATGATTTAAATTACCTTGAAAACATTGTT  
76001 CAATCCAAGATAGGTTTAGACTATTCATTGGGATTTAACAATATTGTTTC  
76051 AAATCCCTGAAGGTTAAGTGAAACATTAATGCCAACTAACCAAGCATCTG  
76101 CTTCCAACACTGCTTTTCAAAATTTTTTAAAAGCAATCATTACTATAAAT  
76151 CCAAGCCAAGGATCGCAATTCATTAAACAAACCCAAGATCCATTACAAA  
76201 AAGATTTATCTATGCAATTGACAGTGATAAGGCATTAAAAATAATAATG  
76251 AACAAAACGGTTCCTAAAACCACTTAACTTTAAATGATGATTTTGCTAAA  
76301 TTTCTCTACAGTCAATTTGAATTAATTAATAAGAGTGGAATGCAAGTAA  
76351 TGAAGATTTAAATGCAATTGATTTTGAAAACCCCAACAATCAGAGATT  
76401 TTTACAACAAGTACAATGCTTTACCACCATTAGATTACAACTTAGCTTT  
76451 AATGTAATAGGTTTACCCAAAGAGACAATTGCTGGACAAATTGACACCCC  
76501 TAAGTATGGATTTTAAACCTTCATGGTGAATATCAAAATACTCCTATCA  
76551 AGATTAAAGGTATTAAGATTGAAAAGATAAAGTGGATAATTTAGGTCCA  
76601 GTTTTGAGTGATCAAAACAACCACATTATTAATCAAGAATTGTTTAAAAA  
76651 TTATTCTTTTGATCCTTTGATAGTTAACAATTCTGCTGCAAAAAAATACC

76701 AACTTGCAATAGGTAGTGAGATTAATATTGCAGTTAACACAGCTTCAAA  
76751 CGGATTGACAATAAGATCATTAATCAAGATCCTTTAGTGAATGCTACCTT  
5 76801 TAGAGTTGTAGGGATTAACAATTCCGCTCATGATCCTGAATTTTTCATA  
76851 GTTATAGTACTGCTTTTAAAGTATTGGAATATCCCAATGAATGGTTCGTA  
76901 AAAAACTTCCATTTAATAGCTTCTATGCTAATTCGCTTTTAAGTTTTGT  
76951 TCAATCTACTTCGCTATTTTCTGAATCTGGTATTTTTCCTGCTACTAGTA  
10 77001 GTTTTTCAACTAATAACACTGTACTTGTGAGTTAATAAAAAACCAT  
77051 AATTACAAGATGGTCAAATGAATCAAACCTCAAGTAATGACTCTTCTAA  
77101 GAAAGAAAATTACCAAAAATTGCAAAAAGCATTAGGAATATCAACTGATT  
15 77151 TGGAGATTAGTAAAGTTAATGAATATGTTGCTATCTTAGCAAGGGTTTAT  
77201 AATGGTTTACCTTACAACCTCTACTATTAGCTTTATTAGCAATGTTGCTGC  
77251 TAACAACGCTTTATTTGGAAATATTGCTAACACCACCAAGCAGATTCAAG  
77301 CTGTTGTAATTGCAGTGATTATTCCTATAATCATGTTGATTATTCTTTTG  
20 77351 GTTCAACTACCTTAATTCAAGAGTTGAAAAAATTGCTATTAGATTAAA  
77401 AGCATTGGGATATTCCAATTTAAAAATTCTCGCTTCATTTTTATCAATAT  
77451 ACATCCCTTTATTTGCCTTTGGTTTGTTGATTTCTATCCCTTTTCTATC  
25 77501 TATCTAATTGCACTACATAATGAGGTAATTTTGCAGCTCATCGATCTT  
77551 TTTAGATGCTTTTTTAAGTTTTGAAAGTGCAATTGGTTCAATGTTAGTTT  
77601 TACTAGCGGTTTTATCAATTACCTTTGTGTTGAATTGATTAGAGTTGAAC  
77651 AAAATTAAGATTGACAAGGAAATCAAAAACCTCCTAATGGATTTTTTCTCT  
30 77701 TTAAACAAAATCATAAAAACCAACCAGAAATTCCTAGTAATGAAGCTGA  
77751 ATTTCTACAGATAGCTACTGATTATTTGGAGGAAAGTCAAACTATCTTC  
77801 AAAAGGGTTTAAAGCAATTAAAAAAGAATATAAAAGATCCATTATTAT  
35 77851 AACCCTAACCTTGAATATAAACGCTTTGTTAAATGAAAAGAAAATTCAC  
77901 TGAAACATTTGAAAGTTATTATGACAGGTTTTTTATTACCAATACAACC  
77951 ATTATTCACTAAGCTTACTTTTTAGCTTTATTAATGAACAGATTGAAACA  
78001 GTTATTGCTAGTTACAACCTCATTTCTAAATGAGCATAATAAGTTAGCTTT  
40 78051 TAATAAAGTTAGTTTTAGTTTTGAAAAGAACTTTTTGAAGCTACACAAC  
78101 AGTTTAACTTAGAAAAAAACACTGCTATTAGTGATGATTTACCGCTC  
78151 CAGTTTAAAGTTAGAACAACCTCAACTAAAAGCCCAAGAGAAAGGGAATT  
45 78201 GAAGAACTTGTGAATAAAATCAAGCTTAAAAATTTAAGTGAAAAAAAC  
78251 AAGAAATTTGTAAATAACTGGTTTAAATAGCAACGAACGTTTGTTTTTA  
78301 AAAAAAGAGTGAAAAAGGTTAATTGACTAACTCGCCAAGACAAAAACA  
78351 ACAAGCAGCTCAAATTGATGATCAAAACATTATTGAATTGAAAAATGTGT  
50 78401 ATAAATACATCACTAATGGCATTACTACAAATGCAGTTCTTAAAGGAGTT  
78451 GATCTTGCCATTAAAAGTCATGATTTTATTGTGATTTTAGGCCCTTCAGG



78501 ATCTGGTAAAACCACATTACTAAACATTATTTTCAGGGATGGATAGAGCTT  
78551 CTAGTGGTAGTGTTATTGTCAATGGTTATAACATGATTGTGTTAAATGAT  
78601 AGAAAGCTCACTAAATTCCGTCAAAAGTATGTTGGTTACATCTTTCAACA  
78651 ATACGGTTTATTACCTAATTTAACAGTTAGAGAAAACATTGAGATAGGAG  
78701 CAAATCTTCAACCAGATCCTAGTAAAAGGATCAGCATTGATGCACTTTTA  
78751 GAAGCGGTTGGGATGGATAGTTTGCAAAGAAGCTTCCTAATGAATTGAG  
78801 TGGTGGGCAACAGCAACGTGTTTCCATTGCAAGAGCTTTTGCTAAAAACC  
78851 CCTTATTAATTTTTGGTGATGAACCTACTGGGGCACTTGATCTTGAGATG  
78901 ACCCAAATTGTTTTAAACAGTTTTTAGCAATTA AAAAGCGTTATCAAAC  
78951 GACAATGATTATTGTTACCCACAACAATTAATTGCTAACTTAGCTGATT  
79001 TAGTTATCTATGTAGCAGATGGAAAAATAAAATCACTACACAGGAACTTA  
79051 AATCCTAAACAGGTTGAAGAGATCCATTGAATTTAGATTATGAAATACTT  
79101 ATATGCCACTCAACACCTTACTTTAAATGCTATTAAGCATGCTAAGGGAG  
79151 GACATGTTGGCATGGCCATTGGTGCAAGTCCTATCTTATTTAGTTTATTT  
79201 ACTAAACACTTTTCACTTTGATCCTGACCAACCAAAGTGGATCAACAGAGA  
79251 TCGCTTTGTTTTAAGTGCTGGCCATGGTAGCATGGCATTATATTCAATTT  
79301 TCCATTTTGCCGGACTTATTTCTAAACAAGAGATCTTACAGCATAAACAT  
79351 GGTCAAATTAACACTTCTTCCCATCCTGAATATGCTCCAAATAACTTCAT  
79401 AGATGCATCAACAGGCCCTTTAGGTCAAGGCTTTGGCATGGCAGTTGGCA  
79451 TGGTGTTAGCACAAAAGTTATTAGCTAATGAATTTAAAGAGCTAAGTGAT  
79501 AAATGTTTGACCATTACACCTATGTGGTTGTTGGGGATGGAGATCTACA  
79551 GGAGGGGGTTAGTTATGAAGTTAGTCAAATGCTGGGTTATATAAATTAA  
79601 ATAACTAATTGTGCTTCATGATTCAAATAGAGTGCAAATGGATAGTGAA  
79651 GTAAAAAAGTTGCTAATGAAAATCTAAAGGTTAGGTTTGAAAACGTTGG  
79701 TTGGAATTACATCCATACTGATGATCAACTAGAAAATATTGATCAAGCTA  
79751 TTATTAAAGCCAAACAATCAGATAAGCCAACTTTTATTGAAGTGAGAACA  
79801 ACTATTGCTAAAAACACCCACCTTGAAGATCAGTATGGAGGACATTGGTT  
79851 TATCCCAATGAAGTGGACTTTCACTTTTGGAGAAAAGACAAATACTA  
79901 ACTTTAACTTTTTTAATTATCCAGATAGTATTTACCACTGATTCAAACAA  
79951 ACTGTTATTGAAAGACAAAAACAAATTAAAGAAGATTACAACaATTTGCT  
80001 AATTTCTCTTAAAGACAAACCACTTTTTAAAAAATTTACTAATTGGATTG  
80051 ACAGTGATTTTCAAGCCCTTTATCTTAACCAACTAGATGAAAAGAAAGTA  
80101 GCAAAAAAAGATAGTGCTACTAGAACTATTTAAAAGATTTTTTAAACCA  
80151 AATTAATAATCCTAATTCCACTTGATTTGCTTAAATGCTGATGTATCAC  
80201 GTTCTTGTTTTATCAAGATAGGTGATGATAATCTCCATGAAAAATCCTTGT  
80251 TCTAGAAATATCCAATAGGAATTAGGGAGTTTGCAATGGCAACAATAAT

80301 GAATGGTATGGCACTTCATGGTGGTATTAAAAGTGATGGGTGGTACTTTTT  
80351 TAGCATTGCTGATTATTCAAAGCCAGCAATTCGCTTAGGTGCATTAAATG  
5 80401 AACTTACCACTATTTTATGTTTATACCCATGACTCTTATCAAGTAGGGG  
80451 TGATGGTCCTACTCATCAACCCTATGATCAACTACCAATGTTAAGAGCAA  
80501 TTGAAAATGTTTGTGTATTTTCGTCCTTGTGATGAAAAGGAACTTGTGCT  
10 80551 GGATTTAACTATGGTCTTTTAAAGTCAAGATCAGACAACCTGTTTGGTTTT  
80601 AACACGTCAACCCCTAAAATCCATTGATAACACTGATAGTTTAAAAACAC  
80651 TGAAGGGTGGTTATATCCTTTTGGATAGAAAACAACCTGATTTAATTATT  
80701 GCTGCTAGTGGTAGTGAAGTGCAACTTGCAATAGAGTTTGAAAAAGTTTT  
15 80751 AACTAAACAAAATGTAAAGGTAAGAATTCTGTCAGTCCCAATATAACTT  
80801 TACTTTTAAACAAGATGAAAAATATCTAAAGAGTTTATTTGATGCTAAC  
80851 AGTTCACTTATCACCATAGAAGCTAGTAGCTATGAGTGGTTTTGCTT  
80901 TAAGAAGTATGTTAAAAACCATGCTCATTTAGGAGCTTTTAGTTTTGGTG  
20 80951 AATCTGATGATGGAGATAAAGTTTATCAGCAAAAAGGGTTAATCTGGAA  
81001 AGGTTAATGAAAATATTTACTTCCCTAAGAAATTTAAATTATCTTAATGT  
81051 TGTATAGGTTTTGAAAAACAGGATTGGCAATTTTTATGCCTGGTTGCATC  
25 81101 TTACTTTCATCCTGTTCTTTTAGAAGTTATATCCCAACTCCTAGTTTAAAG  
81151 AAATACTGTTGGTAATCACAACAGTTATGTTAATAATACTGTCCCTAAAA  
81201 ACAATTTTATGAAAAGTTTATGATCTAACTTTTGCTTTAAATTTCACT  
81251 AATCAGAAAACCAAGAGTTTGGTACTGGTTGTTAATTGACTGAAAAGG  
30 81301 AGATGAAACTAAAGATCTTAATACATTAACCTATTGCTAGTTCCTTCTATTA  
81351 TTTCTCTGTAAGTAATCATTCCTTTAAAAGAAAAACAAGATGACAAGCTT  
81401 TTTATTGCTTATATTGCCACCAATTTACATCTGATAGATGGTTTAAAGAA  
35 81451 TGATCATGATTATCAACCATACAATAAAGATGGAAATGGTCTTAGTTTTT  
81501 CATTTGATCAAAAAACCAATCATTCCTTATTGGGTAGGTTTGCCAATCCT  
81551 AAGATAAATTCCAAACCAGAAGAGATGAACTACCAAGTTCAAACCTCGTTT  
40 81601 AAAACAAGATGCAATGGTGTATTCCAAACCAGTACTTTACCTAAAACCTG  
81651 CTTATGCAGGAATTGATCCTATTAACTTTGATTACCATGAACTAGTGAT  
81701 GAGAGTGGATTTTGAACTAAAAACAAGCACTGCAAACTTCCCTAGAAC  
81751 AAGAACATTAAAAAGTTATGCTGATTTTGAGTTTATAGAGGTACCCTTAT  
45 81801 TCTTAGATAATGCTAATGATGCCAAGATTTATCAAGAGTGAATTAGACCA  
81851 GCAGTTCAAGCTTATAAGGAGCTAGGGGATGTTGAAAATATTTTGGCTAA  
81901 AACCCCATACGCTGAATATATTAATAACACCTACTACTTATTGGGTTATC  
50 81951 CTGTTACTAATAACAATAAGTATCAGTTTATCTTAGGTCAAGATGAAAAG  
82001 TGAAAGTTTTCTCAACAACTTCTGTATTAAAGCACTATCAAAAACAACC  
82051 TCTTCAACAAAGAACAGTTTATGTTGAACGTGATGATGGTCTTCCTACAT

82101 TAACTTTTAATGAAGATAAACTCACTCATGTTCAAGGTACTGATCTAATT  
82151 AATGTTGATCAGATTACCGATACTAATTTAGGAAATGGCTTAATAAATTA  
82201 TGCTGGTTTATCACGCTTTACTTTAAGCTATCACAATGTTGAATATAAGT  
82251 TATTTGGTTATGGCACTATTTTAAATAATACTAATTTTCCAGGTGGATCT  
82301 TCTGGTAGTGCTGTTTTCAACAAGGAAAAACAACATAACAAGTATTTACTT  
82351 TGGTTCAGTGATTAATGTAACAACCTGGAAATAACAGGAATGTTAATTTAG  
82401 GTTTGGGTCAAATTCTTCGTACTTATAACACTAATAATAGTAAGCACAGT  
82451 GCACCATCATCATATGATTTAATTTTTGGTGATAAAAAACCCATCAAGTT  
82501 TTATGCACAGTTTGCAAAGAAAAGCAAACCTCATCTTTGAAATAAAATTC  
82551 AAACATCTGTTAACTCTTCAATCAGCTTTTACAAAGACAAAAATAATAA  
82601 TTAACATAACAATTTGTATTTGTGTTAAGACGTTATCTAACTCTGAGTTTT  
82651 TCTAGCTTGCTTTTTATTAGCACTGCTGTTTTTAACAGGCTGTTCTTTTGT  
82701 TAGACCACAATTTTCGCAGGGGCTTTAGAACCAGTTTAAAATTAACCTTA  
82751 TTCCAACCTGTTAGTGATCCTTATCACATTAACTACGACTTAACCTTTTTCA  
82801 TTAACTTTGCTTCCAACAAAAGAAATACTTATGGTACTGGTTGGTTAAT  
82851 TGATTGGAAAGGAGATGAAAATAACCCTGAGAAAAATGATCCTTTTAAAG  
82901 TTTATTTAGCTACTAACCCTCATGTGATAGATGCTTTAAGAAATAATAAT  
82951 GACTATGAACCATATAACAAGGATAGTAATAACCAAGCTTTTAATAGTGA  
83001 AGAGATCACTAGGTTCTTTTCTATAGGTAAATACACATATCCTAGTATTT  
83051 TTAGTGAATTAAATTTTATTATCAATGCTAGAGAAGCGTTTGTTCGATT  
83101 CAAACCTCTACTATTTCCTAAAACCTGCTTATGCTGCTGTTAACTTTGTTGA  
83151 AACACAAGGAGAGGATGAAAGTTATACAGATTCATTATCAACTGATAATA  
83201 AAAGAGATATTTATGCGGATTTTGCTGTGATAGAAATTCCTTATTCTTA  
83251 ACTAACCATCGCGATTATCAAGTATTTAATGAATTTATTAAACCAGCAAT  
83301 AGAAACATACAAACAACCTAGGAACTCTTCCTTTGAAAAAAACAACCTAG  
83351 ATCAACATAAAAAACGACAACCTTTTACATGTTAGGTTATCCTTTGGTTGAG  
83401 AGTAGCATAGATGCTCTAATTTTGAACCAAAGAAGACAGTACAATAACAG  
83451 TTATACTGAAAAATATACTCCTCAAACCTTTAACCAAAGATCAACGTACCA  
83501 TTGACTTAAGCAGAGAAGTTCCTACTTTAATTCAGAACAAAACAGAAAAC  
83551 TCTACAGGAAGTCAATTACTAGTAAATCAATCTTTAAGTAGTACATCTGA  
83601 AGGGATTATTGAATTTATTAAAGTTACCTGAATTTAACTCAATTATCATA  
83651 ATAAAAGTTACCGTCAATATGGTAGAGGTTTTGCTCTACAAAACACTAAC  
83701 TTTAGACCAGGTTCTTCAGGAACTTTAATGTTAAATAACCAAAAACAGAT  
83751 AGCAGGTATTTATTTTGGTGTTTTAGATTTTGGAGAAGATGTAAGTTTAA  
83801 TGAGTAACATTGGCGTTGGACAAATTCTTCGTGTTCTCCTCAAAAGAACAAT  
83851 ACTAGAAATAGATCAATTGCTACTAATAAAAGCAACTATGATTTGATCTT

83901 TGGTGATAGCAATACAACCTAACTTTTATGCAAAATTTGCTAGACAAAATA  
83951 ACACCCATCTTTATCAGATGATTTCAAATAGTAAAGATACAAAATTAAAG  
5 84001 TATGTGAATACTGTTGAAAAAACAGTAAAGCTAGTATTAAATAAAACAA  
84051 AATAGTGACTTTCTTTTTTATACTCATAAAAAATGGAAAATCAAAACAGT  
84101 TGTAGTTCTGTAAAGAAAAAGAGTTATATAATCCAAAAAGCCTTTTCT  
84151 TTTTGCGGTAATTTCTTTCTTTGTTTTTCATAATATTTTTTGCTTTAGCAG  
10 84201 GTTCATTTACCAAATTTGCATTAGAAGAAAGCAGGGGTATAGTTTCTT  
84251 GTTATTGTCTGTTATCTTCTAGGAACAGTTTGTTTTTTGTTTTTATCTA  
84301 TTTTTGGTTTTGATTCTTATCTGAATTTTTTGCAAATAGAGTTCTAGTTA  
15 84351 AGTTATGAGATTTACCTACTAAAAAGAGAAGAAAAAGACATGCAAAAAA  
84401 CAAAGATAATTAGTTAAGTTTTAATAACTCAGTTGGCAAATAAATTAGGG  
84451 AGTTATTAGAACGCTATTTTTTATTAATTTAAGTGTGTGTTAAAAATTA  
84501 TTAAGTACTTTTTTAACCTGTTAAAAAGTAGTTATTTTATTAGTTGGAA  
20 84551 AGTGCAAAAAGAATTAAATATTTCAAATGATAAAAAGACTTGTTTAAATG  
84601 AAATAGAAACAAGCAAAGTTAAATTTCTAACAACAACCTTAATTTTGTG  
84651 TGATCAATATTAATAACACTCTTAGTTGTTGTTAGTGTATTAGCATTAA  
25 84701 TTTCAATTTATTAGGATCTACTAAACAAGGATTACCAAATACCAATGAAA  
84751 TAGAGACACTAAAAAGTTCATTAGCCTTGCAATTATCACAAAATGGTGTG  
84801 ATCTTATCAATAGCACTACTTGCTTTTTTTTAGTTGGATGGCAATTGTTGG  
84851 AATTCACAGCTTTTTTAGTTGGAATTTTAGTTAATCATCAAACACTTAAAA  
30 84901 TAAGTAAAAAGTATGTTATTTTAGGTTGATTTTTCCAATTATGGCATT  
84951 ACAAATACTcTGTAATTAGAAAAAAATTAAGAGCTTTATTAGGAGAGGGT  
85001 AAGGTTCAAAAAGGACTCaAGTTTTAACTATTAGTTTTATTGTGTTTTG  
35 85051 AAGCTTGCAATTGATAATAGGCTTTTTTGTATGACTTTTTCCCTTATGCTG  
85101 GTGAGGCAGGAATTAATATAGGAATTAATTTATCTATTTTTAATTTGGCT  
85151 CAGTTAGTAGGCTCAGATATAAATGTAATAACTTACTTTACAACCTTTTTT  
85201 AACGCTGCTTTTTGCATTTCTTTCATGAGCCGTATTGCATGTTTTAGCTT  
40 85251 GCTTTATTTTGGTACATTTGACTATTTATAACAACAAGAATGAATAAAA  
85301 ATTAAAGCTATTTACATTTTGGCTTTAACCTTAATTGATTTAATGGGTTT  
85351 AATTTTGGCTTTTGGTATTATTGTTGTTAACAATACAAATCTTCAAGTG  
45 85401 TTGATGCAAAATCAAATTCCTTAGCATTAAATTTTAAAGTTCATTATTTT  
85451 GGTAGTTCTATAGCAGCCTTTTTAACAGTTTTAAGTTTTGCTAGTTCAGT  
85501 TGCTTTACTTGTCAATTTAATAAAAAAAGATAAGGGATTAACCTTAAAAA  
85551 ATTAGTTAACCTCCCCAACCTCTATTTTCTGTTACTAGTGCCTAAGGTG  
50 85601 GTATTGGAGTATCACAGCTCAGTAAGGATGTAGTCAAAGAGAGTTTGGG  
85651 GGTGGATACATCAGGTTCAACTTTTGATCCAACCTAAAAGGTTGAAAAAAG

10

15

20

25

30

35

40

45

50

55

87501 TATCTTGTTTGAAAAGTAATGGAGAGGCGAGGAATGTTGTTAGCCTCCTTC  
87551 CTCTACTTTCAACCCAACAAGGTGAAAAGTGGTCAATACCAAACCACCAA  
5 87601 CACCTACAACAAGTTAATTGAACCTGACAAGTGACAATCAAGTAGTGATT  
87651 TGAACAATATGACCAACTTGTTAAAACTCCTAACAACTAAAAATGTGAAA  
87701 GCAAAGTTGGGGAAGACAGCCCAATCTCAGGAAAATAGTGGGGGGGTGAA  
10 87751 ATGATAAAATGTTTTTAAATAACTACATTAATTCTCTTAACTTACTAA  
87801 ATTATTTTTCCATTTGAACTATTATTTGAAAAAGTTATTAATTGCAAG  
87851 TTGATAAGAAAATGAAGCAAAATAACAAGAAAGAATTATCTAAATTTAA  
87901 ATAGACTAGAATTAAATTAAGACCAAAATGTTGCATGCAACAACATATG  
15 87951 CTCTTTTAGTTGTTTTTGGAAATTTTATTAGTTCTAATTGGACTAGGATTT  
88001 TTATTTTGAGCTTTAAAAATTTCACTTAAAGAACAAAAGAAAGGTCAAAT  
88051 TACTAATGATTTGACTTCCAATAACTCACTTAAAAATGAAGTTCCTAGAG  
88101 GGAGTTGATGAAAAAGAAACAACAAATTAGTTTTATTTTTGCTTGCAATA  
20 88151 GTTTTTTTAATGCTAGGAATAGGTGGACTTGTTTTCCCTTCCTAAGCTGTT  
88201 TGGTTAATAAAATTTAGTAGTTTTTAAATGCAGATTAGTTTAGTTAAAT  
88251 CCGCAATAAGTTTAAACAAAGAAACCGTGGTTCTTTTCGTCAGTGAGTTG  
25 88301 GTAAGCTTTCCAACGGTTTGATGATCCCTATTGCAGTTTTGCCTTTAGCA  
88351 GGTATTTTTTTAGGAATCGGTGATGCCATTTCTTCCAATTCATCTGGCAT  
88401 TGTGTTGTTGAAATTTTTTGGTGAATTTATTAAACAAGGTGGTAATGTAG  
88451 TTTTGTCTAACTTACCTATTTTGTGTTGCAGTTGCAATTGCGATCACCTTT  
30 88501 TCTCAAGATGCAGGGGTTGCTGGATTTTCTGCTTTTGTTTTTGGGCCAC  
88551 AATGAACGCGTTTATGAGTTCATTAATTATTCTGTTGATGCAATAATA  
88601 CTGCTTCAGGTTATAACATCCTTTATTGAAAAGCAGTACCTCAGTCAGCA  
35 88651 ATTGCTTCTACTTTAGGATTAAATTCACTTTCAACTTCAGTTTTTGGTGG  
88701 GATTATAGTAGGGGCTTTAACTGCATATTTATATAACAAGTTTTATGCAA  
88751 TTAGATTGCCTGATGTAATTGGGTTTTTTAGTGGTACTAGGTTTGTTCCT  
88801 ATTATTTGTATGACTATTGCTATTCCAGTAGCATTACTTTTATTGATGGT  
40 88851 TTGACCTGGTGTTTCTATCTTATTAAATTTAATAGGAACTGGGCTTGGAA  
88901 TCTTAGGTGGAAGAGGATATGGTGCTAACAGTTTAATCTTTGGATATATA  
88951 GAAAGAGCACTAATTCCTTTTGGAGTACATCATGCCTTTTATGCACCATT  
45 89001 ATGATATACAAGTGCAGGCGGTAGTTTGCAAGAAATTGCAAATCAACAAG  
89051 TTTGGATTAGAGCTCCTGGTAGTGATTATGTAACCAGAGTGATAGGTTGA  
89101 GAAGATTTTAATACTCCAGGAAAATGAGTTATTCTGCTGCTTTAGCTAA  
89151 TGGAAACAAGTGGAAATGATGAATGGAGCTACTACAACAGGACAAGATAGTA  
50 89201 CATCTGCACTTTCAAAATACATGAGTAAAGAATCAACAACTTTCTAAGT  
89251 TGAAAAGAACTTGTGATGGTCTTACACGTAAAGGTAACCTTTGATGAATT

89301 GGCTAAAAACGGTTTATTAGATGGTTCTAACAAGATTTGAATTGGTTTAA  
89351 ACCAGTCAGGGATCTTAGGTAAAAAAGTACTGTTAAGTGATGGTAAGGAC  
5 89401 TACACTATTACCTTTTAAACTTTTGCTAACACCACGCCAACATTCTGAAG  
89451 CCATGGTGCTCATGCACTTTTACCAATTAGTGGAACCTCCAAGTGCAATAA  
89501 CTAATGGAGTTACTGTTAATGGTACTGCTAATTCTAAAACCTATAATGTC  
89551 AGTCAGTTCAGTGTGTCAGTTCCTTCTTTAAACCCAGCACAAATATTCCCA  
10 89601 AGGTAAATTCCTCATGCTAATTGGAATTCAGCAGCTGGACTTGCAA  
89651 TGATCTTAGCTGCTCCTAAGGGTAGAAGAAAAGAAGCTAGTTCTATTATT  
89701 GGTAGTGCTGCATTCACTAGTTTTCTAACAGGGATCACCGAACCTTTTGA  
15 89751 ATTTACCTTTCTTTCTTAGCACCATGGTTATTCTATGGTATCCACGCTG  
89801 TATTAGCTGCAGTAAGCTTTTGATTAATGAACTTATTGAGTGCTAACGTT  
89851 GGACAAACCTTCTCAGGTTCTTTCATTGACTTTATCTTGTATGGGGCTTT  
89901 ACCTGATGGTAGGGGTTGATTAGCAAACCTTACTTAGTACCTATTATTG  
20 89951 GTATCTTTTTAGCATTGATTTATTTCCCTACCTTCTATTCTTGACAATT  
90001 CGCTTTAACTTAGCAAACCTCGGTAGAGGTGGTAAGTTAATTACTAAAA  
90051 GGAATATTTAGCAGCAAAAGCAGCTCAAAAACTGATCAAACCTACTAACA  
25 90101 CTAACCTTTAATCAAACCCAAATTGAAGCTGGTATGTTACTAAGAGCTTAT  
90151 GGTGGAAGTGAAAACATTGCTGAATTAGGGGCTTGCACTACTAAATTAAG  
90201 AGTAACAGTTAAAAACCCTGAACTTGTTAATGAACTATTATTAAAGACT  
90251 TGGGAGCAGCTGGGGTAATGCGTACCACTCCAACATTCTTTGTAGCAGTG  
30 90301 TTTGGTACTCGAGCTGCTGTTTATAAATCAGCAATGCAAGATATTATCCA  
90351 AGGCAAAGTAAATTGAACAGAGTTGCAAAAAGTCTTAGATAAAAAATGATA  
90401 GTACTGTTGAAAAACCAGAAATAAAACCAACCCAGTTTTTAAAGTTCAA  
90451 GATGAAATTGTGATCCTCTCACCAGTTAATGGCACCTTAAAACCGCTCAC  
35 90501 CCAAGTTCCTGATGATACCTTCAAAAATCGTTTGGTAGGAGATGGAATTG  
90551 CTATCTTACCTAGCGATGGGCACCTTCAAAGCACCAGGTGATGTGGGTGTG  
90601 AAAACTGAACTTGCTTTCCCTACTGGTCATGCCTTTATCTTTGATGTTGA  
40 90651 TGGTGTGAAAGTAATGCTTCACATTGGGATTGATACAGTAAAAATTAATG  
90701 CTGATAAAAAACCAGGGGAACAACTTGAAGTGTTTGATGTAAAAACAAAA  
90751 CAAGGAGAATACACTAAATTAAAGAGTGAAAGTGTTGTTGAAGTTGATTT  
45 90801 AAAGAACTTAAACGAAAGTATGATCCAATCACTCCTTTCATTGTGATGC  
90851 AAGAATCACTTGATAACTTCAAGTTGGTGCCAATTCGCCAACGTGGTGAA  
90901 ATTAAAGTTGGCCAACCTTTATTTAAACTAATTTATAAAGATAAGAAGAG  
90951 TTAATCAATAAACTCGATAATAACTAAAAGCCATAAAACCTTGGTTTTG  
50 91001 TGGTTTTTAGCTTGTTTATAACAATATTATTGCAGTTTTACTGCATAATG  
91051 TAAAATTACACAGCATGTCAGATACAAATACTGAAAAACCTGAGTTAGTT

91101 TCCCTTAATAAGTTAAGTGAGATGCGCACTAACATCGGGATGGTTAAACG  
91151 TTATTGAAACCCAAAGATGGGATTCTTTATCGAACCTGAACGTAAGCATA  
5 91201 ATAACGATTTATTGAAGCTTGATCTACAGTACCAAGCGTTAAAACTGCT  
91251 TATAACTTCATTAAGGATGTTGTTAAAAATCACGGACAAATCCTTTTTGT  
91301 TGGAACAAAGAATGATTATGTTAAAAAACTGGTAATTGATATTGCTAAAA  
10 91351 GAGTTAATGTTGCATATATTACCCAGCGCTGATTAGGTGGTACTTTAACT  
91401 AACTTTAAACCCCTTTCTATCTCAATTAACAACTCAATAAATTAGTTGA  
91451 ACAGCAAAGCAAATGCAAATGATCTAACCAAGAAAGAAAACCTGTTAC  
91501 TTTCAGAGAGATTGAAAGACTTGAAAAGTTCTTTGGTGGGGTCAAAAAT  
15 91551 TTAAAAAGACTTCCTAATCTAATAGTTATAGATGATCCTGTTTATGAAAA  
91601 AAATGCAGTTTTAGAAAGCAAACAGCTTAAAAATCCCTGTTGTGGCACTAT  
91651 GCAACACCAACACCAATCCAGAGCTAGTTGACTTTATTATTCCAGCTAAT  
91701 AACCACCAACCCCAAAGTACTTGTATTATTGATGAATTTACTAGCAGATGC  
20 91751 GATAGCAGAAGCGAAGGGTTTTGAAACCTTGATGCTTACAAACCAGATG  
91801 AACAGATCCAAATTGAAATTCCTCCCAAACAAGAACGCCAAGTTATTAAC  
91851 CGTTCCAATACCAGAAACATCACTAACCAGCGCTTAAACATTAACCGTCA  
25 91901 ACAACAAGAACTTTATAGAGCAGTGAACAGTTGAACAGGACTTAGTGAA  
91951 CAAGCGGCAATTAAGTTCGTCAAGAACATGGTGCTAATTTCTTCCTGA  
92001 GAAAAAGCTACCCCTTTTGGTTGTTATTTCTTCAACAATTTAAAGTT  
30 92051 TAGTTGTTATTCTTTTACTGCTAGCTAGCTTGTATCGTTTGTAGTTGCT  
92101 ATTGTCAGTGGTTTGAGAAGTAACTGAACTTTAACCATGATCTGATTAT  
92151 TGAATGGGTTCAACCTTTTATTATCTTATTAAGTGTTTTGGCAATTAC  
92201 TAATTGGTTCTATCCAGGAATTTAAAGCCAGAAATCTGCTAGTGCTTTA  
35 92251 AAGTCCTTGACAAAGTCTTTCACAAGGGTTTTTAGGAATGGTGAATTAAT  
92301 TAGCATTAAATGTTAGTGAAGTTGTTGTAGGAGATATTATTTTGTGTATG  
92351 CAGGAGATATTATCCCTGCTGATGGCAAATTACTACAGGTTAATAACTTA  
92401 CGTTGTTTGGAAAGCTTTTAACTGGTGAATCAACTCCAGTTGATAAGAC  
40 92451 TATTGATAGCAATGAAAAAGCTACTATTCTTGAACAGACAACTTAGTTT  
92501 TTTCAGGGGCACAAGTAGTTTATGGTAGTGGCGTTTTTCAAGTGGAAGCA  
92551 GTTGGGATTAACCAAGTTGGAAAAATTGCTAAAAGTGTGATGATAG  
45 92601 TGTAATAAACTCTCACCCTTACAACAAAACTAGAGAAGATAGGAAAGT  
92651 GATTTAGTTGGTTTGGGCTTGGTCTTTTGTGCTAGTTTTCTTGTCCTAA  
92701 ACTGCTTTATTAGGATTTGATAATTTCACTAATAACTGATCAATAGCTTT  
92751 AATTGGTGCTATTGCGCTTGTGTTGCAATTATCCCTGAAGGGCTTGTTA  
50 92801 CTTTTATTAATGTGATCTTTGCATTAAGTGTGCAGAACTAACTAAGCAA  
92851 AAAGCCATTATTAAGTATTTATCAGTAATTGAAACACTTGGATCAGTACA



92901 AATTATCTGTACTGATAAACTGGTACTTTAACCCAAAACAGATGAAAG  
92951 TTGTCGATCACTTCTGTTTTAATTCAACAACCCAACTGATCTAGCAAGA  
93001 GCATTGTGCTTGTGTAATAATGCTTCTATTTCCAAAGATGCTAATAAAAC  
93051 AGGTGATCCTACTGAAATTGCTCTCTTGGAATGAAAAGATCGCAGTCAAT  
93101 TAGATTTAAAAACCTATTACAGGGTTTATGAAAAAGCCTTTGATTCAATC  
93151 AGAAAACCTTATGACAGTTGTTGTTCAAAAAGACAACCGCTTCATTGTGAT  
93201 TGTTAAAGGTGCTCCTGATGTGTTATTACCATTATGTAATAACGTTCAAA  
93251 ATGAAGTAAAGAACATTGAAAACCTTACTTGATCAAAGTGCTGGTCAAGGC  
93301 TTGCGTACCTTAGCAGTTGCTTTAAAGGTTTTATATAAGTTTGATCAAAA  
93351 CGATCAGAAGCAAATTGATGAACTTGAAAACAACCTTGAATTCCTTGGGT  
93401 TTGTTAGTTTACAAGACCCACCAAGAAAAGAAAGTAAGGAAGCGATTTTA  
93451 GCGTGCAAGAAAGCTAATATAACCCCAATAATGATTACAGGGGATCATCT  
93501 TAAACTGCAACTGTAATTGCTAAAGAGTTAGGCATTTTAACTTTAGATA  
93551 ATCAAGCAGTTTTAGGTAGCGAACTAGATGAAAAGAAGATCTTGGATTAC  
93601 AGGGTATTTGCTAGAGTAACTCCCCAACAAAAATTAGCCATTGTTAGTGC  
93651 TTGAAAAGAAAGCGGGATTTACAGTTAGTGTTACTGGTGATGGGGTGAATG  
93701 ACGCACCTGCATTAATCAAGAGTGATGTAGGGTGTTGTATGGGGATTACT  
93751 GGGGTTGATATTGCAAAAGATGCTAGTGATCTGATTATTAGTGATGATAA  
93801 TTTGCTACTATAGTAAATGGTATTGAGGAGGGTAGAAAACTTTTTTAA  
93851 CTTGTAAACGAGTTTTATTAAACCTGTTTTTAACTTCAATTGCAGGAACA  
93901 GTTGTAGTTTTATTAGGACTATTCATCTTAGGACAAGTTTTTAAACTAA  
93951 TTTATTACAACAAGGTCATGACTTTCAGGTGTTTAGTCCTACCCAACTGC  
94001 TAATTATTAACCTGTTTGTTCATGGTTTTCTGCTGTTGCATTAGCAGTA  
94051 CAACCTGTTAAAGAAAAATTGATGGTAGGTAGTTTTTCTACTAAAAATCT  
94101 GTTTTACAACCGCCAGGGATTTGATTTAATCTGACAATCACTATTCTTAA  
94151 GCTTTTTAACTTTATTGTTCTATAGCTTAGGAATTATATATGCAATTAAT  
94201 AACCGTGATTTACAACTAGCGGGGATCTAATTAATCGTGCTGGATCAAC  
94251 GTGCGGTTTTTTTTATTTTGGGTGCTAGTGCTGCTTTAAACTCATTAAACC  
94301 TAATGGTAGATAAAACATTGCTTATGACAAACCTTGGTTTTTTAAGTTA  
94351 GTTTGAATAGGTTCACTTGCTTCTATACTGGTATTTTTATTGATCATCTT  
94401 TATCAACCTTTAGGGTTAGTGTTAATGTCTTGCAAGATTTAACTAATC  
94451 ACCCAGTTTTAATAAGCTATAGTTTTGGGGGAGTTATTTTGTATATGGGG  
94501 ATGAATGAAGTTGTAACTTATTAGATTAGGTTATGGCAATATTTAACT  
94551 TCCTTAAGTTAATTTCAACCAAAAACAGAATTCTCAGTAAGGCAAATAGG  
94601 ATTGCCAGTGAGGTTGAGAGTTATAAAAACTACTACCGTAACTTAACTGA  
94651 TCAACAGTTATTTGAAGAGTCAAATAAACTAGTTGATCTTGTCACTAAGC

94701 AAAATTACACCATTCTAGATGTTTGTGTTGCTGCACTTGCTTTAATTAGA  
94751 GAAGTGGTTTACCGTGAGACTGGTGAATTTGCATATAGGGTGCAGATCAT  
5 94801 AGGAGCTTTTATTGTTTTAAGTGGTGATTTTGTGAGATGATGACTGGTG  
94851 AAGGTAAGACCTTAACCATTGTTTATAGCAGCATACGTTTCTGCACTTGAA  
94901 AAGCGTGGTGTGCATGTTGTTACTGTTAATGAATATCTAGCTCAAAGGGA  
10 94951 TGCTAATAATGCAATGAAGATCTTAAACGGGTGGGATGAGTGTGGTT  
95001 GTAACCTTGCTAATCTCTCCCCTCAGCTAAAACAAGCTGCATTTAATTGC  
95051 GATGTTACCTACCACTAACAGTGAAGTGGGGTTTGATTATCTTAGAGA  
95101 TAACATGGTCCACAGTTATCAAGATAAGAAGATCAGAGAGTTGCACTTTG  
15 95151 CAATAGTTGATGAAGGTGATTGAGTTTAAATTGATGAGGCGCGAACGCCT  
95201 TTAATTATTTTCAGGTCCTAGTAAAAATGAGTTTGGGTTATATGTTGCAGT  
95251 TGATCGATTTGTTAAATCATTAACTGAACAGGAGTTTAAGATTGACCCCTG  
95301 AATCACGTGCTGCTTCTTTAACTGAAGTGGGATTAAAAAGCAGAGCAA  
20 95351 ACATTTAAAAAGAAAACCTTTTTGCTTTGGAAAACAGTGATCTTTTTCA  
95401 CAAGATCATGAATGGTTGACTGCTGTGAAAGTTTTTGAACAGGGCAAAG  
95451 AGTACATTGTTGCTGATGGCAAGGTTTTAATTGTTGATCACTTTACAGGT  
25 95501 AGGATATTGGAAGGGAGAAGTTACAGTAATGGCTTACAACAAGCTGTACA  
95551 AGCCAAAGAATATGTTGAGATAGAACCTGAAAATGTGATAGTAGCTACCA  
95601 TTACCTACCAATCCTTCTTTAGGCTATACAACCGCTTAGCAGCAGTATCA  
95651 GGTACTGCTTTAACTGAATCAGAGGAGTTTCTCAAGATTATAACATGGT  
30 95701 TGTAGTACCAGTGCCAATAACCGTCCTAACATCAGAAAAGACCGTTCTG  
95751 ATAGTGTATTTGGTACCCACAAATTAAGTGAATGGCAGTTGTTAAAGAG  
95801 ATAAAAAGATCCATGAACTTCTCGACCTATTCTGATTGGAAGTGTAA  
35 95851 CATAGATGATTCTGAACTCTTACATAATCTGTTACTAGAAGCTAATATTC  
95901 CCCATGAGGTTTTAAATGCTAAAAACCATTCAAGAGAAGCGGAGATAGTA  
95951 ACTAAAGCAGGACAGAAGAATGCAGTTACTATTTCAACTAACATGGCTGG  
96001 AAGAGGAACTGATATCCGTTTAGGTGAAGGGTTGCTGAAATGGGTGGTC  
40 96051 TTTATGTATTGGGAACTGAAAGAAATGAGTCAAGAAGGATTGATAACCAA  
96101 CTAAGAGGGAGAGCTGCTAGACAAGGTGATAAAGGGGAACTAAGTTCTT  
96151 TATCTCACTAGGTGATTGATTGTTTAAACGTTTTGCTCATGACAAGATTG  
45 96201 AAAGAGCGATTAGCAAATTAGGTAATGAAACATTTGACAGTGCCTTCTTT  
96251 TCCAAAATGTTAAGTAGAACCACAAAACGGGTGGAAGCAATTAACTTTGA  
96301 CACTAGAAAAACCTGATTGATTATGACCATGTTCTTGCAAGTCAAAGGG  
96351 AATTGATTTACAAACAACGTGATAAGTTTTTATTAGCAAACGATTTAAGT  
50 96401 GAAATGATCGACAAAATGCTAGAAAAGTTTGTACAACAGTTTTGTGATCA  
96451 ATATAGAAACCAAAGAACCAAACTTAATTAATCACATTGCACTAGCAG

96501 AAGCTTTAAATCTTGAGATGAACATGCAAAACACCATTAATCCAAAGGTG  
96551 TTTGAAAACATGACTTTTGATGTTGCTGTTGATAAAACCCGTAACCTTAGT  
5 96601 AGCTAAAAAGATTAGTGATAAAAGTTAATGTTTTGACCAAACCAATTGCTT  
96651 TAAACAGGTTTCGTGACATTATCATAAECTTCGATGGATAAACATTGAACT  
96701 GAACACTTGGATAGTGTTTTTAAGTTAAGAGAAGGGGTTGTACTTCGTTT  
10 96751 TATGGAACATACGAGTCCTTTAAATGTTTACATTAAAGAAACAGATATCC  
96801 TTTTTAAACAATGTTGCAAAAGATTGCTCAAGATGTCATTGTGCAAATT  
96851 GCTAACCTCACAACCTCCAGATGAATTTGATCATAGCTTAATGCAAGCCAA  
96901 TGCTTTAAAGAACTAGCAGCAATTAAAGCAGATGAAAAATCAAACCAAG  
15 96951 AGTAATAGTTTATTTTCAACTTCCACTAATATATACCTACTGGTGATCA  
97001 ACCTGAAGCAATTAAGAAATTATCAGAATTTAAACTAAGCAGCAGGTTT  
97051 TATTGGGGGCCACAGGCACAGGTAAAACCTTTACAATTGCTAATGTAATT  
20 97101 CAAAACAGCCAACTCCCAACAGTTGTTATTGCTCATAACAAAACCCTAGC  
97151 AGGTCAACTCTTCAATGAATTAAAGCAACTGTTTCCTAAAAATGCAGTTG  
97201 AATATTTTATCTCTTACTTTGATTTTTATCAACCTGAAGCTTACTTACCC  
97251 AGTAAAGGGATCTACATTGAAAAAGTGCTACAGTCAATGAAGCGATTAA  
25 97301 ACGCTTAAGAGTCTCAACACTGCATTCACTTTCAACAAGAAAAGATGTTA  
97351 TTGTAGTAGGTTCTGTTGCTAGTATTTATCCCACCTCATCTCCCAGTGAT  
97401 TTTGTTAAGTATTGCTTGTGGTTTGTGGTTGGCAAAGATTATGATTTGAA  
30 97451 AACCATTAAAGATAGGTTAGTTAGTCTTAACTATGTTGTTAATAACAAC  
97501 AATTAACCCAGGAAAATTTGCTTTTCAAGGTGATGTTTTGGAGGTATTT  
97551 CCTGGTTACAGTGATGCTTTTGTGATCAGAATCTCCTTTTTTGATACTAA  
97601 AGTAGAACAAATTTGTCAAATTGACCCACTAACAAATAAGATTTTAAACC  
35 97651 AACTCTTTGAGATTAAGATAGGTCCTGCTGATGAATATGTTGTAAACCAA  
97701 TCTGATCTTGATATAGCAATTAAAAATATTAACAAGAACTTCAGGAACG  
97751 AGTTAATTATTTCAATAAGCAAAATCTTGTTGAAAGAGCACAACGTTTAG  
97801 CCACCATTACTAACCATGATCTCAATGATCTGAAGGCTTGGGGATTTTGT  
40 97851 AGTGGAGTTGAAAACTATGCTAGACACTTAGAGTTGAGGATGGCTAACTC  
97901 AACCCCTTACAGTATCTTTGATTATTTTAAGGGGGATTGGTTACTGGTTA  
97951 TTGATGAATCACACCAAACCTTACCACCACTTAATGGGATGTATAACACT  
45 98001 GATCTTTCAAGAAAGCAAAGCTTAATTGATTATGGTTTTGACTCCCTC  
98051 TGCACCTTGATAACAGACCGCTCTCATTTGCTGAATTACAACAAAAATGC  
98101 AAAAAGTTATTTATGTTTCAGCAACTCCAAGAGATAAAGAGATTAGTTTA  
98151 AGTCAGAATAATGTCATTGAACAGTTAGTTAGACCAACTTACTTGGTTGA  
50 98201 TCCTATTATCGTTGTTAAACCAAAAGATAACCAGGTGGAGGATCTCATTG  
98251 AAGAGATTATCAACCAACGCCAAAACAACAAGAACATTTGTTACTGTT

98301 TTAAC TATTAAGATGGCTGAAAACCTCACTGAATACTTAAAGGAACGCAA  
98351 AATTAAAGTTGCCTATATCCATAAGGACATTAAAGCATTGGAACGTTTAT  
5 98401 TGTTAATTAATGACCTGAGAAGAGGTGAATATGAGTGT TAGTTGGGATT  
98451 AACCTTTTAAAGAGAAGGGTTAGATGTCCCTGAAGTTGCTTTAGTTTGTAT  
98501 CTTTGATGCAGATATCCCAGGACTACCTAGGGATGAGAGAAGTTTAATCC  
10 98551 AGATTATTGGACGTGCTGCTAGAAATGAACATGGTCGAGTTGTTATGTAT  
98601 GCTAACCATGTTACTGAACAGATGCAAAAAGCCATTGATGAAACCAAAAG  
98651 AAGAAGAACTGTTCAAATGGAATATAACAAGCTACATAATAAGACACCAA  
98701 AAACAGTTGT TAAACCCCTTACCTTTGTTCAACCAATCAAAT TAAAAGCT  
15 98751 AAGAGTAATGCAGAAAAAATGCTGCATTAATCAAACAATTAACCAAAGA  
98801 AATGAAGAAAGCAGCAGCTAATCAAAATTATGAACTTGCCATTGAGATTA  
98851 GAGATTCCATATTTGAATTGGAAAAAGAAATTGGTAGTAAAT TAAAGTA  
20 98901 TAGCAATGCGACAGTTTATTAAGCTTAGCCTCTTAGTCTTTGTCTTGCTT  
98951 TTC TTAAGTGAAC TTAATCTGTAGGTTCTCTTTACGCTTAGTAAAT TCTAT  
99001 TAAAGCGAGATATAAATCTTCAGTATTTTCTACACTGCTTGTTTGCTAT  
99051 TTTTAAAGAGTTTTCAAAAC TTTTCTAATGCTTTTCAGAAGTTAGCTAAC  
25 99101 TGGGTATTTTGATTTGAAAATGATGTTAATGAACTGTTATCTATCTTTTA  
99151 CTTTAACTTTGATCAGAAGAGTGAAAAAGTAGATTACAAC TTTCTTTAATG  
99201 GTTATAAAGTTACTGCTCAAAAAGTAGTTGAAAAAGAACAGTTATTA ACT  
99251 TGTAAGTTAAGTGATTACTACCGTTTATTTAGAGATAAAAC TTTTGATT  
30 99301 TGAAC TTAACAAC TAATAAGATCCTTATTGGCTGTTTAAGTTTGCTC  
99351 TCTTTATAAATTCATAACTTTTCTCTTAACATATGAAATTAAGTACAATA  
99401 ACTACTATCTGCTTGTC AATATCTGGTGCTTTTGGTACTACTGCAATTGC  
35 99451 TTTACCAACTACAGTAGCAT TGTTAAAAAACCAACAGCAAAACACTG  
99501 AAAAAACAACAAAACCCGATTAAAGATATCCGCTTTGGTTTAAACAATGTA  
99551 CAGGTTCCAAATACCATTCCGCTACACCAAAC TGTGGTTGAAGTGACCAA  
99601 CAACAAAGCAATTGTTGATTACAAAGATGCACCCCAAAAT TCTTTTAG  
40 99651 CTAAAAGTGCGTTAAATAATAAACTCCAAGTTGAGTTTGATAAGTTCTTG  
99701 TTAAGAACAGGAGTGATTAATGCTTTAATGCAGATTTGAAAGAATGGAT  
99751 AGACCAAACATTATTTATCCCAATCAAAGTTT TTTTGATCTTAGTGCTA  
45 99801 ATAAACTCAATTTAACTTTGTCAAATCAAAGCGAAGTGAGTTTAGATCTT  
99851 GAGTTTATTTTACTAACTTTAGTGATAAAAAATCAACCATTAAACTCCC  
99901 CTTTGATGGTAGTGTGGTGGTTAATGCTAACGAGTCATACACCTATT CAG  
99951 TTAAAGCAACACTACAGAACTAAAAGTATTGACTTATTCAAGAGCAGAT  
50 100001 CAT TCTGTAGGGATTAGTTATGCAATACCAACAGTGAGTTTAAATGGCAA  
100051 AACTCAAAATGACTTTAGTTT TTAACCCCTTTAAAAGTAATATTA ACTTTG

100101 CTTTCAAAAATGTCTACAATGCTTTAAATCCGTTTGAAGCACAACAATAC  
100151 CTGGTTGGCCAAGGTAAGTTTTTAAACCAAAAAGTTAATGCTGATGATGT  
5 100201 TAAAAATGACATTAATAATCACATTGAAACCCAGTTTAATGTTGCTAAAA  
100251 TCACAGCAACTCTTTTAGGAAAAGCTTTTAAGCAGTTTGGTGAACATAAA  
100301 AATGGTCAACCACTTTCACTTTTAAAAGTACTAAGTGGATTAAACAATGA  
10 100351 GTTTAAACAACCTTTTAATTATGTCAGACCTGGTTTAGGTGATTTTGTTA  
100401 GTGATTTAATCCAAAGCTCCAGTCAATCAAGTAATAAAAAAACTGTTTAC  
100451 CAGCTATTATTTGAAAACAAGACAACAATTATCCACTTGTTGCAAGATCT  
100501 TAATATTAGTGAACCTGAACCTGTTTTACCAGTTGTTGATATTTGTTTG  
15 100551 AAGGGATTAACAGTGCAGAATCACTATACCAAAGGATCCAATCATTTAAG  
100601 GATTTAATTGTTCCCTGCTTTAAAGCTGATAAGCAACTTAAGAGCTTAGA  
100651 AGCGATTATTTTAGCAGTTTGTAGACAATCCTAATACCTATGTTTTGATC  
20 100701 TTGTTTACCAAAACAAATCGATTCTGTTTAATTTGTTAAGTGATTTTCTT  
100751 AAAAACACCGCAAACACTTTACCATTTCTTCAAGAACAGTTTGATATTGT  
100801 TAACCACTTATTTGCCAATGAAGCGATCTTGATCTGTTTTCCAATGCTG  
100851 ACTTTGTGAGAAGATTGCTGATCTTTTTTTAGCAAAACAAAAGGTACAA  
25 100901 GAAGTTAATAATGATGGAACATAATCAACAAAAATTGTTGATTTCGATTTT  
100951 AGTTGCTACCCCTTAAGGGTTTAGTTGGTGATCAGCTCAGTTCAATCACTG  
101001 AACTGTTAAACATCTATATCTTTGAAAATGAATTTTTAAACAGAAATGAT  
101051 AGTAATAGTTTCAGTTAAAAACAACAACTGATAGTCTAAAAATCTGTT  
30 101101 TAGCGTAATTGGTGATATTTTAAGTGAGACCAATGTTAACAAGATCACTT  
101151 TACACGCAGTTAAAAATAATGAACTTCTTTTCGTTAGTTGAAACAGCTTCA  
101201 AACTAAAAATTAAACATCTTAATGTTCAATACAAAGTTTTAGTTGATAA  
35 101251 GTTTGAATTGAAAAACAGTTTCATTAAGGAACATTAATTTTTTTCCAG  
101301 ATACTAAAGATATCACCCCAACTATTA AAAAGGTACTGTTTGAAAGTGAA  
101351 AATTATAAAACACTCCGTAAGAAGTATGAAAATGAAGGGTTCCAGGTTA  
101401 TCACTGGGCTAAGTTCATTGTCCCAGGTACCTTCAATTCTGCTGAAAACA  
40 101451 CTTTCTATTCTGCTATTGATAAACTAAATCAATTCGCGATCTGTTTGCT  
101501 GACATGTTATTTGGTAAGAGTTTAGAGAGTGTTAATGACAGTGATAGTTT  
101551 TATCAAAATTAATGGTTCATTTACATTAAAGTACCACGGTGATAACTTAA  
45 101601 ATTTACTCCCTAACTACCACTCATTAACTACTAAGAATGTTGGTTATCAA  
101651 ATAGTTAATGTTAATTTTCATATTGATGCAAGATTGCTAACTGCAGAACT  
101701 ACAAACACGGTATTTTCAAATCCAAACAGTTATTAAATCACCTGTTG  
101751 AACTCTCCAAATCCTTATTTGAAGTTTGAAAGACTATCTTTGAAAACCTCA  
50 101801 GTTAACCAAATCTTAAAAAAGAATATACTTTCAAAGATAATCTAAAGTT  
101851 CTTTCCTTTTAAAGCTGATGGCTCCTCGCGCTTAGAATTTGATCTATCAA

101901 AACCTGATCAACGTGTTATTCCTTTTGCTTTTGTTGATGGTTATCAATTC  
101951 CAACTAAAAAAGAGTTAATTCCTAACAAAGAAACAAAAAAGAAGCTAA  
5 102001 TTCTTCACCAGTTTTAAAGCTTTATGATGCAGTTAAAAGAAACGATAGAC  
102051 AATATCGTCCTAATCACCACCATGATGATCTGAGAACTATCCTAGCCTT  
102101 AAATCTCAACTAGAACTTATATTAAACCTTGGTGATAAGCTTAAAGCTAA  
102151 TAATGATTTTATAGATGACACTGTTGTTAATGCTTTGCAATATAAAACTA  
10 102201 GTTTTAAATCTACTCTAAAAGTTAACAGTTTAGGAATTCCTATTAACCTT  
102251 TTCTTTTTTACATTGTGACTTAAATTTAACTTAGAAATTCGAATTGACGG  
102301 TTCATTAACATTAACATCCGTTAATGTTGTTTTCCCATACAGTTTGTATG  
102351 ATACTAGTTCGAATGAATTTACAAGGATAGTCGATCGCTTAAATTTCACT  
15 102401 GATACCAACTTCTATCTAAAAGATGCATTTCTAATTTCTGGTTTGTGG  
102451 TTTCTAGAGTAATGAACTAAACCACTAACTAACTACCACTAGATAAA  
102501 CAATCAAGTTCATCCACCAAAACCCACTAGTTTTTGTCTGTAAGTTGCA  
20 102551 CTTTGATCTTGATATTGATTAAACTAACTAATGGTTTTGCATAAACT  
102601 ACCTAACTTAAGATATCTGTTAACTTACTAATTCATACCGCATTCAT  
102651 CACAAGTTTTTAAACGGAATATCCCCTGTAAACAAACAAGTAATAAGTTA  
25 102701 ACAAAAAAGCTAGTTAGTACTGAaTTTTTAACAACCACTGTAAAATTGGT  
102751 TGACTTGTGAAAATAAATAGTAATGTTAAGATCAAAAAGAAAAGGATTA  
102801 GATAAAATACGCTAACAACCTATCCCACCATACTCAGCTTTATTACTGTTT  
102851 TTGTTTTGATTTAAAACCATCTAGTAATCGTTATTAGTATCATTTTTTTA  
30 102901 TAAAATAATCAAGAACATCAGCACATGATCTTTATCACTAAATTTATGTT  
102951 TGGTTTCAAATGAAGTTGGATTATAAATCCTGCTTTATGTAAATCATGCT  
103001 TTAGATTTAGAAGCTGGTTACTTTTTGTTTCAGGTAACCAGTACCATTTC  
35 103051 AAAAACTGAGAACCTGAAAAAACAGGTTCTTTTTTTATTTCTATTTAG  
103101 TAAATGTTCAAGTATATTCTTAAACGATTAGGACTAGCAGTAGTTGCGAT  
103151 GTTTATCGTAATGTCTATAGTCTTCTTTTTAGTGAACGCTACTGGTAATG  
103201 TTCCCTTGTCAGCCACTTCTGCAAGAGATATTGCTGCAGTGCAAGCACAA  
40 103251 CTACAAGAGTTTGGGTTTAATGACCCTATTATAGTTAGGTATTTTCGCTA  
103301 TTGAGCTAAGCTATTTTCTTTCAAGCTGATGCTTTAGGAATTTATTATG  
103351 CAAACCCTAACCAACAATTGGTGAGATTGTGTTTGCAAGAGTACCAAAT  
45 103401 ACCTTATATGTGGTTTTAATCTCTTTTTAATTGGTTCATTGCTAGGGAT  
103451 CTTTTAGGGATGGTTTCAGGATTGAATAGAGGGAAGTTTTTAGATGCAG  
103501 CAATTAATGTGTTGGTAGTTTTATTGTATCTATTCCTTCATTGTAGTG  
103551 GGATTAGGGTTACTTAACTAGCAGGATTTTTAAATCTACCACCACGGTT  
50 103601 TATTAACCTTTGATGATGCTTTTTTTAGCTTTGATCGTTTCTTGCTGCTAT  
103651 CAATTATCCCGATCCTTTCATTGGTCTTCTATTATCATCAGCTGCTTTTACA

103701 TACAGGATTAGAAATGAGGTGGTGGGAAGTGATGAATCAAGACTATATTAA  
103751 AACTGCAAAAAGTAAGGGACTTGGGATGTTTGCTGTAGCTAGGTATCATA  
5 103801 TCTTTAGAACTCGATTATTCCTTCTATTCCCTTGTTTGTATTTGGAATC  
103851 TCAGGTGCTTTTTTCAGGTGGATTTATTATTGAGTCTTTGTTTGGAGTACA  
103901 AGGGGTATCTAGGATCTTAATTGATTCAGTGCAAGTTAATGAAACTAACA  
103951 TGGTAATGTTTAATATCTTGTTTATCCAAGGGATTCCCTTATTAGCAAGT  
10 104001 GTCTTTATTGAATTTATCTATGTTTTAGTTGATCCTAGAATTAGGATTGC  
104051 AAATAGTTCTAATGTTAGCTTATTAAGTTAAAGTTCTTAAGTTCAA  
104101 GACACCAATGGTTAATGAAGTGAAACAAGATTAACAGTGATAATGCCCAA  
104151 AATATTGTGTTTAACTCGCCACTGCACCACCAGCTATTAGAACTCAATGC  
15 104201 AATTGATTACAAAACAAAACAGTTCAACTAACAAGTGAACAAAAAAGT  
104251 CTCTCAATATCAGTGCAACTGCTAAGTTTATCTTACTTGGTAACAAGTGT  
104301 TTAAAGCTCAAAACAATCCATGGATAGAAATAAAAGTTTTGACCCTAAGT  
20 104351 TATTTAAAGGGTTGATATCAACTTATTAAAGCGAAATGATCAGCTTATT  
104401 GGTAACCAACTACCAATTCAATAGAAATTATCAAGCGCTTGTTTCAAAA  
104451 CAAGTGGGCCATCTTATTTTTCTTTTAAAGTTGTTATTGTGCTATTAG  
25 104501 CAATTATTGTGCCTTTAACTCCCCCTTTTTTCAGCAGTAAGTCTGTTTCA  
104551 ACCAATGCCTTAGCACAAAATCTACCACCACGGTACTTATGGCATAAACC  
104601 AGGTGACATTTTAGTTTATAAGATTACAGCAAGATCAATTGCTGAAATCT  
104651 CTCAAGCTAGTGGAGTTTTAGTAGGAACATTACCTAGTGCAAATAGTAAT  
30 104701 CCCTTAGCAACTAATGTCCAGTATGATATTGCTCCTTTTCAACTCCAAGA  
104751 ATTGCGTAATTATTTCCCTTTATTGGGGACTAATGGACTTGGGATTGATA  
104801 TTTGAACCTTGTTGTGAGCTTCTGTTGCCAAGTCATTGTGAATTGCAGTA  
35 104851 GTAGTAGCAATTATAGCAATGGTGTGTTGGAACCATTTATGGAGCGGTTGC  
104901 TGGAAGCTTTGTTGGACATATGGCTGATAACATTATGAGTAGGATCATTG  
104951 AGATTATTGATATAGTCCCTTCTATTCTTTGAATTATTGTCTTAGGAGCT  
105001 ACATTCCGCTTTGGTGGGGTTAAACAATTTGATGATAGTGTGTAATCTT  
40 105051 TACTTTAATCTTTGTGTTTTGAACATGACCTGCTACTACAACCAGAAATT  
105101 ACATTTTGAAAAACAAAGATACAGAGTACATCCAAGCAGCTAAGACCCTA  
105151 GGGGCACACCAATCAGAATTATCTTTGTTTATATGTTACCTGTTGTATT  
45 105201 TGGGAGATTAGCTGTTGTGTTTGTAGTTTAAATCCCAGCAGTTATTGGTT  
105251 ATGAAGCTTCCTTAGTTTTCTTGGGTAAAACAGCTACTGATATTGGC  
105301 TTAGGGGCACCTTTTAAACCAAGTAAGTTCAAGTGATAATGTAGCTTTAAT  
105351 CTTAAGTTTCGATTGTTAGCTTTGCAGTTTTAACAGTAGCAGCTAGAACAT  
50 105401 TTGCTAATGCTTTAAATGATGCAATTGACCCTAGGGTTGTAAAACGATAA  
105451 AATGGCACTTAAAAGAAGTAATTTCTTTGTTGATAAAGACCAACAAGTAA

105501 AGGATAATTTGATCTTAGACATCACTGATTTACATGTAACTTTAAGGTT  
105551 AAAGATGGGATCTTACATGCTGTTAGAGGGATTGATCTTAAGGTAGAGAG  
5 105601 GGGTAGTATTGTAGGGATTGTAGGTGAATCAGGCAGCGGTAAATCAGTGA  
105651 GTGTTAAATCAATTATTGGTTTTAATGACAATGCACAACTAAAGCCAAA  
105701 CTGATGAACTTTAAAAACGTTGATATTACCAAACTAAAGAAACACCAAGT  
10 105751 GAAGTATTATAGAGGGACATATGTCTCTTATATTTCCCAAGACCCATTGT  
105801 TTTCTCTAAACCCAACAATGACGATAGGAAAAAAGTAAAAGAAGCGATT  
105851 TATGTGGCTTCAAAAAGAAGGTATTTCCAAGCTAAATCAGACTTAAAATT  
105901 TGCTTTATCAAATAAGGAGATTGACAAAAAACTTATAAAAGTAACTAA  
15 105951 AAGAGATCAAACAAACCTACCAACAAAAATAAAACCTATCAATGTAGAG  
106001 AAAAAAACCTTAGAGATCCTGCAGTTCATTGGTATTAATGATGCCAAGAA  
106051 ACGTTTAAAGGCATTCCCAAGTGAGTTTTTCAGGAGGGATGAGACAGAGAA  
106101 TTGTGATTGCTATTGCAGTAGCAACTGAACCTGATTTAATTATTGCTGAT  
20 106151 GAACCTACTACTGCACCTTGATGTAACCTATTCAAGCTAAGGTATTAACCTT  
106201 AATTAAACAACTCCGTGATCTACTTAATATCACTATTATCTTTATTAGTC  
106251 ACAATATCTCTTTAATTGCTAATTTCTGTGACTTTGTTTATGTTATGTAT  
25 106301 GCAGGGAAAATTGTAGAACAGGGTCTGGTTGAAGAGATCTTTACAAATCC  
106351 ACTCCATCCCTATACATGGGCATTGATTTCTTCAATTCTGAACAGAAAG  
106401 ATAAAAACAAACCACTAATCTTATCCCTGGAGTTATTCTTAACATGTTA  
106451 ACCCCACCAAAGGGTGATGCTTTTCGCTAGTAGAAACCAATATGCTCTAGC  
30 106501 AATTGACTTTGAATACCATCCACCCTTTTTTGAAGTTACTAAAACCCATA  
106551 AAGCAGCAACTTGATTGCTGCATCCCCAAGCCCCTAAAGTTGAACCACT  
106601 CAAGCGGTTATTGATAACATTACCTTAACCAAAAAAGCACTGCAATTTAA  
35 106651 AGATCAATAATGGAAAACCAAAACAAAAAAACCACTTGTTAATGTAA  
106701 GGCTTTGAGCATGATGTTCAAGGTCAGAGGAACCTTTTTTAAAGCCCTTG  
106751 ATGAAATTGGTTTTTACTGTTAATGAAGGGGACTTCTTTGGGGTTATTGGT  
106801 GAGAGTGGTAGTGGTAAATCAACCACGGGAAAATGTTTGATTAGATTAAA  
40 106851 CATTCTAGTGGTGGAAAGATTGAGATTGCCAACCCTTACTCTCAGGAA  
106901 AAAAATTACTAAAGAGAATAACCAAGTGGTTAAACAAAACATCCAAATG  
106951 GTGTTTCAAGACCCTTATTCATCTATTAACCCTACTAAAAATGTGCTAAC  
45 107001 TGTGATTTCAGAACCGCTGGTAATTAGTAAAACTGTTTTTGGGGAAACAA  
107051 AACAATACTTAAAGAGTTTGCAAAGCTCTCTTTTAAAGTAAAGAAAACA  
107101 TTGTTAAGGAATGATATTGAACTTGAAACCAAGTTTCACAATAACTTTTT  
107151 TAAAACCGTTATTAAGCAAATTAATGAATCATTGTTTAACTTTGAAGATC  
50 107201 TTGATTACAAGGATTTTAAACCATCACATTTAAGGCAAAGAATCATAAAT  
107251 GAAACAGATAAATTCATTGAAAAAATTAGAAGTGAGTTTGCCCTTTTTTA



107301 TGATTTTATGCTAACCAATCAGTACCCTTGCAAAAGGCATTAGATGATG  
107351 CGAATTCCTCTTTAACACCATCTAGTGTTATTGAGTTAAAAACCAGTTA  
107401 AAAGCATTACAAAAACAAGCAAAGATTTCAAAGGCAGCATGGGATATTTT  
107451 ACAAGCCCTAAAGCAAAACCAAAAGGAGTTGAAAGATTATGAAAATTATG  
107501 TCCATTTTGAAGCTCCAAAAAAGCCACGAATCTATCTTAATACCTGACTT  
107551 TTAACAACCAAAAGCTACATTAAAGATTCCAAGCAAAACATGCAGCTTAC  
107601 TGATGATATCTTTGCTTTTTCATATAACAGTATGGTTGACAAGAAAAGAA  
107651 ACTTGGTTTAAATTCTTCTAAATACTATAAGCTGTTACCTTATTTCTAT  
107701 GACCAATCAGTATTTGATAATGCTGATCAATTTGATGAAATTGCTAACCT  
107751 TATCTTTTTTGATTTAGTTGAAACATTGCTTGGTGTAAGTAGTTTATTTA  
107801 ATGATGCATTAGCAGCTGATAAAGTCCCACTAATTAAGTTTGCTAAGTTC  
107851 TTAAATAAGTTATGTGACTTGCCTTTTTAACCTTAAAAAGAGCTTTAA  
107901 AAAACAAGAGTAAGTTGTAGCTTTAGTTTTAACAGTGAACCTGAAATCT  
107951 TGTTTGCCAACAGCTGCTATGATTTGCAACAAATGCCTCAAATCATTAAA  
108001 CCCTTTTGAGAGAAGCTTTTAAATGAACAGAACTACCAAAAGATTATTGA  
108051 TTCAGTTTCAAGACTGAATGTAATGATTGCAAATTACATTACCAAAGCTT  
108101 TTGAAATTAAAAAACTATTGATGAAAACTAAGGGAGTTTAAACAACAA  
108151 AATTTAGCTTTAAAAAAAGCTTATTCAGCTAACAAGAAAAGTGAGGCAAA  
108201 CAAAGCTTCCATTAATGAGTTAAAAGTCAATTTAAAAACACTTAAAAAAC  
108251 AGCTTAAACAAGAGAAAAATACTACTAAAAACAATCAAAAAAGGAATTA  
108301 AAACCACTTTTAAAGAACACCATACTGCTTTAAAACTCCATGATGAGTT  
108351 TAACCATGATTTACGCAAGTGGTTCAAAAACTTAACCTTTATGGTTAAGA  
108401 AATACAACCGACTGGAAAAACAGCCAGAAAAAGTTTTGTTTAGTTAAAAAG  
108451 TTAAAGCGCTTTTCAAAAAACAGGATGAAACACTGCAAAGTGAATTAAG  
108501 ACCAAAACTAAAAACATTGGGTGTAATTAACCTTTGAGTACAAACGTGCAG  
108551 TCAAAGAGTCCAATGTCTTTCGATTGGTGCAATTTTGCTAAAAATATCTTT  
108601 AAACCATTCTTGTTTTTTAACCTCACCAAGATTTTTATGAGAAATAAGGT  
108651 CTATGAAGCACTTGATAGTGTGGTTTAAAAAGAGAACATGCTTACAGAT  
108701 ACCCCATGAATTTTCAGGCGGACAAAGACAAAGAATTGCTATTGCCCGT  
108751 GCTTTAATCACTAAACCCAAACTGATTATTGCAGATGAATTGATTAGTGC  
108801 ACTTGATGTTTCTATCCAAGCCCAAGTTATTAACATCTTGAAAGACTTGG  
108851 CTAAAAACACAACCTTAACGTGCTTTTTCATTGCCCATGATTATCAATG  
108901 GTGCAAACCTGTTTGTAACCGTTTGATCATTATGCATAGGGGCAAGATTGT  
108951 TGAACGGGGCAGTGTGGATGAGATCTTTTCAAATCCAGTTCATCCCTACA  
109001 CCCGTTCCCTAATAAAAGCATCTCCTAAGTTAAGCAAAATCAATGTTGAT  
109051 CTCGCTTCTTTTGATGAAAACTTCACTTATGATAGTGATTATTTACTAAC

109101 CAATATGCCCTTTTATATTAAAGTTCCTAACAGTGAAGAACATGAACTTT  
109151 ACTGTACTCAAAAGCAATTTGATAGTTGAATCAAAGAGGCTACGCCGATA  
5 109201 AATTAATTTAAAATTTTCCAAAAATGTGGGAGCTAATTAAGCGTTTGTAC  
109251 CACAGCAAAATATGGCTAAAAAACAGTTACAAGAATCGCTAAGATTAAC  
109301 CTAATTGGCGGACAAGCAAAACCTGGCCCTGCGCTTGCTTCTGTAGGGAT  
10 109351 TAATATGGGTGAGTTTACCAAACAATTTAATGAAAAACCAAGGATAGAC  
109401 AAGGTGAAACGATCCCTTGATAATCACTGCTTTTAACGATAAATCATT  
109451 ACTTTTGTCTTAAAACTACCCCTGTTAGTAACTTAATTAAACAAGCTGC  
109501 TAAACTAGAAAAAGGTGCTAAAAATGCAAAACTATTGTTGAAAAATCT  
15 109551 CCTTACAACAAGCTAAGGAGATTGCGCAATACAAGTTAGTTGATCTTAAT  
109601 GCTAACACAGTTGAAGCAGCATTAAAAATGGTGTTAGGTACAGCTAAACA  
109651 GATGGGAATAGAGGTAAGTATTAATGAAAAACTATCAAAAAGGATGCA  
109701 AGCTGTTACCAAGCTCATTGATAAAAACAAACCTTTATCCTATCCAAGAAG  
20 109751 CATTTGAATTAATTAAAAAACAGCAATTACTAAGTTTGTCAAGTTCAGTT  
109801 GATATTGCTGTTAGTTTAAACCTTGATACTACTAAAGCTGAACAACAGTT  
109851 AAGAGGTGCAATTGCTTTTCCTTTTAGTATTGGTAAATCTATCAGAATTT  
25 109901 TAGCTATCACTGATGATGAGAAAAAGCTAGTGAAGCAGGTGCTGATTTT  
109951 GTTGGTGGGCTTGATAAGATAGAAGCGATAAAAAATGGCTGATTAGATTT  
110001 TGATCTAATTATCACTTCTCCCAAGTTCATGGGAGCATTAGGTAACTAG  
110051 GAAACTATTAGGAACAGGGGATTGATGCCAAACCCAAAACTGAAACA  
30 110101 GTTACTGATGATGTAGTTAGTGCTATTAAAGCTTATAAAAAGGGTAAGAA  
110151 AGAATATCGAACTGATTCATTTGGCAACATCCACCTCTCTTTAGGTAAAA  
110201 CAGATACCAAACTGAGCACTTGCTTGCTAATGCCATGGCTTTAATAGAT  
110251 TTAATTAAGTCTAAACGTCCTAGCACAGTCAAAGGTACTTACATTAAAAA  
35 110301 TATTGCTTTGACAACAACATGGGACCAAGTTTAAAAGTAAAGCTACCTG  
110351 ATTAATGCCACCTATAAACTAATTGTTGGTTTAGGTAACTTAGGTAAAA  
110401 AGTATGAGAAAACCTCGCCATAATGCTGGTTTTATGGTGTTAGATAGACTA  
40 110451 GCTAGTTTATTCCACTTAACTTTGATAAAACCAACAAGTTAGGTGATTA  
110501 TCTTTTTATTAAAGAAAAAGCAGCAATCTTAGCAAAACCTGCTACCTTTA  
110551 TGAATAATAGCGGTCTTTTTGTGAAATGGTTACAAGATCACTTTCAAATT  
45 110601 CCGCTTGCAACATAATGATAGTCCATGATGAAATAGCGTTTGATTTGGG  
110651 AGTAATTAGGCTTAAATGCAAGGGAGTGCTAACAATCATAATGGCATAA  
110701 AATCAGTAATTAGACATTTAGATACTGAACAGTTCAATCGTTTACGCTTT  
110751 GGGATTAAATCACAAAATACGAGTAACATATTGCATGAACAGGTAATGAG  
50 110801 TGAATTCAGAATAGTGAAGTAACTGGAAGTTGCGATTACAAAGT  
110851 CTGTTGAACTGTTGAAGCGTTATATTGAAGGAGAAGAGTTACAAAGGTTA

110901 ATGGAATATTATCATCATGGCTAGTGAAAAACAATATATAGCAGGGGTTT  
110951 CAGGTGGATCTGATTCAATGCTAATGCTTAACTTTACCAAAAGAAGATT  
5 111001 GCTTGTGTTGTTTCATGTCAATTACAACACCAGATCAACCTCATTACGTGA  
111051 TCAAAAGTTAGTAGAACAATATTGTCAAAAATTAAATATTCCACTGGTTG  
111101 TTCACACTGTTGATCCTGATCTAGTTTGAAAGAAGAACTTTCAAAATCAG  
10 111151 GCACGGAATCCGCTTTGATCAGTTTAAAAAGACTGCAAAGCTATACCA  
111201 GACCAACAAGTTATTATTAGCTCATCACCGTGATGATTTCATTGAGCAGG  
111251 CCAAAATGCAACTAGATGCAAAAAACGTGCTGTTTACTATGGGATTAAA  
111301 ACCAGGTGTGAATTGTATGGTTTGAAAATCTACCGTCCCCTAATGAAATA  
15 111351 CTGAAAAGATGAAATCATTGCCCTCTGTAGACAAGACCATATCCCTTATG  
111401 AGATTGATGAACTAACAAGTTACCTATTTATAAGCGCAATGAAGTGAGG  
111451 TTAGAGATAGAAAAATGGTCTAAAATCGAAAAAGAACAGTTTATATTGC  
20 111501 TATCTGTGCAATGAACAAAACAATTGCTCAAAAAGTGTGTATTAAATGA  
111551 AAAAAAGCTAAAAATGGTTATTACAACCTGATGTTAGGGAATTGAAACGG  
111601 TTTTCAATTATTGATCAAAAACAGTTAATTTATAGCTATCTTATTTATCA  
111651 CAAGATTAATGTTAATGGTGAGAAAATTGATGCTATCCTTGATTTTATCC  
25 111701 AACCTAGTCAACAAAAACAATACCGCTTGCAAAACGATATCTTTTTGATG  
111751 GTGAAAAACAGTGTTTAGCACTTTTATACAAAAGCTAAATGAAACATTT  
111801 AACTGTCAAAGCATTAGTTTTGCAATTTAATGATTGTATCCAACTCATTG  
111851 ATGGTAAAAACAACATAGATAATGTGATTACTATCCCTGGGTAAAAAGG  
30 111901 AGTGTTTTTGAACTATTAGGACTATTTTGTAAGCCAATTGGTTCAGTTGC  
111951 TATTTTAGGTAAACGTGAATTTATTTTAAATCAAAGCCAGTTGAGC  
112001 AACAGAAAAAGATTATTGCAACCTCTTGAAACTCAAACCACCTGCAGTT  
35 112051 ATTCTAACCAAGTCATTTCTTGATTGTGGTGTTTGTGTAGCTGTTAATCA  
112101 AACTTATCAAGTTCCTATTTTAAAACTAACTTGTTTTCACTGAACTCT  
112151 CTTTACTGTTGAAACCTATATTAACGAGCAATTTGCTACTGTTCAAAAG  
112201 TTACATGGGGTTTTACTTGAAATCTTTGGTGTTGGGGTATTTTAGAAGG  
40 112251 AAAGAGTGGGATTGGTAAATCTGAAAGTGCTTTAGATTTAATTAATAAAA  
112301 ACCACCTTCTAATAGGTGATGATGCTATTGAGATCTACAGATTAGGCAAT  
112351 AGGTTATTTGGTAGAGCACAAGCACTGGCAAAAGGCTTTATGGAGATTAG  
45 112401 AGGTCTTGGCATCATTAATATTGAACGTGCTTATGGGTTACAGATTACAA  
112451 AAGAACAAACTGAAATCCAACTAGCAATTAGTTTGTGAGTTTAGAGGAG  
112501 AAAACAACGCTAGTTTTGAGCGCTTAGGCAGTGATTTAAACTAAAAAA  
112551 TCTGCTTGGGGTTAAGATTAGTTACTATCAGATCCCTATCTCTTCAGGTA  
50 112601 GAAAAACAAGCGAAATATTGAAAGTGCAAGTAATCGATTTTAACTTAAG  
112651 AAAAGTGGTTACAATTCAGCAAACGAGTTTATCTTAAAGCAACGTGCCAT

112701 GTTAGAAGAACAACTGATGAATAGACCAAGTTGATCAACTGCATTTAAT  
112751 ATTGGTGGTGGATTTCATCCAGTGGTATGGGATCATTGTCTCAATTGG  
5 112801 CATTATTTTTGCCATTTTAATGTTTGTCTTTAACTGATTTATTGTTACA  
112851 AATTACAAGACAACAGTTTTTATTTTTTTATCTTTATTGCTGTTTTAACG  
112901 ATGGTTTTAGGCGCTCGCCTCTGGTCATTTGTAATTGGTGATTCCAATTT  
10 112951 TGCTAACAACAATTTCTTTGATTTTCGTAACGGTGGATTGGCCATTTCAGG  
113001 GTGGGATTTTGTTAACCAGTATTGTGCGAGTAATCTATTTCAACTTCTTT  
113051 TTAAATAGTAAGACCAATAAAACCAAACGATTGCTGAATTACTGAATAA  
113101 TAAGAATGAAATAAAAGCTGTTTATGTTGAAAGAAATATCTCTGTTCTAG  
15 113151 TGATGTTAGATCTGATTGCTCCTTGTGTTTTAATTGGTCAAGCAATTGGC  
113201 AGATGGGGTAATTTTTTCAACCAAGAAGTTTATGGGTTTGCTTTAGCTGG  
113251 AACAATGAATGATCCCCAAGCATTGGCTAATACCCAGTGGGGATTTTTTAA  
113301 AGATCTTAATGCCTAAGGTTTGGGATGGGATGTGGATTGATGGTCAGTTT  
20 113351 CGCATTCCGCTCTTTTTTAATTGAGTCATTTTTTAACACTATTTTCTTTGT  
113401 GTTAATTTACTTTGTAATGGATTTTATTAGGGGAGTTAAAAGTGGCACAA  
113451 TTGGTTTTAGTTATTTTCTTGCTACTGGAATCATTGTTTAATCTTGGA  
25 113501 AACTTTAGAGACCAAACCTTTTTATTTTCAAACCTCAATAACCACTAGTAT  
113551 TTTGTTTATTGTCGTTGGTATTTTAGGAATTTTTTATTGCCAGTTTATCC  
113601 ATGTCAAATTAAGAAATTACTTCTGAACTTATTTCTTTCTTTATGCCTTT  
113651 TATAAAGTAGCTGCTTTTTTCACTACACTTTTTTTGAATAACAGAAAGCA  
30 113701 AATGGCACAACAGAAGTTTGCTTTTTATGAAAAATCACTTCCCAATAAGA  
113751 AGCGTTCTTTTTTTGAAATGAAGTATTACAATGATGTAACAACACCCCAA  
113801 ATTTATCGTTTAACTGATCAGGAAATGAAGTTATTTGATAAATTAGAGGC  
35 113851 AGTTACAACCAGCTAGATTTTGTAGAATACTTCAGTTGTCTATATGGCT  
113901 ACAATAGCGCAATTAATTAGAAAACACGCCAAAAAAGAAGGTTAAATC  
113951 AAAGTCACCTGCACTCCATTATAACCTCAACCTTTTAAACAAAAAACTA  
114001 CCAATGTTTACTCACCCTAAAGCGTGGTGTGTCACCAGGGTTGGCACC  
40 114051 ATGACCCCCAGAAAACCTAATTCTGCACTAAGAAAGTATGCTAAGGTTAG  
114101 ACTTACAAATGGCTTTGAAGTACTTGCTTATATCCAGGAGAAGGTCATA  
114151 ACCTACAAGAACACAGTGTTACTTTATTAAGGGGGGTAGAGTAAAAGAT  
45 114201 CTCCCTGGAGTTAGATACCATATTGTTGCTGGTACTTTAGATACAGTTGG  
114251 TGTTGACAAAAGAAGACAACAACGTTCTGCATATGGCGCTAAAAAACCA  
114301 AACCAAAATCTTAACCTTGATCAGTTAAATAATGAGAAAAAATCGTGCTTT  
114351 AAAAAGAACTGTTTTACCCGATCCTGTTTTTAACAACACACTGGTTACAA  
50 114401 GGATTATTAATGTCATCATGAAAGATGGCAAGAAGGGTTTAGCACAACGC  
114451 ATCTTGATGGTGCTTTTGAGATCATTGAAAAACGCACCAACCAACAACC

114501 TTTAACTGTCTTTGAAAAAGCAGTTGATAATGTTATGCCCCGCTTAGAGT  
114551 TAAAAGTGAGAAGAATTGCTGGTTCTAACTACCAAGTACCAACTGAAGTT  
114601 CCCCCTGACAGAAGGATTGCTTTAGCACTAAGATGGATTGTGATCTTTGC  
114651 TAACAAAAGAAATGaAAAAaCAATGCTTGAACGTGTTGCTAATGAAATTA  
114701 TTGATGCTTTTAATAACACGGGTGCTAGTGTTAAAAAGAAGGATGATACT  
114751 CACAAGATGGCAGAAGCTAACAAAGCCTTTGCCACATGCGTTGGTAGTT  
114801 ATTTATTATGTCAAGAACAGTTGATTTAAAAAAGTTCCGTAAGTTTGGCA  
114851 TTATGGCCCATATTGATGCTGGGAAAACCCACATCAGAACGTATTTTG  
114901 TTCCATTTCAGGTAGAATTCAAGATTGGTGAAACCCATGATGGTGAATC  
114951 AGTGATGGACTGGATGGAACAAGAAAAAGAAAGGGGTATTACTATCACCT  
115001 CTGCAGCCACTTCAGTGAGCTGAAAAAAGTGCAGCTTAACTTGATTGAC  
115051 ACTCCTGGCCATGTTGACTTTACAGTTGAAGTGGAGCGTAGCTTAAGGGT  
115101 TTTGGATGGAGCAATTGCGGTATTGGATGCTCAAATGGGAGTAGAACCCAC  
115151 AAAGTGAACAGTATGAAGACAAGCTTCACGCTATGAAGTACCACGGGTA  
115201 ATCTTTGTTAATAAGATGGATAAAACCGGTGCTAACTTTGAGCGCTCTGT  
115251 TTTATCAATTCAACAACGCTTGGGAGTGAAAGCTGTTCTTATCAATTTT  
115301 CCATAGGTGCTGAAAATGATTTCAATGGCATCATTGATATCATCACTAAA  
115351 AAAGCTTATTTTTTTGATGGTAATAAGAGGAAAAATGCTATTGAAAAACC  
115401 AATTCCTGAACAGTATGTTGATCAAGTTGAAAAAGTTTACAACAAGTTAG  
115451 TTGAAGAAGTTGCTAGTTTAGATGATCAACTCATGGCTGATTATCTAGAT  
115501 GGTAAACCAATTGAAATTGATGCAATTAAAAATGCAATTAGAAACGGGGT  
115551 AATTCAGTGTAAAGTTTTTCCCGGTATTGTGTGGTTTCAAGTTTAAAAACA  
115601 AGGGAATTAAAGTCTTACTTGATGCAGTGGTTGATTTTCTCCCTTACCT  
115651 GTTGATGTCACCTGCTAAAGCAATTGATGCAACAACAAGAGATATC  
115701 TATTAAAGCTAGTGATGATGCTAACTTTATTGGCTTAGCATTTAAAGTTG  
115751 CTACTGATCCTTTTGTGGTAGATTAACTTTTATTAGGGTTTATGCAGGA  
115801 GTTTTAAAGTCTGGTTCTTATGTTAAGAATGTTAGAAAAACAAAAAGGA  
115851 AAGGGTATCACGTTTAGTGAAAATGCACGCACAAAATCGCAATGAAATTG  
115901 ATGAAATTAGAGCAGGGGATATCTGTGCAGTAATTGGCTTGAAGATACT  
115951 ACTACTGGAGAACTTTAACTGATGATAAGCTTGATGTGCAACTAGAAGC  
116001 AATGCAATTTGCTGAACCAAGTATCTCTTTAGCAGTAGAACCTAAAACTA  
116051 AAGCAGATCAGGAAAAGATGTCAATTGCTTTATCAAACTAGCAGAAGAA  
116101 GATCCTACTTTTAAACCTTTAGTGATCCTGAAACAGGGCAAAGTATTAT  
116151 TGCTGGAATGGGTGAGTTACACCTTGATATCTTAGTTGATAGGATGAAAC  
116201 GTGAATTTAAGGTAGAAGTTAACATTGGTGCACCTCAAGTTAGCTTTTCGT  
116251 GAAACCTTTAAATCAACTAGTGAAGTTGAGGGTAAATACATCAACAATC

116301 AGGTGGTAGAGGTCAATATGGACATGTTAAAATCCGTTTTGAACCTAATA  
116351 AAGATAAGGGCTTTGAATTTGTTGATAAGATTGTGGGCGGAAGGATTCCA  
116401 AGGGAATATATTAAACCAGTTCAAACTGGTCTTGAAAATGCAATGAATTC  
116451 AGGTCCCTTAGCAGGTTACCCAATGATTGATATTAAAGCTACCTTATTTG  
116501 ATGGTTCTTTCCATGAAGTTGACTCAAGTGAAATGGCTTTTAAAATTGCT  
116551 GCATCCTTAGCTTTAAAAGAAGCAGGTAAACAATGTAACCCAGTTTACT  
116601 TGAACCTATTATGGCAATAGAAGTTACTGTACCTGAACAGTACTTTGGGG  
116651 ATACAATGGGTGATATCAGTTCAAGAAGAGGGATCATTTGAAGGTACTGAA  
116701 CAACGTGATAATGTTCAACTAATAAAAGCAAAAGTACCTTTAAAGAGAT  
116751 GTTTGGTTATGCCACTGATTTACGCTCTTTTTCCCAAGGTAGGGGTAATT  
116801 ATGTAATGCAATTTAGCCATTATGCTGAAACTCCTAAAAGCGTTGTTAAT  
116851 GAGATAATTGCTAATAAAAAATAGATACTTAATAAAAAATATACTTTACT  
116901 CAATGAGTTTTTCCAAAAGTTTTTATGCACTACAATATCATTCTTTTAG  
116951 TTGATGGTACGCTTAGTTTAGAACAAGCTAACCAAGTTGAACAAAACAC  
117001 CAAAATTGCTTGAAAAGGCAACTGAATTTAAAAGTGAATACTTAGGTTT  
117051 AAAAGAGTTGGCTTACCCCATTAAGCAACTTTCTGCTCACTATTACA  
117101 GATGGAGTTTTCATGGTGAAAGCAATTGTACTAAGGAGTTTAAAAGAGCT  
117151 GCTAACATCAATAAGCAGATAATAAGAGAGTTAATTATTACAGAGAAAA  
117201 AGACTATGGTTATTTAGGTTGAGTTAACCCTAACCAAACTGTCTT  
117251 TGCAGAAGCTAACCAAGTATAATGAGATTATTGCTAGTGAAAATAATCCT  
117301 GATAACCCAGATGCGCCTGTCACTTCTGGTCTAGCTTCTGTAAACCACG  
117351 GCTATCAAGAGTTGAAAACAAAAGGAACGTGAACCTGAAAAGTGAACGG  
117401 TTGTTACCAATCAGGTAACTTTGATACTGTACAGATCAATCCTTATCGT  
117451 CCTAGGATAAACCGCTTTTTACAAAACAACCAACAAACCTCCCAAGCTAA  
117501 TAATAACCAACCTCGTTTTTCAAAATCAATTTAAAAAAGGAGCAAAACCTT  
117551 AGATGAACCGGGTCTTCTTGTGTTGGTAAACTCAGTTTACTCCCAACCGT  
117601 TTACAGACAAAAATGGTACGTTAGGAGCTACTTTTCCATGGAATGTCT  
117651 TGATTCCAGTGGTTTAAATAATGCCAAATCATTATTAGAGTAACTGCTT  
117701 GAGGTAAAGTTGCTAGTTTTATTGTTGCTCAAAATCCTGGGGTGATGCTT  
117751 TTTGTAGAAGGAAGATTAACTACATATAAAATTACTAACAGTGAAAATAA  
117801 AAACACCTATGCTTTACAAGTAAGTCTGATAAGATCTTTCATCCTGATG  
117851 AAAAACTACCAATGAAGAACCTATTAAATCAACTGTAGTTGATTCACCC  
117901 TTTATGAATCCCAAGCAAGTGTTACAGAAGCTGAGTTTGAACAAGCATT  
117951 CCCCCATCAAGATGAACTGATTTTAAACAACATTACCCCTATATTTGAAA  
118001 ATGATGTCCAAGTAGAGGAGGAAAGTGATGATTAATAAAGAACAGGATTT  
118051 AAACCAATTAGAAACCAACCAAGAACAGAGTGTTGAACAAAACCAACTG

118101 ATGAAAAGCGCAAGCCAAAACCAACTTTAAAAGAGCAAAAAAATATTGT  
118151 CGATTTTGCGCCATAGGTCAACTAAGGATTGATTTTATTGATGATTTGGA  
118201 AGCAATCAAACGCTTTCTCAGTCCCTATGCAAAGATTAATCCTAGAAGAA  
118251 TTACAGGTAATTGCAACATGCACCAACGTCATGTAGCTAATGCTCTAAA  
118301 CGAGCACGTTACCTAGCTTTAGTGCCATTTATTAAAGATTAAATATGAAG  
118351 ATAATTTTGAAGCAAGATGTTGCTAAATTAGGCAAGCGGTTTGATGTTGT  
118401 TGAAGTTAAAGATGGGTTTGCTATCCATTTTTTATTTCCAAAAAACTAG  
118451 CTGCACCTTTAACAAAGAAAGCAATTGCTAACCGTGATTTGTTTTTAAAA  
118501 CAACAACAAGAACAATACCAAAAAATCGTGCCTTAGCTGAAAAATTGAA  
118551 ACTAGTAATTGAACAAACACCATTAACTTTTCAACTCAAACAACACGATG  
118601 GCAAGCCATATGGTTCAATCATCACCAACAAATAATTAATTTAGCAAAA  
118651 CAACAAAGACTTGATTTACAGCGCTTTATGTTTAAAGATAATGTGCGCTT  
118701 ACAGTTTGGTGAACACAACTAATTTTGACCTTTTGGAGAGATAACTG  
118751 CAACTTTAACTGTTATAGTGAACCCCTGAAAATGGGACAACAACTAGTTT  
118801 TAAATATGCAAATGATAGCAACATTGAACGTGCTGAAAGACGTTTGATGC  
118851 AAGCAGTTGCTCAAACAGTGAGGGCATTGATCTAATTTTCAATAAACTT  
118901 GAACCAATTGATTTTTTTGCAACCCCTTTCAAACCTATTTTTCAAACGTC  
118951 AAAAGAAAACCTACCAATTAAATAACCCCTATTATTGGTTCTGGTTTACTAG  
119001 AAGCGGTTAAGTTTAACTTGATGCTAATGATCAATCCACTAAAAGTGAA  
119051 CTTGAAATTTTATTACAAAGATCTTATTAATCCGTTTACCACCTAACCA  
119101 AACAGAGATTAAACACTGGTTGATGTTGTTAAAAAGCTTCTATTTTTTC  
119151 GCAGGTTACAACAGTTTGCTAAGCGTGTTTACAACGAGGAATTTAAGTTA  
119201 AAAGAAGATCGTTTTGAAGGCTATTTACAAGCTATTCAAGATGATTTTGT  
119251 CAAGATTATCCACAGTGCTTTTAGTAACATCTTTGCTTTTAGCTATGATG  
119301 AGATTGCCAATCAAGAGGAAGCATTAAATAAAAAGGTTACCGTGGGGAA  
119351 TTGATCATCAGTGGACTTTCAAGTGGATTTTTTAAATTAGATCAACTTAC  
119401 ATCAGGTTGAAAACCAGGAGAGTTAATAGTAATAGCAGCTCGCCAGGTA  
119451 GAGGTAAACTGCCCTTTTGATTAAATTTATGGCTAGTGCAGCTAAACAA  
119501 ATTGATCCTAAACTGATGTGGTCTCTTCTTTAGTTTAGAGATGCGTAA  
119551 CCGGGAAATTTACCAAAGGCACTTAATGCATGAAAGTCAAACCTAGTTACA  
119601 CACTAACCAACCGGCAAAGGATTAATAATGTCTTTGAAGAGTTAATGGAA  
119651 GCATCTTCAAGGATCAAAAACCTTACCTATTAAACTCTTTGATTACAGTAG  
119701 TTTAACTCCAAGAGATCAGAAACCAATTACTGAAGTGAGTAAACCA  
119751 GTAATGTTAGGTTAGTAATTATTGACTATTTACAACCTTGTTAATGCTTTA  
119801 AAAAAATACTATGGTTTGACAAGACAACAAGAAGTGACAATGATCTCTCA  
119851 ATCACTTAAAGCATTGCTAAGGAGTTAATACCCCTATTATTGCTGCAG

119901 CTCAACTTTCTAGAAGGATTGAAGAAAGGAAAGATTCCAGACCAATTCTT  
119951 TCTGATTTAAGAGAATCAGGTTCAATTGAACAGGATGCGGATATGGTTTTT  
5 120001 ATTTATCCATAGAACTAATGATGATAAAAAAGAACAGGAAGAGGAGAACA  
120051 CAAACTTGTTTGAAGTGGAGCTTATCTTAGAAAAGAACAGAAATGGTCCC  
120101 AATGGCAAAGTTAAACTAACTTTCGCAGTGACACTTCTTCTTTTATTAG  
10 120151 TCAATATTTCCCCTAGTTTTGATGACCAATACAGTTAATTTATGAACTGA  
120201 AGTTTTACAACTACCTTTAATTACTACAGCATTAGTTTTGTATTTTTA  
120251 ACTGCTTGTTCAACACCCCAATCTTCCTTTTTTCTCCCTGCACAAACAAC  
120301 TATTAGTACTTTAAAAATTAATGGTATGGAAAACAAAACAGGTATTTTTC  
15 120351 TTGAAACGCAGCGTTCTCGTGGTAGTTACAATCCCACCGCTTCACTTACT  
120401 ATGATTAAGTTAGGAGATGAAAAAGAGTTTAAAAACGTAGATACAACCAA  
120451 GCAAGATGAAGTTTTGTTTGGCAACATTTATGGTGAATCTCTTCATTGC  
20 120501 TTAACCTCAGAATTATCCAACCGATGTTAACCTACTGAACTTAGTTAAC  
120551 AACTCATTAAAGTCAGATTGGTAGTACTAATGACTTAATTACATTCAAAGA  
120601 TAGTGGATATAAAGATCAACTTGCAAAAGCGCTTGCTAACAATCTCATAG  
120651 TTGCTGATGAAGGTAATAATAACTTTTGGTTTGGTTTAAAAGCCCTAAAG  
25 120701 TTTGATACGGTTAAACTCCAAGCTAATAATACTGCTACTAGTTCAACAAG  
120751 AGCTTCAACTACTCAAAATACTAATAATAAGATTGATGCACGTGAAAAAA  
120801 TCACCATTAATGGGAATGGTGAACAAATAATGATCAAAATGCTACTGTT  
120851 CAAAAGTTGATAGGTATTGAAAATATTGAAGTTGAGTTTAGCTTTGTAA  
30 120901 AACTGGTTTTAATGGAAATGAGATTAAGTTTGAAGATTATGTAACAGATT  
120951 CTTCCCCACAACATCTTTATTAAAGCAAGTTTGAAAAAGTAAGTGAAAT  
121001 ACCGAGTTGACCCACACCAGCTTTAAATTCAAACCTCAATTCTTCAATGT  
35 121051 TTTGTAACTTATCAATTGGAAGCAAACCAAAAAAGCCAATATCTTCCCA  
121101 ATGGCTTTAGCTTTCTTTTCCATCTAATTAGAAGGAAAGATAGATAGT  
121151 TCAAAAAGCTATTGAAACAATCTTGTTGATTTTTCAAAAAGAACCACAAA  
40 121201 TGAAGAGAACACAATGCTACTAACTGATTTGCAAAAGAAACAAGATCAAG  
121251 TGAATCGGTTTTGTGGTTTTATTGGTCAAACCACTTTACTTTAAGTGCT  
121301 AACAGCATTAAATGAAAAGCAGTTTAACGATGCTAGTACTGCTGATTTTTT  
121351 TAAAGCAATCTTTCAAAAAGTGAGTATCAATGAATAACAATTTTAGCCAT  
45 121401 TCAGTTTTGAAAAGAAAAGTTTAAATTAATGGTAAAATTATTCAATAAC  
121451 TTTCTTGTTAGTTGTAGTTTTCAATACTGTTTGTATTTTGAAGTTTCAAT  
121501 TTAAAAAATTCGTAGTTCTAGATCTTAAATATGTTATTTAATTGTCTT  
50 121551 TTTTAATTTCAATAATTGTTTGAACACAAAAAATATCTTTAAGGTCA  
121601 AGGCCTTACTACTTTCACTTTTTTCTGCTGCTGTTACCATCACTATTTTT  
121651 GCTTTACCTATCTTTGCAACAATGGTTCTAAACTGATTTAGGTTTGCT



121701 TTCTAAAAATAGTGCTGATTTTTTTAGGTAGTTCAAAAAGAAGTCTTGCTG  
121751 GCTTTGATACTCCTTTTTAGTCCAGATAACCTCCAGTATTTAGAAAAAGAA  
121801 ACTGATTATGATCAGAAGTTTAAAAGTTTACTGAAAAGTTTAAAGATGA  
121851 AAAAAATACTAACAACCAACTTGGTATTGTTGATATCTATAACTTATTCA  
121901 GTGGTTTTTCACAAGAGTGTCAAAGCACAGTTGACTTAATGAACCAACTG  
121951 CAAAAGCAAGTTGAAGCTGCTAATGCTATCTTCCCAGTTGATGATGCTTT  
122001 TGTTAAATTACCTAAAGTACCTACTGAATTATTTAAGTTAGTTGATGATA  
122051 ATGTCTTTTCTAAGTTAAATCCTAAGGGCTTAAATATCTCTGATAATATT  
122101 GCTGCACTTTTTGAAAGATATAACCTTAAATCGATTGAACTTAAGAACTT  
122151 TGACTTAGCTTTCTTGAGAAAAGCTGATGTAATTATCAAAGACAAGGTTC  
122201 GATATAACTTTGAGATGCAAATGCAGTTTCAAAGTGTATGTTGGTGGA  
122251 GGAATACCGTTATTAACTTAGACTTTACTTTAAAAGCCCAAACCGTTAA  
122301 CTTTGCTAACCTCCAAGATTTACAAACACTTTTGTAAAGTTGGTAATG  
122351 ATCTTTCCACCCAAGTCTTTTGGATTCCAAGTGTAAATAAATTAAGTATG  
122401 AATGCAGGTAATGATCTTACCCATATTGCTAAAAGTGTGATTGGTGAATC  
122451 GTTTTTCCAAACCAATGTAACTTAGCTAAATCAGTTATTGAATATGATA  
122501 AGGTTCAACCATTTGGTTAAACAAGCTTTGAAGAGCGAGTTTTAACTCCT  
122551 TTCAAAAAGGAAAGAGAAGCTGCTAAAAAGCTTATGAAGAAGAACAACG  
122601 TCGCTTGGAAGAGGAACGTAAGCGTCAACTAGAAGAGCTAAGGAGAAGAG  
122651 AAGCTGAGGAGAAAAGAAAAGCTGAAGAAGCAAAACGAAATCAAGAAAAA  
122701 GCACGCAGAGAAAGAGAAGCTTATGAAAAATCATTTAACTCCTTTAAGA  
122751 CTTTAAATTTTACTGGTTAACTAAAGGTAAAGATGTTACTAAAAAGCTG  
122801 ATTTAATTGATGCACTTAAAACCGCTATTGCTACACCAGCATACAGAAAT  
122851 AGAACATTCTCTTTATTAATCAAAGGTTTGTAGTGGAGTTGAACGTTA  
122901 TTTCAACGCTAACAGAATGATAAAGAGTTGAAAAAAGTGCATTTGGTG  
122951 AAAAAAGGATCCAATTCCCTAGAGCAGATGCTGGGGTAAATGGTCTTTAC  
123001 ATGAGTAATTTTTTGAGGCATGAATTGACAAGCAAAGCAAAATTTTCACT  
123051 TAACCTAAAAGATATAAAAGTTGAAAATACGGTTGAAGATACTCAATTGT  
123101 ATTGGAAGGATAATGGCATTCAATTTAAAGCAAGCCAATCCTTATAAATTC  
123151 AATCTAAATATCAAGATCAAGTACAACGGCTGGTATAATGTCCACTGGTG  
123201 AAAGTGGCTCCCTGCTAAAATTTTAGGGATTCTACAGACTGAAGTGGTG  
123251 AGATGAATTTAACATTGTGTCAACGGTGACCTATCAGAAATTGTTGAT  
123301 AAACATGATTACCCTGGTACTTTCTTTCAATTTACCGATAAAAAATGAATT  
123351 GCTATTTACCTTAGCAGTTAGAGAACAAATTAAGGTTGATAATAATCATT  
123401 TTATGGGTCTGTTAAAAAGCCAAAACCTTCATAATCTTCAGCTTGCTTCT  
123451 GGTGCTACAAAACCTCCTGTTGTTGATTAGCTAGTTATTCCACTTTGT

123501 ATTATTGACTGAAAAATCTTAATCTATTAAGAAATTTTGTGATCAGTTACT  
123551 TTTACCTAGATAAAATTTAAAGTTTATTTGTGGTAATGGATGATCTATTCC  
123601 AAAGAATGGTTAGCTGTGTTCTACCGTCATGAAGAGCTTTTATTGATGAG  
123651 GAAGTTAAAAAACCTTATTTTCAAGCTTTATTAGAAAAATTAAAGGCTTT  
123701 AAAAGCAACAATAATTCAAAACCAGAACTTATTTCCGTGTTTTAGCT  
123751 TCTTTAAGCCAATTGATACAAAGGTAATTATCTTTGGTCAAGATCCCTAT  
123801 CCTAGTCCTAATGATGCTTGTGGACTTGCTTTTGCATCCAATAATTCOA  
123851 AACCCCTGCCAGCTTAAAAAGAATAATTTTACGTTTAGAAAAAGAATATC  
123901 CTTGCTTAAACAAGAAAGTAGTTGACAACAAACTTCCTATTGAATTGA  
123951 GCAGAACAGGGCGTTTTATTACTAAATGGAATTTAACAACACTACTGTATT  
124001 TATACGCAACGCCCATAAAAATTGGGGTTGGGAGGAGTTTAACTGTAATT  
124051 TGCTAACTTTTCTAAAAATCAAACATTAAACCGCTGTTGGTATTTCTG  
124101 GGTGTTCAAACATAAACTTTGTTGTTAAGAGTATTGGTAATGTTGATGG  
124151 ATTTGAGCATTTATCATATCCCATCCCTCACCCTAAGTGGTAATTTGT  
124201 TTCTAACAAACCCTAACGATCTGTTTAAACAATTAACAATTGGTTGAAA  
124251 CAACATAACCAAAAAATAATTAAGTGAAGCTGTTTAAATGCTAGTTT  
124301 TGACCAATTAAGTTAATTAACAAAGCTGTAGTTGACACTTGTTTTATT  
124351 GATTAGAAAAACAACCTTGTAATTAATTTAACTAAGTGAATTATTAC  
124401 TTAATTGCACTTTAGATGGGAGAGATTAAAAATACTGCACCAACAAGCGA  
124451 TATTTCCACTTCAGGATTTATCTATTTTGCAGTTGTTTTCTAATCATT  
124501 TAGTCTATCTTTTTTTTAAAAACATTCTCTTTTGTCTCTTTAAAGA  
124551 TATCCTAAAAACACACCTAAATTTGGGGTTAGCAATATTACTACTATTGC  
124601 TATGATTATTGCTGTTGCTGTATCTGTTGTTTGGTCTTAATGGCTTTAG  
124651 CAGGGGGGTTAACAGCAGCGCTGTTCCGTGGTTATCCTGGGTCCGTGTT  
124701 ACCTTAGAGTTAATTTCTAGTGAAGATTTAGGACTTTTATTGGTCCTAT  
124751 AATTGGTATTTTTCAGCAGCTACCATTGACTTTTAACTGTTATTTTTT  
124801 CAGGTGGGGTGTAAATATTGGTTATGTTTTAGGAGCAATCCTAACGGGA  
124851 ATGATTGCTGGAATTTTACGTGAAGTTTAAATTTCAACTTCTTTTTTAAA  
124901 TAACAAAACTTTAAGTGATTTTGCCATCTTGTTTTATCAGTGGGGATGG  
124951 TATTTGCCAGTTTTTTAGTAACCCAGTTTTTTGTTATCTCAGTTACCCAA  
125001 AACTTATCAGCATTTCAAAGTAATGATCAAATTGTTTTACGTTTTAACGC  
125051 CTCACCTTTAAATTTTCAAGTATCTCATGCAAAGATATGTTCAAATTATTT  
125101 TCTATTTGCGATGGTTGTAATCATCAATGGTAGTACTTTACTTTGTT  
125151 TGAATAATCAAGCAAAAGCACTTTAACTATGCTTATTTCAAGTTTTTCTT  
125201 TCGTAGATATAAACATGCTAATCACCATTACCTTATTTGTGTTAACAA  
125251 AAGAAAACCTGGTTTTATCTAATCTGAATGTAATTACATTAGCAACCACC

125301 AGTTTGCTAATGATTAACATTGCATTTATTCCTATCTTTGATACCCAAAC  
125351 AACTGGACAACTTATGATTTTTGATTATTAGTTAGATTATTGTTTGCTC  
125401 CTTTGATCTTCTTACTTGATATTATTGTTATCTATCCAATCTTGTTATTG  
125451 TTAACCCCAATCATGTTAAAAGGGTTTAAACAGTAGCATCAGAAACCCA  
125501 AACAAAAGGAATCAAAAAGAGTTTTTCAGATATGCAAAGCTTAATTATGC  
125551 CCAATGTTATTAGTCACAAAAACAGCAGTTAATTAGAAAAGAGATGCAA  
125601 CAGTTAGCAAAAACAATCAGAATTGATTTATCAGACAAAGAAGTGGATGC  
125651 ACTTGTTGAAGAGTTTAAAGAGATCACAAAGAGTTTTAATAAGGTAACCTA  
125701 AAATTGATACCACTAATGTTCAACCGATGTACGCTCCATTTGAATTTAGT  
125751 CCAACCCCACTAAGAAAAGATAAACCAGTAGTTGATAAACACGCTAAGCA  
125801 ACTACTTAATAACTGTTGTGAAGTTAAACAGGTTTTGTAAAGGTATAGT  
125851 TGTGCGATCAAATATTTTAAGTCTCAGGGCGATACTTGATAAAAAACCTA  
125901 GTGCCATTAACGATGTTTTAACATCAATTAATGCAAAGATAGAACTGAAT  
125951 AAATCAAGTAATTTTTTATTGAAAAATACTGTTGAAATTTATTCAAAAAA  
126001 AATTAATAAAAGTGATGAAAAGATTCTGCTAAATAACATCCCTTATGTTT  
126051 TGAAAGATAACATCGCTACTAAAGATATTGTCACCACTGGTGGTTCTTTG  
126101 TTTTTAAAAAATATCTTCCCCCTTTTCAGCAACTGTGTTTGAAGTGT  
126151 AGAAATGAATGGCGCGTTGCTTGTGGTAAAGCTAATATGGATGAATTTG  
126201 GCTTAGGTGGAACAGGTAGTTATTCTGCTTTTGGTGTGTTTCATCACCT  
126251 GAAAATTCAGTTTAATTGCAGGTGGTTCTTCTCAGGTTGAGCTTACGC  
126301 AGTTGCTAAAGACATTGTTTCTTTTCCATTGCAACTGACACTGGTGATT  
126351 CGATTAGAAGACCTGCTAGTATCTGTAATGTTGTTGGCTTTAAACCAACT  
126401 TATGGTTTGATATCACGTAATGGGGTATTTCCATATGCCCAAGTATGGA  
126451 CCATGTGGGGATATTGCTAAGTTTGTAGTGATATTGCCATTGTTAGTG  
126501 ATGTTGTTATTAAACATGATAAACTGATTTTTCTTCCCCAAAAATCACCT  
126551 GATGAAAACCAGTTTTTCAATGAGTTGGCCATTCCCTTTACAAGATCAAT  
126601 TCGCTTCGGTTATTTAAAACCACTAGAAAACTGTTTAAACAAACACCTCC  
126651 AAAAAAATGAAATAATCTCAAAAAACCTTAGAACAAAAAACTACCAG  
126701 TTGATTCCACTTGATTTTGATGTGGAACCTTCTCAAAGTAATTGATTCTAT  
126751 TTACAAAATAATTAGTTATAGCGAAGCAGTTAGTTGTTATAGTAATTTAA  
126801 CTGGCATTGTCTTTGGTCAAAAGGTGTTTGAACCTAATTCACCAAGTAAT  
126851 TTTGATCAAACCTATTACCAGAAACAGAGATCAGTTTTTAGGTAAACAACT  
126901 AAAAAAGAAGATTTGTAATAGGGGCATTGCAACTGATGAGAAGAATTTTG  
126951 AAAAGTACTTTGAAAAAGCTCAGAAAATAAGAAGAGTCTTAGTGGATAAC  
127001 TTTCTGAATCTCTTTAGTGATGTTGATTTTGTATTATCACCAAGCGCTTC  
127051 TTGTTTTGCTAGTACCATTGAAGATATTCAAGCTAATAAGCCATATACAA

127101 ACATTATTGATGACTTTTTACAATTAGCTAATTTTGCTGGTAGCCCTTCT  
127151 ATAACATATCCCTTGGTTAGTTCAAAACAAAAGACCAAACAATTGGTTTAAG  
127201 TATTAGTGCTAACTGTTTTGAAGATAAAAACTCTTACAAATTGCTTATT  
127251 GATTTGAACAACCTTTTTGATTTAAACCATGATTAAATTTGAAGCGATTAT  
127301 TGGAAATTGAAGTCCATGTAGTTTTAAATACTGCTAGCAAGATGTTTTCAA  
127351 AAGCACCTAACCGCGTTGATAATCAAAAAATCAATCATTTTATTGACCCA  
127401 ATAGATTTAGGTTTACCAGGCACCTTGCCTCAAGTTAATGAGTTAGCAGT  
127451 TTACAAGGCATTATTATTAGCTGATGCATTAATAATGAAGACAGTAACAA  
127501 ATAACTTGTTTTTGATCGAAAGCACTATTTTTATCAGGACTTACCTAAG  
127551 GGTTTTCAAATCACCAACAAAATTATCCTTTTGCTAAAAATGGTGTAGT  
127601 TACCATTAATGTTGATGCTATTGAAAAACCAATTTATATTGACCGGTTTC  
127651 ATTTGGAGGAAGATACTGCCAAACAACACTTTAACCATGACCAAATTCG  
127701 CTTGATTTAATAGGTGTGGTGCACCTTTAATTGAAGTTGTTACTCTTCC  
127751 TGTTATCAACACTGCAAAAGAAGCGAAAGCCTACCTACAGAAGTTGAGAC  
127801 AAATTCTGATTGTTAACAATATCTCCAATGCCAAATTGGAAGATGGTTCA  
127851 ATGCGGAGCGATTGCAATGTTTCAGTACGTTTAAAGGTCAAAGGCAACT  
127901 AGGAACTAAAATTGAAATTAAAAACATCAACTCACTTAATAATGTTGAAA  
127951 AAGCGATTGATCTTGAGATTAACCGCCAAGTTAAAGCACTTATTAATGGT  
128001 GAAACCTTGAGTCAAGCAACTTTAAGCTTTGATGATAAAACCAACAACAA  
128051 TGTTTTTATGAGAAAAAAGACAATACGATTGACTATAGGTACTTTATTG  
128101 AACCTAACATCATGACTAGTAATATTGATGATTATTATTAGAAAAACCT  
128151 GTTGCTTTTCAGTTAGAACAGTTTCAAAAAGAACTAATTGATAGTAATGT  
128201 CAATCCTCAATTAGTCCAATTAGTAGTTGATGATGCAACTATCTTTAGTG  
128251 CTTTTCAAACATTAAATAGTGTGATTAAAAACCCCAAGAAACCATCAGG  
128301 TGGTTATGTATTGAACTAATAGGTCAACTCAATAAAACCAACAGTTCATT  
128351 AACAGCTAATTTAATTCAAGATCTAATTACCCTAATTGAAATGCTAAAAG  
128401 CAGCAAAGGTTAACCAAAAACAAGCTAAGCAGTTAATTACTTTAATGATT  
128451 GAACTAAAAAAGATCCAAAATCGCTAGCTAAGCTCCATAATTTAGAGCA  
128501 AATTACTGATCCAAAAGAGTTACAAAAGATCATTAAAAAATCTTTCAGG  
128551 AAAATGAAAAAGAGATCCTGAAAAACATTGATAGAATTGAACGGATTCAA  
128601 AAGTTAATTATTGGTCAAGTTATGCATAAGACCAATAATCGAGCAAACCC  
128651 CCAACAAGTTTTTATAATTGTTGAAAATATGCTTCATGAAGTTCGGGAAA  
128701 GAGATAGCTAAAAAAATCAAATTATTTATCGCTATATAATCCTTAAAT  
128751 TCAAAGCTTTGAATGACCTGCTAACACCCGTATCTTCTCAGAACGCCAAC  
128801 TAGAAATCCGTTTCAACTCCTCACGGAGTCAAATTCGCTCTGTTCTCGCT  
128851 ACGCTTTTAAACAAAATATAATCCGCTACACTAAAAATACCCCTGGTTA

128901 TTTTGTGTGTAAAGATGTAGGCTTTAGTTTTTTTCATAAAACCCAGGATA  
128951 ATCTGAAGGTGAAATATGCTAAACTTTCAACTTTGATTAAAAAGCTGTTA  
129001 TCACAGGATGATGCTAGTGTTTTTGCCAATATTGACAGTACTGTGCACCT  
129051 TGATAAATTTAAGGGAATTGAAGCTAAGTTTTTTTGATGAGAATAAAAAAC  
129101 ACTTTTTTAAACGTTTGTTTTTTTGCTAAAGATGATATTTTAAACATCCTT  
129151 GATGAAAACAACCTCCAGCAACAGTTCTTCAGGGAGTTTGCTTACAATGG  
129201 GATTGCTATTGAAAAACGTCATTGTGTACCTCTGTTGACAAGGAAAGTG  
129251 GGTGCTTGGTGATGTATGACATGTATTATGATGACAATGATAATTTTGTA  
129301 GTTGCTAGCAAAAGTAACTTCCTTAACCTGAATTGAAAGTAATCAATGC  
129351 TTAAAGTGAATGCTGATTTTTTAACTAAAGATCAAGTTATCTATGATTTA  
129401 GTGATAGTAGGTGCTGGCCCTGCTGGGATTGCTAGTGCCATTTATGGTAA  
129451 ACGTGCTAACTTAAATTTAGCAATTATTGAAGGAAACACTCCAGGAGGGA  
129501 AGATAGTAAAACTAACATTGTGGAAAACTATCCTGGTTTTAAAACCATA  
129551 ACTGGTCCTGAATTAGGTCTTGAGATGTACAACCACTTGTTAGCATTGTA  
129601 ACCAGTTGTTTTTTATAACAACCTTAATCAAAATTGATCATCTTAACGATA  
129651 CATTATCTTGTATTTAGATAACAAAACGACAGTTTTTAGCAAACTGTT  
129701 ATCTATGCAACAGGGATGGAAGAGAGAAAACCTGGCATTGAAAAGGAAGA  
129751 TTATTTTTATGGTAAAGGGATTAGTTATTGTGCTATTTGTGATGCGGCTC  
129801 TTTACAAAGGTAAACAGTTGGTGTGTAGGAGGAGGTAATCTGCAATA  
129851 CAGGAAGCAATTTATCTTTCAAGTATTGCTAAAACAGTTCACCTTATTCA  
129901 CAGACGTGAAGTGTTTAGAAGTGATGCATTACTAGTTGAAAAATTAAAAA  
129951 AAATTAGTAATGTAGTTTTTTCATTTAAATGCTACTGTAAAACAGTTAATA  
130001 GGTCAAGAAAAGCTCCAACTGTAAATTGGCAAGCACAGTTGATAAATC  
130051 AGAAAGTGAAATTGCAATTGATTGTCTCTTTCCTTACATAGGCTTTGAAA  
130101 GTAATAACAAGCCAGTTTATAGATCTTAAGCTTAATTTAGATCAAAATGGT  
130151 TTTATTTTAGGAGATGAAAATATGCAAACTAACATTAAGGGTTTTTATGT  
130201 TGCTGGGGATTGTAGAAGTAAATCATTCCGGCAAATTGCCACTGCAATTA  
130251 GTGATGGGGTAACAGCTGTTTTAAAGGTTAGGGATGACATTTAGTACACA  
130301 GATTAAAGCTGAACTGGTCCAAAACAAATTAATTGATAAACTGAAATG  
130351 TCTTTTTAGCAGGTTTTTTTCAAACAACCTAAAGCTACTTTACAACCGT  
130401 AACTGAAGTTTTTAAAGTGCAATCTGAAGCATTAAGGAACAATTTGTTCA  
130451 AAATCTTAAGTTTGACTTTAAGACAAAAGCTAGTAAGAAATACTTTCTTT  
130501 TTGAGTTTAATGCAGATATTAACGTAATTAACACTCTTTTAAACTTGAT  
130551 GTGACAACTAGTGAATTGGTAGTTAAACAAGTTTATCTCATTGCTGCTTT  
130601 TTTAAGTGAGGTAGTGTTAGTGATTTAATAAACTCCAATAACTTTCACT  
130651 TGCAATCAGTTCCAACAATGAGTTTCAAATTCACAACCTTTAAAATTG

130701 TTTAGTTTTTTTAAAAAACAGTTAAACAAAACCAGTTAGTTGTTTATCT  
130751 TAAAAGTTATGAAAAGATCTGTAATTTTTTAAACTGATTCAAGCCTTTG  
5 130801 ATGGTTATCTTGCTTTTGAAAATAAGCAACTAGAGAAAAGTTTTACTTTA  
130851 AACCAGTTAAGAAAAAGTAATTTGGAAGTTGCTAACTTAATGAAGACAAT  
130901 CAGATCTAATAATCAAACTAATCAACTCCAATAAAATCATTTATTAATA  
10 130951 GTAGTAGTTTTGCAAAAAGACCGCTTAATTTTCAGCGTTATTGCTTAATT  
131001 AAAAGTGATCATCCTGATTGATCTTTAGAACAGATAGCAAACTTTTTTTT  
131051 CACAAAATATAACATAAAGATTAGCCGAGTGAATCCAACATTTTAGTG  
131101 TTAATCTAAAAAACTATGCCAGTAGTTTAAATTAGTTTACAAGCAATG  
15 131151 CATCCAATCCAAATAGTAATGTTTATTATGGCTGTTATCTGTTAATTAT  
131201 TGGACTTTTGCTTTCTAACCATGGTTCTACTGGAGGATTAGCTTCTCTAT  
131251 CAGGTCAGGACTTGGAGATCTTTCGTAAAACCAAAGATAGGGGTTTTGTA  
131301 AAGATCTTACAGATTATCATGTTTATCTTAGTAGTTTTATTTTTAATTCT  
20 131351 TGGGTTGATATTTAGTTTTGCACCAAGATAACAATGAAGGTTTTAACTGA  
131401 ACTCCAAAAGCAGATATTTACCATTGTCAAAAAGGAAAATGGTAAACCTA  
131451 TTCCCCCTGGAATAGTGGTAAGAATGATGGAAAATAGTCCTAATTTTCCA  
25 131501 GGTAAACATCTCATCTATCGGGCCATTGATGATCTGCTTGATTGAGCCAT  
131551 CTTAAGGAAAGCTGGTGGGGTTACAAACCAGCTATTAGTTAACTATGAAC  
131601 CTGCTGAGCCTTTACTTGATAAAAACTACAAGGGATTTTAACCTTAGGA  
30 131651 AATAAGAATAGTGGTTTTATCCGCTCTTTGGATGATGATAAACTGTGTA  
131701 TTATGTCCATTACTCTAATTTAACTGGAGCTTTAGATGGGGATCTTGTTGG  
131751 AGTTTTGTAAATTAGATAAACCCCAATTGGTGATAAGTTTGATGCTGCA  
131801 GTTATTACTATTCTAAAAAGAGCAAGAATCTTGATGCAGGTAATTTTTT  
35 131851 AGTAGATCAAAATGAGTTTGCCTTGGAAATACAAATTGTTGCTGATAACC  
131901 CTAGATTTTATTTAACTATGATTGTAAATCCTGATTCTATCCCAAATAAC  
131951 TTAGCATCTAACACCAAGATAGCTTTTCAAATTGATGAGTATGATCCTGA  
40 132001 TAACAACCTATGTAAGGTTTCTGTACAACAAGTTTTGGGTAACAATGATG  
132051 ATCCGCTAATTAATATAAAAGCAATCATGTTGGACAATTCATTGTCTTT  
132101 GAAACTAACGATGTAGTTGAACAGCATGCTAACAAGTTAAGTTTGTATAC  
132151 TGAAGAACAACATAAAGCTTACCGTCAGGATTTAACTGATTAGCTTTTG  
45 132201 TGAAGTTGATCCTACAACATCAAAAGACCTTGATGATGCTATTTATGTC  
132251 AAAACAATACCAACAGGTTTTGTGCTTTATGTAGCTATTGCTGATGTTGC  
132301 ACACTATGTTAATAGAAATAGTGAAATAGACATTGAAGCAAAACACAAAA  
132351 CAAGCTCAATCTATCTACCTGGTCATTATGTTGTGCCCATGCTACCTGAG  
50 132401 CAATTGTCAAATCAGCTCTGTTCTTTAAATCCAGCACAAAACGTTATGT  
132451 TGTGTTTGTGAGATTAGTTTTGATAATCAGGGAAGGATTAAACAAACA

132501 AGCTTTACCCAGCAACAATTATTTCCAAAAATCGTTTTAGCTATGATCAG  
132551 GTTAACAAGTGGTTAAATAATAAATCAGAATTAACTGTGATGAAACAGT  
132601 TATCAACAGCTTAAAAGCAGCTTTTACACTAAGTGATCTAATTCAAGCGC  
132651 AACGTCAAAAACGCGGTACAATTGATCTTTACACAAAGAACTGAGATA  
132701 GTTGTGATGAACATTATTTTCCCATTAAGATAAATTTTTTGGTTCACGA  
132751 TAAAGCTGAAACCATGATTGAAAATCTCATGGTAGTGGCCAATGAGACAG  
132801 TTGCTTGGGTGTTAACTAACAACAAAATTGCTTTACCATACAGAGTTCAC  
132851 CCAAGACCAAGCAAAAAGAAGTTACAAAGTTTGATTGAAACAGTTGGTGA  
132901 GTTGAACATAACTAAACCCCAATTTAACTTAGATACTGTCACTTCAAGCC  
132951 AAATAGCTAGCTGATTAAATGAAAACAAAGATAATCCTAGTTATGAGATC  
133001 TTTGTAATCCTCTTATTAAGAACACTAGGCAAAGCTTTTATAGTGTTAA  
133051 TCCCTGATGCACCTCAGCATTGGTTCTAACCCTATACCCACTTTACTT  
133101 CACCGATTAGAAGGTATATAGATCTAACCATTACAGGTGTTGTGAATG  
133151 CATCTTTTTACTCCCGATCAATTCCTGATAATGAAAGAGATCAACTCAA  
133201 ACAAGAGTTGGAAAAAATTGCTGATACAGTTAATGATACAGAGATTAAAA  
133251 TTATCAATTGTGAAAGAAATGCCAATGATTATCTAACACGCTGTTATTA  
133301 TCAAAAACAAATTGGCAAAACCTTCAGCGGATTTATTTTCAAGCAATTACTAG  
133351 CTTTGAATTTTTATGAGAATGGATGAAAATAACTTTGATGGGTAAATCA  
133401 AAATTACAACCTATCCCTGATGATTTCTTTATTTTTGAAAAGGAAAAAATG  
133451 GTATTGAAAGGAAGAAAACTAATAAGGTTTATAAAATTGGCGATCGTTT  
133501 GGAAGCTAAACTAAGTGAGATTGATTTTATCCAAAAACGTGCTATTTTAA  
133551 CACTCATATAATTAGCCAATGGTTGTTAATATCCTGCTTTTATTACCCT  
133601 TATTTTTTTACTTTTACTGTTTGTGTTTTTTAATTGCTTTTGCATTTCTAA  
133651 ACAAACGGGTAGAAATTATGTTGTACGTACTTGAAGTAGTGTTCAGT  
133701 AAGTCCAAACAAAACCTTGATAAAAAGAACTTTTTTGACAATTTAACTTC  
133751 AACTTTATTAAGACTTTCAGTTGATAAAATTGGGGCTATTATTGCCATTG  
133801 AAAACGTGATTCACTTGAACCTTATATCAACATTGGTTATCGGGTTAGT  
133851 TCTGATTTTTCCCTGAACTGTTAGTTACTATTTTTTACAACAAATCATC  
133901 TCCTTTACATGATGGAGCGGTGATTGTTAGAGATTACAAAATTATTAGTG  
133951 TCTCTTCTTACTTTCCAATGACAAGACAATTAATTGATGTTTCATATGGT  
134001 TCAAGACACAGAAGTGCCTTGGGATTAAGTGAAAAGTCTGATGCAGTTGT  
134051 TTTTATTGTTAGTGAAACAACCTGGTAAAATATCAGTTGCTTTAAAAGGGG  
134101 TTATTAACAACTTGCTTCCAACCTCAGATAGGTTGCAAGATGAAATTATC  
134151 CATTACTTGTCTTCAAAGTAGGATTAATCACTTTTCATTCTGGTTTTTTA  
134201 AACCATGGATTCAAAGGGTTAATTCCTTGGTAAAAAAGCGTCCCTGTAA  
134251 GTGATCAAATTCATGCTGTAAACACATTCCAAATAGTCCAGTTGCTTTAA

134301 TGGTAATCTCTTTTTTTTCAAACCAATCATAACCTTTAATAGTGATCCAT  
134351 TCACTACGAATTACATAACCTTTGTGCTGCTTTTTAACACTTAAACACCC  
5 134401 CTCACCACTTTCTAAAAATGCTTTATTTTCACTTTGATCAATAATTTTAG  
134451 GATTGATCAGTAGGCACCTTTTTTTCTTTGTTTAAATCATTGAGGTGGATG  
134501 TAAACAGTTGTTTTCAATAGCCAATCTGGTTAGCAGCTATCCCAATTCC  
10 134551 TGGAATAATGTCATATTCTTGTGCTTTACCATCATATGAAGCATCAACAT  
134601 ATGCAATCATCTTTTTAATACAGGTTTCAATTTGCTCATCTATTGGAAAA  
134651 TTAACAGCTTCAGTTGGCTTGTTAATCAAAGCATTATCATCAAAAACAAG  
134701 CCAAGTTTtagTTGGTTGAAAAGTCATTGATAAAAACAGTAAAGTTAAAA  
15 134751 TTATTCTAACAATTGAAGTGAACAATCAGGGGAGAATTTTGTCACTACT  
134801 GGTCTAGCGGTGTTGGCAAAAGCACCTTGTTAAAGCCTTATTAGATCA  
134851 TTTCAAAGaACAACGTCTACAGTATCTCTGCAACTACAAGAAAAAGC  
134901 GCATTAGTGAAAAAGAGGAATTGATTATTTTTTAAAGATAAAGATGAG  
20 134951 TTTGAAAACCTTAATAAAACAAGATGCTTTCATTGAATGGGCTTGCTATAA  
135001 TAACCATTATTATGGAACGCTCAAGTCTCAAGCTGAACAAGCAATTAAAA  
135051 GCGGAATTAATTTAATGCTTGAAATTGAGTATCAAGGTGCTTTACAGGTT  
25 135101 AAAAGTAAATATCCTCATAACGTTGTTTTAATTTTCATTAAACCACCTTC  
135151 AATGCAAGAGTTGTTAAAACGTTTAAAAAAGCGTAATGATGAAGATGAAA  
135201 CCACAATTAaaaaacgTTTtagAACAAGCTAAGATAGAGTTTCAACAGATT  
135251 GATAATTTTAAAGTATGTTGTCACtaACAAAGAGTTTGATAAAACCCTTAA  
30 135301 TGAGTTGAAATCAATCTTACTATCTGAGTTTATTTAATGCAAGCTGCTAA  
135351 TGATCATTCTTTACCGGTTTATCAAAAAAGGTCCTGTAAGAAAGGAAA  
135401 ATCAGGACTTTTATGGATTTAGTTTTAATCAAATAACCTACTAATAGTT  
35 135451 GTTGTGATGGTCTTGGTGGTTATAAGGGTGGCAAGATTGCTAGTAACTT  
135501 AGTAGGTAAACTCTTCTTAGTTTATTTGAAGGTTTTGAATTTAACCAGT  
135551 GAGATGAAACTACAGTTAAAAAGTGGTTTGAAAATACTTTAATACAAGCA  
135601 CGCTTTCaACTAGAAAATTGTTTTCAAACAGTTTATGAAGCACAAATCCA  
40 135651 GTTTGCTAGGATGGCTAGCACCTTGGTCTTGGGAATTTTAACTAAAAGTG  
135701 ATATTTATATCTTTTGAATTGGTGATTCCAGAGCTTACTTATTATTTGAA  
135751 AACCAAGCTAAGTTAGTTACTAAGGATCACAATCTTTATAACCAGTTAGT  
45 135801 TGCTATGAATGCTGATGAGAAATTACTTTTAAAGTTATTCTAATCAACTTT  
135851 TAGCATTAAcAAATACTATTTCAAAGAAACAAAAAGACCATTAGTTTAT  
135901 GGTTTTTATAACACAAAAATTGAACAACAAGAATTTTATTATTGTGTTC  
135951 TGATGGACTTTATAACTTTGTTGAAAAGAGCTTTTTTTTGAAATTATCA  
50 136001 CTAATTCtAAAAACCTAAAAcAGCAGTGTTTAATCTTTATAGAAAAAGT  
136051 ATTGAAAATGCAAGTAATGATAATATTACTGCTGCCCTTGTTAATCTGCA



136101 AAAATGGAAGCAATCTTAAAGATAGGTGATATTGTTGAAAATAAGTATCA  
136151 AATTGAAAAGCTTTTAAATAGGGGTGGGATGGATTCCCTATCTTTTTTTAG  
136201 CAAAAAATTTGAACCTTAAAAAACTATGGACCAGTTCAAAAAAACAGTAT  
136251 GGACACTTAGTTTTAAAGGTGGTTCAAAAAAATCCTAAGATTAATGAAAA  
136301 TAATTGGAAAAAGTTCCTTGATGAAATGGTAACCACAAGTAGAGTGCACC  
136351 ATTCTAACCTAGTGAAAAAGTTTTGATGTGGTGAACCCTTTTTTGAAAAATA  
136401 GTTCGTGGTAATAAAACAATTGCTCTCAATCAGATAGTGATGATTGCAAT  
136451 GGAGTATGTTGATGGCCCTTCTTTAAGACAATTGCTTAACAGAAAAGGCT  
136501 ACTTTAGTGTTAGCGAAGTAGTTTTATTACTTTACAAAGATAGTAAAAGCC  
136551 ATTGATTATCTCCACAGTTTCAAGCACCAAATTATCCACCGTGATCTTAA  
136601 ACCTGAAAACATCTTATTTACTAGTGATTTAACTGATATTAACTATTAG  
136651 ATTTTGGCATTGCTTCAACAGTAGTTAAAGTTGCTGAAAAAACCGAAGTT  
136701 TTAACGTAGTAAAAATTCACTGTTTGGCACAGTTAGTTATATGATTCCTGA  
136751 TGTTTTGGAAAGCACAGTTAATAAAGCTGGTAAAAAGGTTAGAAAACCAC  
136801 CCAATGCCCAGTATGATATCTACTCGTTAGGAATTATTCTATTTGAGATG  
136851 TTAGTTGGTAGAGTTCCATTTAACAAGTCAATTAACCCCAACAAGGAAAG  
136901 AGAAACAATCCAAAAAGCACGCAATTTTGACTTACCTTTAATGCAAGCAA  
136951 CTAGAAGTGATATCCCAAATAGCTTAGAAAAATATTGCTTTTCGTTGTACT  
137001 GCTGTGAAAAGAGAAAAACAATAAGTGACTTTACAGTTCCACAAAAGAAT  
137051 TTTAGAAGATTTGGCGAATTGAGAAAATGAACAAGCGATGATTAAACCTG  
137101 CTAATGAAAGGGTTTTAGAAGGGCAGGTGGAAATTAGAGAAATGATGCTT  
137151 GAAAAGCCCTTAGCTTGGTATTTCAAACTTGAGCCTTATCAATCTTTAC  
137201 TATCGTTTTTATAGGGTTAATTATTGCTGCAATAGTTCTTTTATTAATTT  
137251 TTAATGCCAGATTCTAACTTTGGGATAGTGCTTCAGTCATTAGCAAAACA  
137301 ATGCAAAGTATTTTGAATAACCAGATAATAACTGCTTTTCCTCAAAAGA  
137351 AGTTACAGTGAAAAAATGATTTTAAGTTGATGGTTGGTGATAGGGTTCAA  
137401 CTTGAAGATGGTGCGATCACTAAAGTTTTAGCTAGAAAAAATGAACTTAC  
137451 AAGACCAAGGGTTGCTAATGTTGATCAGATTGTTTTAATCCAATCACTAG  
137501 TTCAACCTAAGATTAACTGAATTCAACTGTTGAAATTATTGGTATATTTTC  
137551 AATGCTAAATTAATTGATGAAATACCTATTTTAATAACAAAAACAGACCT  
137601 TGATTTTGATCCAATGGAAAAACAAAAGTTAATCGATTTAAAAACAGTTTA  
137651 ACTATCAGTTATTTTTTGTCTTCTAAAAATGAACCACTACCTTCAGAATTA  
137701 ATCGATATTTTTAGTAAAAAACTAAGTGTTTTTACAGGTCAATCTGGTGT  
137751 TGGTAAATCTAGCTTAATTAATCGTTTAGATCCTTCTTTAAAAACAAAAGA  
137801 TTCAAGCCTTATCAGTTAATAAATTGGTAAGAATACCACTACTAAAACA  
137851 ACACTTTTTTCATTTAGAGGCGGTTTTATTGTGACACCCCTGGTTTTAA

137901 TGTAATTTCTATTAAAAACCTCAAAATTTTAGCAGCCCAACACTTTGTTG  
137951 GTTTTAGAAAATGATTAGTAAGTGTCATTTTTCTAACTGTTATCATCAG  
5 138001 TATGAAAAAGATTGCTTTGTAACCACAAGTGTTATGAAAAACAGATATCC  
138051 TTCGTGATTGTATGAGAAGTATAGAAAAATGATTAATTAATCAACTGC  
138101 AAAAGTGTTTATGAGTGATAAATTATTAACAATTGACTTAAGTCATGTTT  
138151 ATGGATTTGATAAAGAAATTATTTTAAAGAAATACCAAAAAAAGTAGAT  
10 138201 CAAATTCACCAAGATTTTCTAGCTCATAAACTTGCTGATGGTCACATGAC  
138251 TGGGTGGTATGACCAACCTGATCAAAACCACCAATTCCTTTTAAAAACCA  
138301 TTAATCAAATTGACAAAAAGTTTAAAAGTTTAAAAGTAACTGACATTGTT  
138351 TATGTTGGTATTGGTGGTTCTTTTACTGGTATTAAAACAGTTTTAGATTT  
15 138401 CTTAAAACCAAAACAAAGAACAGGATTAAAAATCCACTTTGTCCCTGACC  
138451 TTTCTGCTTTTCAAGCTGCAAGTGTTATTAAGGAAATTAAAAATAATCA  
138501 TGGGCTCTAATTACCACTTCTAAGTCTGGTAGAACCTAGAACAGCACT  
20 138551 GAATTTCCGCATTTTTAGAACTTATTAAACAAGCGTTATGGCAACAAAC  
138601 ACTACCAAAGAGTAGTTGTTATTACTGATGAAAAAAGGGATTACTAACC  
138651 AAAATGGCATCAAATCATGGTTACCAAAAGTTAGTTATTGATTCAAATAT  
25 138701 CGGTGGGCGTTTTTCAACTCTATCTCCTGCTGGTTTGTACTAGCCAAAC  
138751 TTTTTGGTCATGATCCTAAGGCCATCTTAAAGGAACATTACAAGCCAA  
138801 AAGGATTTGCAAAACAACTTCACTTGAAAACAATTCTGCATACCTTTATGC  
138851 AGTAGTTAGACATTGACTATACACCACAAAAAATTCAAATTTGAAGTTT  
30 138901 GCATTGCTTATCACAGTTTGTATGAATATTTGTTATTACAGCATCGACAA  
138951 CTTTTTGGTGAATCAGAAGGTAAAGACGATAAATCTTTATTTCTACTTT  
139001 TTCGATTTTTACTGTTGACTTACACTCAATGGGACAACTCTATCAAGAAG  
35 139051 GGGAAAAAGTGTTTTTGAACAGTAATTGATGTTAAAAATCCACTTGTT  
139101 AATATTAATTTACCTCCATCTGATTTTGACAAATGATGATGAACCTTGATTT  
139151 CTGTTAGATAAAAAGCTTAAATGAGATTTTCAAGTGTGCAATTGATTCAG  
139201 TTATTAAAGCGCACTACCAAGCAAATGTAAGCATTATTAAATTAACTTTA  
40 139251 AAAGAACAATCTGCATTTATGTTTGGTTATTTTTACTTTTGACTCTCTGT  
139301 TGCTACAGTGATGAGTGGATCATTATTAGGGCATAATGTCTTTAATCAAC  
139351 CTGGCGTTGAAGTTTATAAAAAGTTAATGTTTGA AAAACTAAGAAGTGGC  
45 139401 CACTAAGGTTGTTTTTCACTCTTACCCTTTTAAATAGGTTTGACAAGT  
139451 CACTTTTAGAAAGTTACTTTCAAGATGGATTGAGGTTAATCCATTATGAT  
139501 GTGATGGACCAATTTGTTTATAAATACTGCTTTTAAAGGTGAATATTTGGA  
139551 TGAATTGAAAACAATAGGTTTGTATGTTAATGTCCATTAAATGGTGGAAC  
50 139601 AGATCATCCCTCAAATAAATTTTTATCTTTCACAACCTAATGTGAAAAGG  
139651 ATTTCTGTTTATGTTGAACCATTTAGTTTTGCAAAGATTAAAGAATAAT

139701 CCAACTAGTTAAAGAAAATGGTAAAGAAGTTGGTCTTGCTTTTAAATTTA  
139751 CAACCAATTTACAACATATACCAACCATTTTTTACAACCATCGACTTTATC  
139801 ACTTTAATGAGTGTTCCTCCTGGTAAAGGTGGTCAAGCTTTTAACGAAGC  
139851 TGTTTTTACAAATTTAAAGATTGCTAACCATTACAACCTGAAAATTGAGA  
139901 TTGATGGTGGGATTAAAGTTAATAACATTGATCAAATTAAGCCTTTGTT  
139951 GATTTTCATTGTAATGGGAAGTGGCTTTATAAAATTAGAGCAGTGGCAACG  
140001 TCAAAAATTGTTGCAAACAATCTAATTAACTTTATTGATGAAATCAGTT  
140051 ACAGTCAAGCAGTTACTACAAACCCACGAAAATTTAATAACAAGCAGAT  
140101 TAACTATCAGGTTGGGTAAATAAACGTGCTAGTGCTAACATCATCT  
140151 TTCTAGCAATTAGTGATGGCTCTAGTATTAATACCCTACAAGCAGTAGTA  
140201 AAACAAGAAGATAACCCCGAGTTTTCTCACTGTTACAACTGTTAATTT  
140251 AGCAAGTGCTGTTATGGTTTGAGGGGAAATTATCTTAACCCCAAAGCTA  
140301 AACCAACCACTGGAGTTGAAATTAAAGCAGGTGAGTTTATTAGCACAAGCA  
140351 GAGTCTGATTATCCACTGCAAAAAAAGAACATAGTCAAGAGTTTTTTAG  
140401 AAGTAATGCGCATCTAAGAGTAAGAGCAAAAACTTACTTTGCAGTGATGA  
140451 AAATAAGGAGTGTTTTGTACACGCAATCTTTGAATACCTCTTTAAAAAT  
140501 GATTTTATCTTAGTGCAAAGCCCTATTTTAACTAGTAATGATTGTGAGGG  
140551 AGCGGGGGAAACATTTGTAATTAAAGATAGTGAAACTTTTTTTAATAAAA  
140601 CGACTTTTTTAACAGTAAGTGGCCAGTTTGGAGCAGAAGCTTTTGCGCAA  
140651 GCATTTAAAAAGGTTTTACCTTTGGTCCTACTTTTCAAGCTGAAAAATC  
140701 CCATACTAATCGTCATCTTAGTGAGTTTTGGATGATCGAACCTGAAATTG  
140751 CATTTGCTAACTTAAAGATTAAATGCAGTTAATACAAAACCTAATTTAA  
140801 TTCTTAATTAAAAAGTGATGGAAAATGCTAGTGATGAACTAAATGTTTT  
140851 AGCAAAGCAATTTAGCAATGACATTATTAGCAACTTAAAGACAATCATT  
140901 GTACTAAAAAATTTCCAATCATTGAATACAGCAAAGCATTAGCGATTCTA  
140951 AAGGAATCTAGTGATACAAAAAACTAATTTTGAACCTAAACGACTTTAG  
141001 TTTTGGTATTGACTTAAAAACAGAACATGAACGCTTTTTGTGCGAACAAAT  
141051 ATTTTCAAAATCAACCGCTTTTTGTTATTAACTATCCAAAGGAGTTAAAG  
141101 GCATTTTACATGAAAACAAATACTGACAATAAACTGTTGCTGCAGTTGA  
141151 TCTTTTATTACCAAAGATTGGTGAGATTGTGGGGGAAGTGAAGGGGAAA  
141201 GTGATTTAAACCAACTTAAGAATAGGTGTCAATCTTTAAACATTGACACA  
141251 AAAAGTTTGAACCTGATATCTTGATATGAGGAAATGGGGTTATTTTGCTAG  
141301 TGCAGGTTTTGGTTTGGGCTTTGATAGATTATTAGCTTATATATGTGGAT  
141351 TGGAAAACATCAGAGATGCTATTCCTTTCCCGTGTACATGGCACCATT  
141401 AACTTCTAAATTCGCTGCTTATAAAAAAAGATTGCAAACCTGGTTAACAG  
141451 TTTACAGAAATTTTATTGCTTTACCTACTATTATTTTATTGCTTTAGAT

141501 AATCAACTAGGAGTTTTAGCTAACTTTTCTGTTGGTGCAATTAGCATTAG  
141551 TTTACAGATCAGTTTATTGATTGGAGGATTTTTGTTTTAACTGCAGTTA  
5 141601 TATCAGATTATTTAGATGGATATTTAGCAAGAAAATGGCTAGCAGTTTCT  
141651 AACTTTGGTAAATTATGAGACCCCATTTGCTGATAAAGTGATTATCAATGG  
141701 TGTTCTTATTGCACTAGCGATTAATGGATATTTTCACTTTAGCTTATTAA  
10 141751 TTGTTTTTATAGTCCGTGATCTTGTGTTGGATGGAATGCGGATTTATGCT  
141801 TATGAGAAAAAGGTGGTTATTGCTGCTAACTGACTTGGAAAATGAAAAAC  
141851 TATCATGCAGATGGTTGGTATTGTTTTTAGTTGTTTTGTTGGAGTTTTA  
141901 AACAAAGTGAAATAGCTTCTTTGAATAGTGGACTGTTCTTTTGATTACTA  
15 141951 ACTCAACTGCCATATTATTTAGCAGCAGTTTTTCAATTTGGTCTTTTCAT  
142001 TGTTTATAACATCCAAATATATCAGCAACTAAAGGCTTATAACTCCAAGT  
142051 TATAATCCTTATTAGGCATTGGAATAACTTTGTTTGCCAATTTAATAGCA  
142101 GAAAAACTCCAAAAGTTACAACCTTAGTGTTGCAACAGCTGAATCAGTTAC  
20 142151 TGGTGGCTTATTAGCTCATTGTTTAACTTCCATTGATGGTGCTTCTAACT  
142201 ATTTTAATGGCGGTGTTATTGCTTACAATAACCAAGTTAAGATTAACTTA  
142251 CTGAATGTTCAATCCTCCACAATTGCAAACCATGGGGCAGTTTCCAGTTT  
25 142301 CTGTGCTAGGGAGATGGCAGTTGGGGTTAAACAAAAGTTTCAAGCTGATG  
142351 TGGGTATTGCTTGCACTGGGATAGCAGGTAGTAAAGCAGTTGAAAATAAA  
142401 GCAATAGGATTACTTTTTTCTGTATTATTATAGGAAATAAGGCTTATGA  
142451 TTTTGAGTTTGAAATGAACCAAAATAATCGTAAGGATAACATTGAATTAT  
30 142501 TTACCAATAAGATCTTGAATCTTCCACTATTTGTTAACAAAGCTAGCT  
142551 TAATCTAAGTTATGAAACGTACTTTAAATATAGGTATTGTTTTGTGTGAA  
142601 AATTTTCTTTCAGACCAACAAAATGCTGTTGATAGTTACACCCAAGTTA  
35 142651 TGAAGATGTTAGGATGTTTGAATTTGGGTAAAACCTTTCAATCATTAC  
142701 CTTTTAACATCCAAGAAACCCTTATATTTTGTAAATGCTGAACAACATAAA  
142751 ATAGTTGATAAAGCTGCTAAAAAATACAAAAACACTACTGTGTTTTTTTC  
40 142801 ACGTGATACTGATGTAGCTAATGTTTATGAAGCTAAGGTATTTATCCAAG  
142851 AAAAATACAAATTAACCCAAGATTACAAAAAAGAGGTGTTAGCTCTTAT  
142901 TATGACAGCTGTTGCTTTATCTTAATTGAAGCGAATCGTCCATTAACTGC  
142951 AATAAAGACAGTTAAAAGTGTTTATGAAAAAGCACTGATAGAAAAAGCAG  
45 143001 CTATTGCAGTATTACCATATAATGGTACACTAATGAATGGTAACAATGAT  
143051 GTTGTCTTTAGCCACTTGCAAGATAAAAAATAGGTTTAACTATTGAAAACA  
143101 AAGCAAGGCTTATGAAGTACAATACCCCCAAGCATATACTTTAAATAAAC  
143151 TTAATCAGTTTTCAAAACAGCAATTTCTAAGGGCTAGAAGTATGTTGGAC  
50 143201 TTAATGAAGATTTCTAATAAATCACCCTTAAGTATTGTTGATGGTAGTGC  
143251 TTATGCTTTTAGGGTTGTTACCAACCTTGATTTTGAAATTTTATTAGGTA

143301 TTTTAAAAAATGGATAAAAAATATTTTCAATTAGTACAAAGTTTTGCTAA  
143351 AACGCAAAATGTGCGAGCTAATTACACCTCACAAGACAAAAATATTAGTT  
143401 TAGATTTTGTAGTTTGTGAAACAGTTAGTCAATCACTAACAGGTTTTCTA  
143451 ATTTTAAATAATTTCAATAAAATTGTTACAACCTAATTGAACTGATAAAACA  
143501 AAAGCAAACATGATTATATGTAGATCAGCTCTGAATTGTTGATCTTTCCA  
143551 ATAACAAAGCCTTAACTGATGCTACTGTTTGGATTATTAAACAAGAAAAA  
143601 TTGCCTGTTTCAGTTGCGGCTTTTAGCAACCAACAACCTCAACCAAGTTTA  
143651 TCGCAATTCATCCACAAGTCCTTTGTATCTTAGTTATGTCAAACCAATCG  
143701 AAGTTCAACAATTTTTTACACTTTCTCCATCCATTAACAATAATCCTTTT  
143751 TTAAATCAAAATCCTTTAACTGAATCACCATTTGATAACAATAATCAGCT  
143801 GTTTCAGCAACAAAGAGCGTTGAACCTTCAATGGAAACAATGGAATTTT  
143851 CCCGTTTATGGATGAATTTGATCAGATTACAAAGAACTTTTCTGATATA  
143901 GAGCTTGAACCTATGCAATTCACCCAAAGTTTTGATGATTGGAGCAAAGA  
143951 CTAGGGTTGCAATAGTTGGCGGGATTGGTTACATAGGTAGTTGTTTTGCT  
144001 AGTTTTATCAAAGAACAAAATGATAAGCTAATTGTTACTGTTATTGATAA  
144051 CAACAAAAATAACCATGTAATTAACTCTTAAAAAAGATTGGAATTGAAT  
144101 TCTATTTGCTGATTTACTAGATAGACATAAGCTAACTGAAGTAATTGCA  
144151 GCAATTC AACCTGATGTGGTATTTCACTTTGCTGCTAAAACAAGTGTAAG  
144201 TGAATCAGTACATAATCCATTGAAGTACTTTGATTGCAATGTAATTGGTA  
144251 CTTTAAACCTAATTAGTGCAATTAGTAACCTTACAGAAGCCAATTAAATTA  
144301 TTTTTCGCTTCTAGTGCTGCAGTGATGGTCAAACAACCTAATAGTTACAT  
144351 TAGTGAAGAGATTGTAATAACTGAAACACAAGCAACCAATCCTTATGGAT  
144401 TGAGTAAGTTTTTTAGATGAATTAATCTTAAATGCAGTTGCCAAAAATAGT  
144451 CAACTACAAGTTGTTTGCTTACGCTTTTTTAATGTGGCAGGTGCAATTCT  
144501 GCCATTTGGTAATTTTAATGGTAATACCACGCTTTTAATTCCTAACTTAG  
144551 TAAAAGCCTTTTTTAAACAAACTCCCTTTTTTTTATATGGCAATGATTAT  
144601 GCAACTAAGGATGGTAGTTGCATAAGAGATTACATCCATGTTTATGATAT  
144651 ATGTAATGCTCATTTCTTATTATGAAAGTGGTTAAATGATCATCGCCAAA  
144701 TTAAATTTGAAACCTTTAACTTGGGGAGTGGGATAGGAACTTCTAATTTA  
144751 GAAGTTATTGATATTGCTAAAAAAGTGTTTTATCCTAGTAGATTAAATTT  
144801 AGAAATTAGACCAAAAAGAAGCTGAGATCCAGCAATTTTAGTAGCAAATG  
144851 TTGCTAAAGCAAAACAAACCTTTCAATTCAAAATAACGCGTAATTTGAAA  
144901 GATATGATAAGTGATGAGCGTAATTTTTATGAGAATTTTTATAATGACGC  
144951 TTATTAAGTGGTGTTTAATTAATGGAAAAAGTTGCCTTCAAAATGGAGCA  
145001 TATCTCCAAAAGTTTTGACAATGGCAAAATTAAGGCTAATGTTGATGTTA  
145051 GCTTAGTTGTTTATGAAAATACTGTCCACACCATTTTGGGGGAGAATGGT

145101 GCAGGAAAATCAACCCTGACTTCGATTTTATTTGGTTTATATAAACCTGA  
145151 TAGTGGCAAGATCTTTATTGGTGAAGCAAGTAAATTTTAAATCTTCTA  
5 145201 AAGATGCAGTAAACATAAAATCGGAATGGTGCACCAGCACTTTAAGTTA  
145251 ATAGAAAACCTACACGGTTTTAGATAACATCATTCTAGGGAATGAAAGTAG  
145301 GTTTGGGTTTTTACCTTTAATTAATCGTAAAGTAAGTGAAGCAAAGATTA  
10 145351 AAACCATCATGGAAAAATATGGAATCTTTGTTGATCTTAAACAAAAAGTT  
145401 AGTAACTTAACAGTAGGTGAGCAACAACGGGTTGAGATCCTAAAGGTTTT  
145451 ATTTCTGTAGTAGTAATATCCTTATCTTTGATGAACCCACTGCAGTTTTAA  
145501 GTGATCTTGAAATTCAAACTTTCTCAAGATTATTGCTAACTTTAAAAAG  
15 145551 CTAGGAAAAACAATTGTTTTAATCTCTCATAAATTAAATGAAATTAAACA  
145601 AGTTGCTGATACAGCTACTGTCTTAAGACTTGGCAAGGTAGTTGGTAGTT  
145651 TTGATGTTAAAAACAACACCAGTTGATAAGATTGCGCTTTTAAATGATGGGC  
145701 AAAGAGTTAAAACAAACTAAAAACACCACAGATTTTGTGCTAAAGATGA  
20 145751 ACCTGTTTTTAAAGTTCAAAACCTGAATTTGTTTCTCAATAAATCTTTAG  
145801 CATACAAGTTCTTAGTGAGGTGCAATAACATCCATAAAGCCCAACAAATT  
145851 AAGAAAAATAAACCATTAAGAGACTTATGGATAATTAGTTTTTTAAATAA  
25 145901 ACTAACCACCAGTAACAAAACCCCTAAATTAGTAAAAGGCTTGATTAATA  
145951 AGTTAGGACTTTCTATCAAGAAAATACAGATGAAACCATTAGTTTTGCT  
146001 ATCCATAAGGGAGAAAATTTTGTCTATTGCTGGGGTTGAGGGTAATGGTCA  
146051 AAGTCAGCTTGTTAATTTAATTTGTGGAATTGAAAAAGCTGCTAGTAATA  
30 146101 AGTTAATTTTAAACAATATTGATATCTCAAGATGATCAATTAGAAAACGG  
146151 ATTAATGCTGGGATTAGTTTTGTTTTGGAAGATAGACATAAATATGGCTT  
146201 GATCTTAGATCAAACCGTGAGGTTTAATACGGTTAATAACCAGATTAATA  
146251 ACCGTCCTTTTAGTAGTTGAACTTTTAAAACCAATGGAGATTGCTCTT  
35 146301 TATAGCAACACTATTATTAAGAAAGTTTGATGTTAGGGGCAGTGCTGAGGG  
146351 TAGTGCTGTTGTAAGAAGACTTTCAGGTGTAATCAACAGAACTAATTA  
146401 TTGGTCGAGAAATGACCAAAACAAATGACCTTTTGGTGTTAGCACAAGTA  
40 146451 ACCAGAGGCCTTGATATTGGTGCTATTGCTTTTATCCATGAAAACATCTT  
146501 ATTAGCTAAAGCTAATAATAAGCTATCTTATTGGTTTCATATGAACTTG  
146551 ATGAGATCTTAGCACTTGCTGATACAGTGGCTGTTATCAATAAGGGGAGA  
45 146601 ATAGTTGGTATGGGAAAAAGAGATTTAATGGATCGCCAATCGATAGGTAG  
146651 ATTAATAATGCAATAAAAGACTATGACAATGTGGCAATTTAAAAGTTACT  
146701 TTAAACACCACCTGGTGTTTTGAAAAGACCGATTTTACATAGCTCTGAG  
146751 AAACAAATGCAAAGAAGAAGTATCCTCTCTTCAGTGGTTTTGATAATCCT  
50 146801 CTCTTTTCTTATATCGTTTTTACTGATTATTTCAATTCCTGGAGGTAGAG  
146851 GTGCGAGCTTCTTTGCACTGTTTACTAAGTTATTTTATAGATAACACTAAT

146901 ACTGAAAATTTCTTAAGACAGATTGCTATTTATATCCTAGCTGGATTAGC  
146951 ATTTAGTTTCTGTATGAGTGTGGTATTTTCAACATTGGTATCTCAGGGC  
147001 AGATGATGGCTGGAGCCATCTTTGGGTTTTTAATGATTCTCAAGGTGTTT  
147051 CCAAGTTCATTTTCGACCTGGTTTTTGGAGGTCAGATTATTACTGTATTATT  
147101 GATGGTAATAGGTAGTGTAGTGTGGCAGTTGTTGTTGCAACTTTAAAGA  
147151 TTTTTTCAAGGTTAATGAAGTTGTAAGTGAATTATGTTGAACTGAATT  
147201 GTAGTGCTTATTAGTGCTTATTTAGTAGAGACTTACATTAAAGATAATAG  
147251 TGGGGGTACAGCCCAATTCTTTTCCTTACCACTCCCTGATGAATTTGCTT  
147301 TATATAACtTCTCTCCTTTAACAACAAAAGTTTGGTTGATTAGCTTCACTT  
147351 ATTATTGCTTTTCATTAGTGTATTATTGTGGCAGTAGTATTAAAATACAC  
147401 AGTTTTTGGACACAAATTAAAGTCAATTGGCAGTAGTGTATTGTGTTCTC  
147451 AGGCAATGGGTTTTTAATGTTAGAAAATACCAGTTCTTATCGTTTATTATC  
147501 TCAGGAATTTTATCAGGACTATTAGCAACGGTTGTTTACACTGCATCAAC  
147551 TGAAAAAGTATTGACATTTAACAATGTTGGGGATAGTGCTATTTTCAGCAG  
147601 TACCAGCTACTGGTTTTGATGGGATTGCGATTGGTTTAAATTGCTTTAAAT  
147651 AACCCCTTTAGGATTGTTATTGTTTCTGTTCTTATTGCTTTTGTTAACAT  
147701 TGGGGCAAGACCTGCTAATTTAAACCCTAATACTGCTAGTTTAGTTTTAG  
147751 GAATCATGATGTATTTTGCTGCACTTTATAACCTAATGGTTTACTTTAAA  
147801 CCATGAAGATACCTAGTGAAGCTGAACATTGGAAAGATAAATCTCACCAC  
147851 ATATGAAACATATGAAAACAACTAGCTGCTAACCTAGAGTGACTAAGTT  
147901 TCCAACGCTTCTTGTCAAAAACAGAAAAAAGAATGACAAACTAAATTT  
147951 AATTGGTTTGATACTAGTTTATTTGAACAATATGCAAAAAACAAACAAGA  
148001 AATTGTTCAAGAATACCATCACAATTGTGCAACTAATTTAATTGCTTGGT  
148051 GATTGAATGCAATCCAAAGTGGCAATATTAAACCTTCACTACTTTTAAAG  
148101 TTGGAATTTGTTAATTTTAAACACCAACAGAAGTTTGTATTAAATTGGTT  
148151 TAAAAATGAAAGTGAATCACTGCGTGATTCCAATCACAGTTTGAGAGAA  
148201 TCAATAAGTTAGTGGAAAGGGAGTTTGTTAAGTAACAATGTTAAGTTTAG  
148251 CACAATTAGAAAGTTGGTTTTTTATCGCTCCAGCACTGCTTTTAGCAGTA  
148301 TTGAGTGGTTATCTCGCTGAACGCGTTGGGATCATTAAATTGCTATTAA  
148351 TGGTGGAATGGTGTGTTGGTGGGTTATTTATGGCACTCTTATCGTATGGAT  
148401 TTACAAATAACTTAAATCAATCCGCTCCCTCCTGATCACTATTTATCACC  
148451 ATTCCCTTATCAGTTTTATTTAGTAGTGTATAGGTTGTTTATTTGCACT  
148501 AGCAGCAGTTAAGTTAAGAGCAGATCATGTTATTGTGGGAAGTGGGATTA  
148551 ACTTGTGGCTAGCGGAATTACCCTTTTTATTAGTCAGAATGCTGCTAGT  
148601 TTGTTTTCCGATACTACCTTAAGAGTAAGGTACTTATTTCCCATCCAAAC  
148651 TACTGTAGTATAGAAGCAATTGGTGTGTTGTTTTTAGTTTACTTCTGA

148701 TTGGGTTTGTATGGTACTTGATGAGTTTTACTAAAACGGGTTGAGATAC  
148751 CGTGCGGTAGGTGAGAATCCTAATGTAATTGATACCCAAGGGATTAGTGT  
5 148801 TTACAAATACCAATGGATAGGCGCAATTTGTTCAATGATGGTAGCTGGAT  
148851 TGAGTGGTAGTTTGTGTTTTAAGTGTTCCTAATTTCCCTTTAACAGC  
148901 GGAGATGTAAATGGCTTGGGTTTTATTGCTATTGCCATTATGATTATCTC  
10 148951 AATGTGAAGAATTATCCCTAGCATCTTATTGGGTTAATCTTTGCATATG  
149001 CCTATGTTTTTACCAATAGTCAAATAGGATCTAATAGTAATTCCTACTTG  
149051 TTAAGAACGATCCCTTTTCATCATCTCATTACTAGTAATGTTGTTATTGG  
149101 TTTTCTTAATGTTGCCCAAAAAATATAGGTAAACATTTTGACAAGGGTT  
15 149151 TAAGATAAACAAAAACCTTATTTATAGTTAAGTAAGTaGTTTTATTAAATG  
149201 ATTA AAAACCTGGTGGTGATTGAATCACC CAATAAAGTTAAACATTAAA  
149251 ACAATATCTTCTAGTGATGAATTTGAGATAGTCTCAACCGTTGGTCACA  
149301 TCAGAGAAATGGTGTATAAAAACTTTGGTTTTGATGAAAATACCTATACC  
20 149351 CCTATCTGAGAAGATTGAACTAAAAATAAACAGAAAAATCCCAAACAGAA  
149401 ACACCTGCTCAGTAAGTTTGAGATCATCAAATCAATCAAAGCTAAAGCTA  
149451 GTGATGCACAAAACATTTTTTTAGCTTCTGACCCTGATAGAGAAGGGGAA  
25 149501 GCCATCTCTTGGCATGTCTATGATTTATTGGATCAAAAAGATAAAGCTAA  
149551 GTGCAAACGAATCACTTTCAATGAGATCACTAAAAAAGCAGTAGTAGTG  
149601 CATTAAAAACAACCGGTAACATCGATCTTAAC TGGGTTGAAAGTCAGTTT  
149651 GCCCGCCAAATCCTTGACAGGATGATAGGTTTTAGATTATCAAGATTATT  
30 149701 AAATAGTTATCTGCAAGCAAAGTCTGCAGGTAGAGTTCAATCAGTGGCTT  
149751 TGC GCTTTCTTGAGGAAAGAGAAAAGGAGATAGCTAAGTTTGTTCCGCGT  
149801 TTTTGGTGGACAGTTGATGTTTTATTAAACAAAGAAAATAACCAAAAAGT  
35 149851 AGTTTGTGCAACAAGTCTATTCCTTTGGTTTTAAGAGAAATTAACCCTG  
149901 AATTAAGTGCTAGTTTAAACTGGATTTTGAAGCTGCTGAAAACGTATCA  
149951 GGAATTGACTTTTTAAATGAAGCTTCAGCAACCAGATTTGCCAACCAACT  
40 150001 GACTGGCGAATATGAAGTTTATTTTATTGATGAACCTAAGATTTACTATT  
150051 CATCTCCAAACCCAGTTTATACCACCGCTTCACTTCAAAGGATGCAATT  
150101 AATAAGTTAGGATGGTCTTCCAAAAAGTAACAATGGTGGCCCAAAGACT  
150151 GTATGAAGGGATTAGTGTTAATGGGAAACAACTGCATTAATTAGTTATC  
45 150201 CAAGAACTGATTCAATTAGGATTTCAAACCAATTTCAATCAGAGTGTGAA  
150251 AAGTACATTGAAAAGGAGTTTGGAAGTCATTATTTAGCTGATAAAAAATAA  
150301 GTTAAAAAGACATAAAAAGGATGAGAAAATCATCCAAGATGCCCATGAAG  
150351 GGATCCATCCTACTTACATTACTATTACCCCCAATGATCTGAAAAACGGG  
50 150401 GTGAAACGCGATGAGTTTCTCCTTTATCGTTTAATATGGATTAGAACAGT  
150451 TGCTAGTTTAATGGCAGATGCTAAAACATCAAGAACTATTGTTTCGTTTTA



150501 TAAACCAAAAAACAAGTTTTATACCTCTTCAAAATCACTTTTATTTGAT  
150551 GGTTATCAAAGGTTATATGAAGAGATTAAACCTAATACTAAAGATGAACT  
5 150601 TTACATTGATCTTAGTAAGCTTAAAATTGGTGATAAATTTAGTTTTGAAA  
150651 AGATCAGCGTTAATGAGCATAAAACCAACCCACCACCACGTTACACCCAA  
150701 GCTAGTTTAATTGAAGAGCTTGAAAAATCTAACATCGGTCGTCCCTCTAC  
10 150751 TTATAACACTATGGCCAGTGTTAATCTAGAAAGGGGCTATGCTAACTTAG  
150801 TGAACCGATTTTTTTTATATCACTGAGCTTGGTGAAAAAGTTAATAATGAA  
150851 CTTTCCAAGCATTTTGGGAATGTAATTAATAAAGAATTTACCAAGAAGAT  
150901 GGAAAAATCTTTGGATGAAATTGCTGAAAACAAAGTAAACTATCAAGAAT  
15 150951 TTCTTAAGCAGTTTTGAACAAATTTTAAATCTGATGTTAAACTAGCTGAA  
151001 AATTCAATTCAAAAAGTGAAAAAGGAAAAAGAATTGGTTGAAAGAGATTG  
151051 TCCTAAATGTAATCAACCGTTGGTATATCGTTACACCAAAAGAGGTAATG  
20 151101 AGAAGTTTGGTGGTTGTAGTGATTTTCCTAAGTGTAATACAGTGAGTTT  
151151 AGTAATCCTAAACCAAACTAACCTTGAAACACTTGATGAATTGTGTCC  
151201 TGAGTGTAACAATAAACTGGTTAAGAGGAGAACTAAATTTAACGCTAAAA  
151251 AGACCTTTTAGGTTGCAGTAATTTCCCTAACTGCCGTTTATCAAAAAAG  
25 151301 GATAATGCTGCTGAATTTAAACAATAACAGCGTTCTTATTGTTGCGTTTG  
151351 TAATTGTTTCTTTATTCTTTCTAATAATTGTTGGGTTTGCTTTAAATTTA  
151401 GCAATTGCTTTTTCACTCCATTTAAAGCAGAATAAAAAATAACAAAAATA  
30 151451 CATCTTAAATGACCAACAGATCCAGTTAAGATTAAGTAAAAACAAGCCC  
151501 AATTAACAACTTTACTTAACTTTTATCAACAAAAAATTGAAAGTGTAAC  
151551 AGAGAAAAAAGTTGGTTAGAAAGTCAGTTACAGGTAATTGATAAAAAGGA  
151601 TTTAAAGCAAGCGCAAAAGTTAACTTTACATTTAAAAAAGACCAAATAT  
35 151651 TAGCTCAACTTAATGAAAAGCTGATTCAAAAAAAGTTGATCAGCCTTTA  
151701 GTTAATGAACTACAGAAAACCAAACCTTCTATCTTGAAAGGTTAGTTGA  
151751 TCAAAAGATTAACTCAGTGAAAATAATTTCAAAAGTGCTTTTCTTAAAA  
40 151801 CGAAGGTAAAAGAGACAGCATTTAATATCTTTGCAGCTAAAAACAAGGTG  
151851 AACTGGGAGTATTTTAAACAGGTGTGTGATGCTGATTGCACTTTAAAAAA  
151901 CTTAGAAGATGAAGTGGAATTACTTTTTCTAATTGGAGTTATTTGAGAA  
151951 GGATGCAAGCTCTATTAGCGTTTGAAAACTAATTAGCAAAATCAAAACA  
45 152001 GTCAAAATTAATGAATTGGTTATTAATGAACTTTAGATGAAGTGAAAA  
152051 CGAAATTAGCCAACTGCTTTTCAAGCGGGTGAAAAAATAGTTAAGGAAT  
152101 TTCAGATAACTAATTTAAACGAGCAAATTACCAGACTAATTGGCTTGCAA  
152151 AAATACTATTTTGGCACTGATCAGCTCAATCTCTTAGAACTCGCGGTATT  
50 152201 AACCAACCAATTAGTAATTTTACTGAACAAAAAGTTCAAACTAGATTTAG  
152251 ATTTAGAACTTCTTAAAGCAGCTAGCTTGTTTAACTATTTAAAGTGAGTA

152301 GATAATAACCAGTTCTTTCAAATATTAAACACAAAACCTTAACCAGCTTTT  
152351 AATTAGTGATCAAGTTATTGCAATCATCCAACAACAAGAACTTAGTTTTT  
5 152401 ATCCTGATCAGTATGGGATGTTAATTAATGGAGTGAAAACAATGATTAGA  
152451 GAGCATAACACCATTGATTTTTGAAAACTGGTTTTTCTCAACTCAACAAA  
152501 ACTTATTGATAATTTTTATCTCTATGATTAAATATGATCCATGCAGTTG  
10 152551 AATATAACAACCTGCTTTTATTACTTTGTAGTGTTAAACCCCTTGAGATT  
152601 AAGTCATTAGCAGAACCTGATCTTTTTGTGTTTTGTAAAAAATTTTTT  
152651 AGCTAAAAAGCAAAAGCAAAATCCAAAAGCGGTAAACTGTTTATCACTA  
152701 CCAAAATTTAGCGATCTAATTACATTAGATTTTATTAGAATTGTTTCAA  
15 152751 CTAATAAATTGGCCTTATGGTAACAGAAATTAGAAGTCTTAAACAACCTG  
152801 AAGAGATCTTTTCAGCTAAGAAAAATGTTATTGTTGACTTTTGAGCAGCA  
152851 TGATGTGGTCCTTGTAACCTAACCAGCCCTGAGTTTCAAAAAGCAGCAGA  
152901 TGAATTTAGTGATGCTCAGTTTGTTAAGGTTAATGTTGATGATCATACTG  
20 152951 ATATAGCAGCAGCTTATAACATTACCTCTTTACCAACTATTGTTGTTTTT  
153001 GAAAACGGGGTTGAAAAAAGAGAGCCATTGGCTTTATGCCAAAAACCAA  
153051 AATTATTGATCTTTCAATAACTAAAGTCCATGATTGATCTGCTTGGTTT  
25 153101 GGATCTGGATGGAACGTTATTATCTAAAACTAAAAAATTAACAATCCAT  
153151 CAAAATTAGCATTAACTAATTTAATTGCTAAAAAACCAAGTTTAAAGGTG  
153201 ATGATTTTAACTGGTAGATCAGTTTTTTCTACTCTAAAAACAGTTGAAAA  
153251 GCTGAACAGTTTGTAAAAAACCAATTGTTGATTATTTTTGTGTTATG  
30 153301 GGGGTGCTAACTTTATCAAATTGAAGCAAATAAGCCACAAGAAAGATAC  
153351 AAGTTTGTCTGGAAAACAGTGTTGTTGAAACTACCTTTAGTATTATCAA  
153401 AAAACACCGCGGATTATGTTTAGCTTACTTAGATAGTTATGTCTCTCCTT  
153451 ACCTTTGTTTAGCTGGTAACAAGCTCCTTGGGTGGTTCATAAATACTTT  
35 153501 TGGTATAGAAAAAGGTGTGTGTTTTTAACCAGAACCATTAAACAAGG  
153551 TATTCTAAAGATTAGTGTTTACTTTTTAAGTGCAAAAAGGTGTAAAAAAG  
153601 TTTATGAAATCTTAAAAAATACCTTTCAAGAAAAGGTTAATGTTTTAAGT  
40 153651 TTTTCTAATAATTTAATTGAGATAACTCATCATGATGCTAATAAGGGTTA  
153701 TGCAATTGAATATATGGCCAAAAGAGAACAACCTTCACTTAATAGAATAG  
153751 CAGTTATTGGTGATTCTTGAAATGATTATGCAATGTTCAAAAAGCTAAA  
153801 TATTCCTTTGCAATGTCAAAATCCCCTTCCCAGTTAAATTAATTGCTAC  
45 153851 CAATACCAGTAACAAAACCAACCGTTACCGCTTTAGTACCTTACTTAATT  
153901 TAATTAGTGAAACAATCATTAAATCAAAAAGCTGATTAGATGTTAAACCAA  
153951 ATGCTTTATAAAACATTTTTAATGTTTCATCAGCAACTTTTTAGCTTGG  
50 154001 TTTTACCATCATTTAGGACTTTTAATACCATTTTCATCAGTAATTTGTGC  
154051 TTTTTAAATTTAAGTGATTCTATGACATTAATAACAGCACTACTGAGGT

154101 CATTCTTTAAATCTAAATAACTTTTATTCTGATAATATTTAACAAGATCA  
154151 GAGCCGATTTTTTTTACTTAAATTATGGTTAACTTCTTCTTTTAAAAGTGC  
5 154201 AGTTAAAATAACAAGTAAATTAGTAACACCAGGTTGGGTTTTTTTAGCAA  
154251 AACGAATCTTATTAAAACTATCAGTTGTGGCTTTGCGCACTTTTTTGATG  
154301 ATTGTTTCTTTACTATCATCCAGATAGATAACACCATTTTGATCAGGATT  
10 154351 TGATTGACATCTTTTTTAAAGGATTTGATAGATCCATGATCCTGTTGG  
154401 TATCTTTGTTTTCTATAAATACAGGTAATTTTCAGTTTTAACTTAAATTTT  
154451 TTTGCTACACGTTTAGCTAAATCATTGGTTAATTTCCAAGTGCTGCTTCTG  
154501 ATCATTACCAACTGGAACAATATCAGGTTGATAAAGCAAGATATCAGCAG  
15 154551 CCATTAACACTGGGTAAGTTAACAACCAAGTTGGGATAGTAATGGTGTTA  
154601 TTACTATTTCTTTTTTTCGCTAATTTCTTTGTTTTAAATTGGGTCATTCT  
154651 TTGTAATTCACCTAGATTACTTTGTGTCAGCATTAGATAACCTAACATGG  
20 154701 TATGTTCCATCAGATCACTTTGTAAAAATAAGTTCACTTTTCCATAATCA  
154751 AGTCCTAGTGCTAATAAAGTTTTTAAACAAGTTGCAAGTTGTTATCTTTGAG  
154801 CATTGTTGGTTCAAAATCAACAGTAATAGCATGAAGATCAGCAACAAATA  
154851 AAAACAGTTGGTATTGACTTTGGAGTTGTTTTAAACCTTGCATTACGCCA  
25 154901 AGAAAGTTACCTAGGTGTGTCTTCCAGAAGCTTGAATCCCTGTAATTGC  
154951 GCGCTTTATCATTATTAGAATTGATAGGGTAATTAAAGGTTATTTTAATG  
155001 AAAAAAGCGGGTAAAAAAATAGTGATGCAGGTAAGACTTTTATCTTAAT  
155051 CTCATCATCCTGTTTCATCCTGTCAGAAAGCCATTGAGTTTTTTGATCAAA  
30 155101 ACAAAATTAGCTATGTTGTTGAGAATTTTATAAAAAACCAATTAGTGAT  
155151 AAGCGTTTTAAAGATATTTTAAAGTCTTAGTGAGGATGGTACTGAAAGTTT  
155201 GTTTTCCAAACGTGCTGATCAGATTAAAGCACTAACAGTGTTAGTGTTG  
35 155251 AAGAGTTGAGTATCAGTGAATTAATTAAGCTAGTTAGAGAACGTCCCTTCT  
155301 TTACTAAGAAGGCCTATTATCATCCAATATAATTCTTCAGGAATTCCTAA  
155351 AAGGATGCGAATTGGTTATAACTCATCTGAAATTAAGGTCTTTGAGCGTA  
155401 AACTAATAGAACCAAAGCCTATAATACAACAATAACATCTAAATGAAATA  
40 155451 CAAAATTTTGTCTCCACAACGCCCCAACTGAACCTGTTCTCAATAAGT  
155501 TAAGAGCAGTTTTTAAAACTTGGCAAGCGGTTGAGAATGGTTATGAATAT  
155551 GTGTTTGTTTTAGGTGGGGATGGTTTTTTTGTTCACACTTGCTAACTA  
45 155601 TAACTGTGATAGTTGTAAGGTAGTTGGTATCAATACTGGCCACATTGGTT  
155651 TTTACACTTCTTTTAAATGGAGATGATCTTGATGAAAATTTCAATTCAAAA  
155701 CTAAGTAGCTTTGAGTTTAAAAAGATTAAATTTACTGGAAGTGAAAACTAA  
155751 AAACCACAGTTTCTTAGTTTAAATGAACCTTGACAGTTTACACCAACACTG  
50 155801 CATATCCAATTAACATCTTTATTGATGATAACCACTGGGAATCATACCGC  
155851 GGTTCAAGGTTGCTAATTGGCCCAAGAACAGGTTCAACTGCCCTAGCAAA

155901 ATCTGCTAAGGGAGCGGTTATCTTTCCAAATGTTGATGTTGTTCAAATTA  
155951 TTGAACTAAACCCCTTATTACATCCCAACCAATCACAATTCAATCTCCG  
5 156001 ATTATCTGCCAATGCAAACCAAGGTTGAATTTAGGATCAAAAAAGCTTT  
156051 TAAAGCAGAGCAATTTCCCAATTTTTATGCAGATGGAATCAAGCTTGATT  
156101 TAAAAAATGAAGATACCAGTATTAGCTTTCAGTTGGTTTTATCAAGATCA  
10 156151 ATGTTTCACGCTTCTTTAAAACTAAGGATTTTATTGATAAACTAAAAATC  
156201 AACTTTTATTAAGCAAAGCTAATGAAATGGTTGTTGTGATTGGGTTATAT  
156251 TTTTAGTTTTGGTTTACTCTATCTTTGGATAGTAAAAAATCAAAACAAA  
156301 TTGCTCAACAACCTAACACAAAAGCTGGTTGAATCAACTTCTATTCTTTT  
15 156351 AAAGTTAAGGACTTTGTTAGTGCTTGTGGTGGTAAGGAAAATTTTGTTAA  
156401 TATAAAAACAACACCAACTCAATTAATAGTTACTTTTAAAGATGTTAACT  
156451 CAGTGAGCTTAACAAAGCTTAATGCGCTTAATATCAAAGGAATTAACAAA  
156501 AACCAAAACCAATTTGTTTTGTACTTGGTAACTTTGTAAATGAATTGAA  
20 156551 AAAAAAGATAGAAGATGAACAATAACATTACTAACAGTATTGCCCAATTG  
156601 TTTTTCACACTTCTTTCTTGTCTTTCTGTTTTTAATCATTATTGCGTT  
156651 TAATTTATGCTTGTGTTGCCTATCTTTATTTTCAGTACCGAATTTATAAGA  
25 156701 AAAACCCTAAAAAGCTAACAACTTTAAAGCGAATGAATATGAAAAAATT  
156751 AAGCTATTAAAAAACCAAAATTTCACTGAAAGTAATAAATTAATTGCAAC  
156801 AACTAATGAGTTAAATGAACTTACTAGTCAGCTAGATAATATCTTGGTTA  
156851 GGATTATCAACAAACCACTAGCAAAGTTAGTTAATGATTTTTTAGATGAA  
30 156901 CAGATTAAACAGATAGTTAAGCTAGATAAAAACAGTTCTGATTTTCACTC  
156951 AGAAAGTGATAACCTCCCTTTTTATACCAAACCTTTAATGATTTTCACT  
157001 TTGGTGTTGATAAATTAATAAACATTAACATAAAAAACCCTCTTTATAAC  
35 157051 TGGGTTTATAGCCCCAGTTTTTTAATTAGTGAAAGTGATTTTCGCAAGCT  
157101 TAATGGTATTAGTGGTATCAATAAAAAGCTTTTGGTTGAAAAACTTAGAA  
157151 TTGAAGACATTGTGTTTACAGATCTAAACAAAAGTATGAAGTTAATGTC  
157201 TTGACAGAAAGTCCTATTAAAGCACAAAAACAGTGTTAACTGTGCGCAA  
40 157251 TATCCTGATGAACGATTATGTTGATAATGAAAGGATTGAATCATATGTCC  
157301 AACAAGCTAACTTCTTTTTTACTGAGCACTGTAAAAAGATCGGTAAAGAG  
157351 ATCTTAGAATCACTTAATATTTTTATCTCAAGTAGTTCACTACACCGTCA  
45 157401 TTTTGGCTTTTATGCAATTCGCTATTCAATTTGGACAAAATGTCTTATCCC  
157451 ATAGCCTTGAAACTGCATTTTAACTGCCCCACTTAGCAGCTTTAATAGAA  
157501 CTTGATAGTGAAGTGAAGTTAAAGTGTGGATTGCTCCATGATATTGGTAA  
157551 ATCTAATGATGATAATGGTAAAGAGAGCCATACGATTACAGGCGCTAAAC  
50 157601 TCGCTGAGCAATTTCAACTACCTGATGACATTAAATACACAATTGCTAAC  
157651 CACCACAATAAACATATTGACAATACCTATTGTCGTTTTAACACAAATTGC

157701 TGATAAACTATCTGCTGCTAGAAATGGTGCTAGAAAGTGATAGTTCGCTTC  
157751 TTTTAAACAACATAAAAGATGAGTTGAAAAAGATTGTTGATAAACTATT  
5 157801 AATAATTTTCATACAACGATCTTACTAGGTCAAAGTGGTAGAAGGTAAAT  
157851 GATTTGACTTGAAACTAAAAACCAAAATCAACTGTTAAGTAATGAGCAAA  
157901 TTATTGAAATGGTTGAAAAGATTAAAGCTGAAATTGCTAAGAATCCAATT  
10 157951 ACAAATCACTTCCTTATTAAAGTTGTAATTAGATATAACTTTGAACACAG  
158001 TTTTAACACCAAAAGCTAAGGATGCAATACAGTGCTTTAATACCCTTTT  
158051 TATATTACTAATTAGCTTAGTATTATTTTGTTCAGCTTTAGAAAAATC  
158101 AAAGTGAAAATCAGATAGTGAAAATCTTATTTTTTGCTTATTGCATCGAT  
15 158151 TTTTAGCTTTAATTCTTGCTGTAATGTTGCTCACTTTTTTAAGTCATGG  
158201 GTTGTTAAGTTTAGCGATTTTAATCCCTGTCTTAGTTTTTCAATAATAAT  
158251 GTTTTTTGTATGGTTATTAGTCACTATCCCCTTATGAAAAGACTATTTG  
158301 GAAATTAATAATTCTAAGTACCATGGAGTTGAAAACCCCTAACTTTAAGCT  
20 158351 AATTGATGAAAAGATTGCTGAATTTAATAAGAGTAATGAAAACCTGATTG  
158401 TAAACTACTTCAAAAAGAAAAGGAATTTGCCACAAACCAAGTTACTGTT  
158451 CAGTTTGATACTCAGTCAAAAAGTCAGAAGAAGTGAAAAACCTAGTAA  
25 158501 AAAAATACTGAAAAGTTATCACTTTCTAACAGTAGTTATGGCAGTTAATT  
158551 TGCTAATAACTGTTGGTTTGATAGTTGGCTTAATTTTTGCTTTCAGATAT  
158601 TAGTTGGTAGTTTTCTTCTAAGGAACGTTTGTGGTTTTATTGACATTAT  
158651 AGCCAAACCTTTACCAGTTTCATATTTGGGTACTATGTGTAAGTGAAAA  
30 158701 TGAAAAACCACTTGACCTGCAATTGCCCTTCATTAGAAACATAGTTTAA  
158751 ACCAGATGGTTTTAGTGTCATCTTAGTTTTAAAGCGATTTGTTTTGCTA  
158801 ATAACTAAGTCTTGTAAGTCTTTTTGATCAGTTGAAGAAAAATCAACT  
35 158851 GCATGTTTTTTAGGGATTACTAAAGTATGACCATCAGCTACAGGAAAAGC  
158901 ATCTAAAAAGCAATGGCATGCTCATTTTCTCCAATTTTATAGGATGTAA  
158951 TTGAACCTTGAACAATATCAGAAAAGATACAACTACTGTGGTGTTTTTT  
159001 TCCATAGTAATGTTATTTATAACAAAAAGCATTATAAGATTAAAAACA  
40 159051 TTGATGCAAAAATAGGGATTGATCAAATCCAAACATAACTGTTATATTTA  
159101 GTTTGCGTAAAAATCCATACACTGAATAGGAGTTTTCCACCATTATCCCA  
159151 AACATTTAAAAATGGAATAGTTTGGAGATAAAAAGCATAGATACTGGGAT  
45 159201 AAATGCCTGCTTTTAAAAGAAAGGATTGCAAATTCCTTGGCGGTTTGATA  
159251 AATTTATAAGTTTTAAAAGTAATCCAACATAAATAAGTAAACACCGG  
159301 ATGGATAACATGGAGTAATAGCTCTGAAAAAGCATTCCAGTCATTAATAA  
159351 AAGAACCATTAAACTATATGGTAATTGCGTTGTTATAGTTGAAAACCAA  
50 159401 CCCTGTACATCAGGTTCTATATTAACAATACCTGTGAAGCGTGATAAAGC  
159451 ATAAAAGTTAAAGAAAATAACTGTAAAAACTAGATAACCTGTAACACTTA

159501 AAACCAGTGAACTGTTTTCAAATCATCTGCTTTTATGGTTAAGAAAGTAG  
159551 TATCATACTAAAAAGATTGCAAGGCTATTACTTTGGTAAGTAAAAGTATC  
5 159601 AAAATTAGTAAACCAAATCAGGCTCATTTGACCACTGTTAGCAACACTAA  
159651 TCAGTGCAAGTAATCACCATAAAGATTTGGGTGAATAGTAAAAAGGTGCT  
159701 AGAAAAATTAAATAATAATCGCATTTATTGTTAAGATAAAAGCAACGGTA  
159751 AAAAAATCCAATTGATTTTTTAAGCACGATTTTATTTAATGATATATGA  
10 159801 GTTTTAAAAAGATTGCTGAAATGATGCGTCAAGCAGAACGAGAACTAAG  
159851 AAAAAACATTAGCGTTTGAACAACAAGCCTTTGAATACAACTATAAAAA  
159901 TGGTGCGATTAAGATCACTATTTTAGGTGATCTTACACTTAAATCAATTA  
159951 ACATCGATCCTGTTTGGATTGATGCAAGTGACAAAGTTATTCTAGAGGAG  
15 160001 ATGATTATAGAAGCTACTAATGAAGCGGTTAGTGATGTGAAAACCAAGTA  
160051 TGATAACTTAGTTGAGAAAACTATGCCAAAAGTTCAGGTCTTTTCTAAT  
160101 TAGATTTTCTTTTTTAATAAAGATCTTATCCTTTTTCATTTCCATAAATG  
20 160151 TAGGGATATTAGCAAAGAGTGTCTTAGTAAAATTGCAACATAACTTAAA  
160201 CTAAAGCCCAATAAACACAAGTTGTGGATCACTATTGCTTAAGTTAAG  
160251 AAAGGTCGCCACATTTTATATTCAACATTAGTTCAATCACTTGCTAAGA  
160301 TACCAGTTGTATTACCTGTGATCTGGCCCTTAAACACAGATACCATCAAA  
25 160351 GCTACATAACTAAAGTAAATTAGAGCAAACACATGGATATAGAAAAATGA  
160401 GATTAAAGAAAAACAGTTATCCACAAGATAATTGCTAAGCTTACAAGTA  
160451 AACTGAGAAAATGCATCATGAAATAAATCTGGTTATTTCTGTACCAACA  
30 160501 AAGATGAAATTCACAATATCTTGTTCAATTAACAGGTGTAATAATTAGTTC  
160551 ACCAAAAAGAGTAACCAAAGCTCCAAATAACCCAAAAACAGCTAACACCC  
160601 CACTAATCTTTTTTTGCTTTAAAAAGACAAACACTGGCGCAATAACAGCA  
35 160651 AAAAATGGACAAAGATCTAATAAAAAATATCCTACTTAGTCGTAGTGAATC  
160701 TAAATTTTGTGAAGATTGGGAATTTTGTCCATAAACATCAGGGAATAAAT  
160751 AAATAATCTGCCTACCAAAAAAACATAGACAAACAGTACAATGGCTAGT  
160801 ACTTGAATTAGATAGAACCTAATCTTTAGTTTTCGAACTAAAGGAGTAAA  
40 160851 AGCTAAAACAGAAATTACACCAGCAATAATAAGGATGATGACAAGGTAGT  
160901 TAAGTGTCTGCATTACTTATTGCTTAAATTAAGATAAATAATTTTCCAA  
160951 TTTTGTCTTCAATGAGTGATCGTTTAAATGATCAAGCCCAACATCGCTTG  
45 161001 CAGAACTTTTTAAGGTTAAAACAAATAATAATGACCCTTATTAGTAAC  
161051 AAAAACTAGTCTAACCCATTCTTCAAAAAGCTTTCAAGTTGAATTTGAAA  
161101 AATGTTCAGAAGAAGAGTTGAAGAAAAAGCAACTGTCTCACTAGCTGGA  
161151 AGGATCATTGCTATTAGACAAACCTTTTTAATTATTCAAGATTTTGATGG  
50 161201 TCAAGTCCAACCTTACATCAATAAAAAAATCCATCCTAAGTTATTGATT  
161251 ACTTTAATGAATTTGTTGATATTGGTGATCAAATTGTTGTTAGTGGAAG

161301 CCAATGTAACTAAAACAAAGGTATTAACCTTTAGCTGTTGAAGAGATGAA  
161351 AATCATTTGCTAAGTGTATTATTGGTTCCACCTGAAAAGTGACATGGACTTA  
161401 CTGATATTGAAACCCGCGCTCGCAAGCGCTTTCTTGATCTTACCTATAAC  
161451 TTAGCAATGCGTGATGTTTTCTGAAACGCACTAAGATTATTAAATCAAT  
161501 CCGTAGCTTTCTTGATCAAAATGGTTTTATTGAAGTTGAAACCCCACTT  
161551 TACAAGCTGTTTTAGGAGGAGCTAATGCTAAACCCCTTTAAAACCCATTAC  
161601 AATGCTTTAAAAGCGGATTTTTATCTCAGAATTGCTAATGAAATAGCATT  
161651 AAAAAAATCATTATTGGTGGATTTAACAAGGTTTATGAAATGGGTAAAA  
161701 TGTTCGTAATGAAGGGGTGATACTACCCACAATCCTGAGTTTACCAGT  
161751 ATTGAAATATATCAAGCTTATGCAGATTTTGAAGTCATGCTTGTGCTTGT  
161801 TGAAAAGCTGATTCAATCACTTTGTGAAAGCTTAAACCAATTTAGCTTTA  
161851 ACTGAAATAACAAAACGATTAATCTAAAAACACCATTTTATAAGATAACA  
161901 ATGGTTGAACCTTATTAAGAAAGTTACAGGGATCGATTTTAAATTCAGTAAA  
161951 AGATGATCAATCTGCCATTTTATTAGCAGAAAAACATCATGTTAAACTAG  
162001 CAAAACACCAACAAAATAAGCAACACATCATTAATTTGTTTTTTGAACAG  
162051 TTTTGTGAACAAACATTAATTGAACCTACCTTTGTAACCCATTATCCAAA  
162101 AGCAGTTTCTCCTTTAGCAAAACAAGATCCTTCAAATCCTGAATTCACCC  
162151 AACGATTTGAACCTTTTATTAATGGTAAAGAGATTGCTAATGCTTACAGT  
162201 GAGCTAAACGATCCTTTAGAACAAAGAAAAAGGTTTGAACAACAACCTTGA  
162251 AGAAAAACAGCTTGGTAATGATGAGACAAAGTGAACCTTGATGAATCGTTTT  
162301 TAGAAGCATTAAGTTTTGGGATGGTAAACACTGCTGGGCTTGGGATAGGT  
162351 ATTGATCGTTTGGTAATGTTGTTATGTGAATGTAATCTATCCGTGATGT  
162401 TGTTTTCTTCCCCAGTTGCGTGAACATAAATAGTTTTGATATTTTAATT  
162451 GTTGGTGCTGGTATTAGTGAATAGTACTAGCTAACATCTTAGCTAATCA  
162501 CAATAAAAGGGTTTTAATTGTTGAAAAAGAGATCATATTGGTGGTAACT  
162551 GTTATGATAAAGTTGATAGTAAACTCAACTCTTGTTCACCAGTATGGA  
162601 CCCCATATTTTCCATACTAACAACCAACTGTTATTAACCTTTATCTCACC  
162651 CTTCTTTGAACTAAATAACTACCACCATCGGGTTGGTTTAAAATTGAAAA  
162701 ATAACCTAGATTTAACCTTACCCTTTGATTTTCAACAGATCTATAAACTA  
162751 ATGGGAAAAGATGGTAGAAAACCTCGTTAGTTTTTTTAAAGAAAATTCAG  
162801 TTAAATACTCATCTATCATTAGCAGAATTACAACATAATTGATAATCCTT  
162851 TAGCACAAAACTCTATCAGTTTTTAAATTAGTAATGTTTATAAACCATAC  
162901 AGTGTCAAAATGTGGGGTTTACCATTTGCAATGATTAATGAGAATGTTAT  
162951 TAACAGGGTCAAGATAGTTTTAAGTGAACAAAGCAGTTATTTCTCTGATG  
163001 CAATTATCCAGGGATTACCTAAATCAGGTTATACAAACAGTTTTCTTAAG  
163051 ATGTTAGCCAATCCCTTAATTGATGTGCAGTTAAACTGCAAAGATAACCT

163101 TTTAGTTTATCAAGATGAAAACTGTTTTTTTAAACAATAACTTAATAGAAA  
163151 AACCAGTTGTTTACTGTGGCTTAATTGACAAGCTATTTAACTTTTGCTTT  
5 163201 GGTCAATTTGCAATACCGTTCTCTTGCCTTTAGTTGAAAAAGATTAAACCA  
163251 AAAAAAATACCAAACCTACCCTGTTGTTAATATGCCTTTAGCTAAATCAA  
163301 TCACAAGGAGTGTGGAATACAAACAATAACAAACCAAGGTTCTTTCAAA  
163351 CCGCAAACCATCGTTAGTTTTTGAAACCCCTGGCAGCTATGCAATTAACGA  
10 163401 TCCTAGGTTTAAATGAACCTTATTACCCAATTAACAATACACTAAATGATA  
163451 CTCTTTTAAAGTACTGAAAAAAGCAAGTAAGTTAAAGAATCTACAC  
163501 CTTTGGGAAGATTAGCAACCTACCAATACATTGATATGGATAAAGCAAT  
15 163551 CCTACTTAGTATTAAAAAGCCCAACAACCTGTTAAGTTAATGGAACAAAA  
163601 AAACATTAGAAATTTTTCTATTATTGCCCATATTGATCATGGTAAATCTA  
163651 CCTTATCAGACCGCTTGTTAGAACATAGTTTAGGCTTTGAAAAAGACTA  
163701 TTACAAGCGCAAATGCTTGATACTATGGAGATTGAAAGAGAAAGGGGTAT  
20 163751 TACCATTAAATTAAATGCTGTTGAATTGAAATTAATGTTGATAACAACA  
163801 ACTATCTTTTCATTTAATTGACACCCCTGGGCATGTTGATTTTACTTAT  
163851 GAAGTGTCTCGTTCTTTAGCAGCTTGTGAGGGAGTTTATTGTTAGTAGA  
25 163901 TGCAACCCAAGGAATTCAGCACAAACGATTTCCAATGCTTATCTTGCCT  
163951 TGGAAAATAACCTGGAAATTATCCCAGTTATTAACAAGATAGATATGGAT  
164001 AATGCTGATATTGAAACAACAAAAGATTCACTCCATAACTTATTAGGAGT  
164051 TGAAAAGAACAGTATCTGTTTAGTATCTGCAAAGCTAACTTAGGGATTG  
30 164101 ATCAGTTAATTCAAACAATTATAGCTAAGATCCCCCACCAAAAGGAGAA  
164151 ATTAATAGACCTTTAAAGCATTACTCTTTGATAGTTACTATGATCCTTA  
164201 CAAGGGGGTTGTTGTTTTATTAGGGTATTTGATGGTTGTTTAAAGGTTA  
35 164251 ATGATAAGGTTTCGTTTTATTAAAGTAATTCTGTTTACCAAATTGTGGAA  
164301 CTAGGGGGTTAAACCCCATTTTTTGAAAAAGAGATCAATTGCAAGCAGG  
164351 AGATGTTGGTTGGTTTTTCAGCAGGGATAAAAAAAGCTTCGTGATGTTGGGG  
164401 TTGGTGATACTATTGTTAGTTTTGATGATCAATTTACAAAACCCCTAGCA  
40 164451 GGTATAAAAAGATCTTACCCATGATCTATTGTGGTTTATATCCAGTTGA  
164501 TAACAGTGATTATCAAAACCTCAAGTTAGCGATGGAAAAGATCATAATCA  
164551 GTGATGCAGCATTGGAATATGAATATGAAACATCCCAAGCGTTAGGTTTT  
45 164601 GGGGTTAGGTGTGGTTTTCTAGGTCTTTTACATATGGATGTTATTAAAGA  
164651 AAGATTGGAAGAGAATACAACCTAAACTCATCTCAGCTCCCCCTTCAG  
164701 TTGTATATAAGGTGTTGTTAACAATGGTAAAGAGATTAGTATTGACAAT  
164751 CCCTCTTGTACCAGAACGCTCCAAGATTAAAGCAATCAGTGAACCAT  
50 164801 TGTAAGTCTTTATTGATTTACCTGATCAATATTTGGGCAGTGTTATTG  
164851 ATTTATGCCAAAAGCTTCAGGGGTCAATATGAAAGTTTAAATGAGATTGAT



164901 ATCAACAGAAAAAGAACTGTTATCTGATGCCTTTAGGGGAAATTATCTA  
164951 CAGTTTTTTTTGATAAGTTAAAGTCGATTAGTAAGGGTTATGCATCGTTAA  
165001 ACTATGAGTTTTATAACTACCAACATAGTCAACTGGAAAAAGTTGAGATC  
165051 ATGTTAAACAAACAAAAGATTGATGCATTATCTTTTATCAGTCATAAAGA  
165101 CTTTGCTTTTAAAGCGGGCAAAAAGTTTGGCACTAAGCTCAAAGAATTGA  
165151 TTCCAAGCATCTGTTTGAGATCCCTATCCAAGCAACAATAGGGAGTAAA  
165201 GTAATAGCAAGAGAGACAATCAAAGCAGTTAGAAAGGATGTAATAGCTAA  
165251 ACTTTATGGAGGGGATGTTAGTAGAAAAAAGAAGTTATTAGAGAAGCAAA  
165301 AAGAGGGTAAAAACGCTTGAAAGCAGTTGGGAGTGTTCAATTACCCCAA  
165351 GAGCTATTTAGTCATTGCTGAAAGATGAAGATTAACATTTTTATAATTT  
165401 GTTATTCTTTTGATTGGTTGATACTTTAAACAAAGTATTCACAATAAAAT  
165451 TTCAACACTAATATAAACAATGATAAAGGATTTTAACTCCTGGTGATTTTA  
165501 TTGGTAAAAACCAACTAAAATCTATGCTTTTGGTGGTATCCAAGAAGTT  
165551 GGTAAAAACATGTATGGGATTGAATATGATGATGAAATCATCATTATTGA  
165601 CTGTGGCATTAAATTTGCTAGTGATGATCTACTTGGCATCAATGGGATTA  
165651 TCCCTAGTTTTGAACACTTAATTGAAAACCAAAGTAAGGTTAAAGCATTG  
165701 TTTATTACCCATGGTCATGAAGACCATATTGGGGGTGTACCATACCTTTT  
165751 AAAGCAGGTTGATATTCTCTGTTATCTACGCACCAAGGATCGCAGCATCAT  
165801 TAATCTTGAAAAAGGTTAATGAGCACAAGGATGCTAAGCTCAATAAGATA  
165851 GTTACTTTTGATGATTTTAGTGAGTTTCAAACCAAACACTTCAAAATTGA  
165901 TTTTTACCGGGTAAACCACTCGATTCCCGATGCTTTTGGAACTCTGTGTGC  
165951 AAACCCCTAATGGCAACATTGTTCAAAGCGGTGACTACCGGTTTGATTTT  
166001 GCTGCTGGGAGTGAGATGTTAGATGTTTATAAAGTAGTGAAAATTGCCGA  
166051 GCGCAATGTCCATGTTTTATGAGTGAATCTACTAATGCTGAAGTACCAG  
166101 GTTTTTCCCAAAGTGAAAAGTTAATTTACAGAAACATCCAAAAGATCTTA  
166151 AAAGAAGCAAGGGGTAGGGTTATTTTAACTACTTTTGCATCTAACATCAC  
166201 ACGGATTAATGAAATTATTGAGATTGCTTTAAACAACAAACGCAAGATCT  
166251 GTTTATTGGGTAAATCAATGGATGTTAATGTTAATATTTACGCAAAATT  
166301 GGATTGATGGCAATTGATAGTAATGATATTGTGGAAGTTCGTGATATCAA  
166351 AAACATCCTGATCGTAATATCTTAATCTGTGCACTGGTTCACAAGGTG  
166401 AGGAGGCTGCTGCTTTAAACACAATGGCACGTGGTAAGCATAATTGGGTG  
166451 AGCTTAAATCAACTGACACCATTATTATGTCTTCAAATCCAATTCCAGG  
166501 TAATTATGCTGCAGTTGAAAACCTTGCTTAATGAACTCTCTAAGTTTGGTG  
166551 TTGCTATTTATGAAAATTCATCCCACTAAAACCTACATGCCTCAGGTCAT  
166601 GCCACTCAACAAGAGTTACAGTTGATGCTAAATTTAATGTTTCTTAAATA  
166651 CTTAATTCTATCCATGGTGAATTTAAGATGATGCGAACCATAAAAAACA

166701 TTGCTAATGAATGTGGCATTAAAAGCGAGGATGTGGCGCTTTTAAGTAAT  
166751 GGCCAAGTAATGTATTTAATTGATGAAGAACTTTATTATTCCAATGAAAT  
5 166801 TATTAATGCTGATCCTATTTATATAGAGAGTCATAACTCTTCTCCTGATC  
166851 TTGCAAGAATAATTAAGCAAAGACAAATCCTTAGTCGTGATGGGATGTTT  
166901 GCTGTTATTGTTGTTTGTGATAAGAATAATAACATCATTGGGATTCCAAC  
166951 CTTAATAACAAGGGTGTGTTTCTTTGCACCTTGATTCCAATCCTTTAATGA  
10 167001 CAAAGATAGCCCATTCTGTTAAAAGAACTTTAGAAAGTGTTATCCAAAGT  
167051 AAGAAGTTTAATAGTCATGAACAACTAACAAAGGAATTGAAACGAGTTTG  
167101 TAAGGAAACTGTTTCTTACTTTATCTGAAAAATAAAAACCGTAATCCCT  
15 167151 TAATTTCAACTGTGCTTTCCTGGATCTAATTCCCCAACCTCTATTTTCT  
167201 GTTACTAGTGCCAAAAGTGGTATTAGAGTACCACAACCTGAATAACCAAG  
167251 TAGTCAAAGAGAGTTTGGGAAGTGAAGCAACCCAATCATCCTTCAACCCC  
167301 ACCCAAAGGTTGAAGAGTGGGAGTCCAATGAAGGATACAGGAAAGATGGG  
20 167351 GGAGAACTCAGTGAACAACCTGCTTCATCCATGAGTGGTATGGCTACAT  
167401 CCACTCGAGCCAAGGCCCTTAAGATAGAGGTGGAAAGGGGGAGTAATGTC  
167451 AATCAAGGCGAACTACAATCCAACGACTTTGCCAAAAGCCGTTTAAAGA  
25 167501 TGAGAGCAATAAGAAGTTGGATTACAGAAGGAGTTTCCCAAGGAAAGG  
167551 TTTGAAAACCGGTGTTGAGTACAGATGAGATAACAAGAGAGAGGGGGATG  
167601 GGGGCGACTTAGACTTTCTCCCCTGAATCGGCAATGGTAAACCCCTTCTCC  
167651 AACTCCCCCTCCCCCTCAACTTCTGCTTCCTCAACCCCCCTCCCCACTTT  
30 167701 TTCTAACATCAATGTTGGGGTTAAATCAATGATCACTCAACATTTAAATA  
167751 AAGAAAACACCCGGTGGGTGTTTATACCTAACTTTTCACCTGACATCTGA  
167801 ACAGGAGCAGGTTATAGAAAAGCTAATAACAACAATAACGGCATTCCCTTT  
35 167851 TGAACAGGTGAACCTAGCAATAGTAGTACCCCTTTAATCCCACCTCAG  
167901 CTGGTGGCTCCTCAGCCAAAAAACAACCACCTATTCCTTTTTACCCAAT  
167951 TCCATCAGTCCCACAGTGACTGGATCAACGCATTGACTTTCACTAATAA  
168001 GAATAACCCGCAACGAAATCAACTGTTGTTAAGAGCACTGTTAGGAACTA  
40 168051 TTCCGGTCTTGATCAATAAGAGTGGGGATAGTAATGATCAATTTAACAAG  
168101 GATAGTGAGCAGAAATGGGATAAAACGAATGAAAAAGATGGGAATTTACC  
168151 TGGGTTTGGGGAGGTGAATGGTGGTTTTATAAGATTTTACTTATTTAA  
45 168201 TAGTTAAAAAGTTTTGAATTTTTCTTAGTTTTTTATTGTTTAAATTTT  
168251 AAGAAAGTCTCAAATTTTATCAGTTTATTGGTCAAAGAAGTCGCAAATT  
168301 TTTCTTAGTTTTTTATTTGCTTAATGGTTAAAAAAGCGTTAGTTTTTACC  
168351 TTTATTTAATTAATAAAAAACATTAACTTCGCCACCCCATCACCATTCT  
50 168401 TAAAAGTGATCTGGTTAGTTTGGCACAACTTGATTCTTCTATCAAATCT  
168451 CCGACCAAACCATCCATAACACCAACTGTTTGTGTTGTTCAAGTCCAAG

168501 GATGTGAAGCTTACATATAGTTCAAGTGGCTCAAATAACCAGATTAGTTT  
168551 TGATTCAACTAGTCAAGCTAACAAACCCGCTACATCGTTGAATTTACTA  
168601 ATTCCACCAACATTGGCATCAAGTGAAGGGTAGTGAATAATATCAGtTa  
168651 GATGTACCGAATGTTTCAACAACCATGAACGAAGTTTTGCAAGAATTGAT  
168701 CCTAGAACAACCTTTGACTAAGTATACCTTAAACAGTAGTTTGGCCAAAG  
168751 AGAAGGGTAAGACACAAGTAGCGGTACATCTGGGTAGTGGGCAAGCAAAT  
168801 CAGTGAACCAGTCAACGCAACCAACATGACCTAAACAACAATCCCAGTCC  
168851 CAATGCTTCAACTGGGTTTAAACTCACTACCGGCAATGCGTATAGAAAAT  
168901 TGGATCAATCCTGACCAATTTACCAACCAATTGATGGGACCAAGCAGGGC  
168951 AAAGGGAAGGATAGTAGTGGGTGGAATAGTGAAGAAAACGAAGCTAAAAG  
169001 TGATGCGCCCCTAAGTACAGGAGGGGGTGCTTCTTCTGGAACATTTAATA  
169051 AATACCTCAACACCAAGCAAGCGTTAGAGAGCATCGGCATCTTGTGTTGAT  
169101 GGGGATGGAATGAGGAATGTGGTTACCCAACCTCTATTATGCTTCTACCAG  
169151 CAAGCTAGCAGTCACCAACAACCACATTGTCTGTGATGGGTAACAGCTTTC  
169201 TACCCAGCTTGTGGTACTGGGTGGTGGAGCGGAGTGCACAGGAAAATGCA  
169251 AGTAACAAACCCACCTGGTTTGCTAATACCAATTTAGACTGAGGGGAAGA  
169301 CAAACAAAAACAATTTGTTGAGAACCAGTTGGGGTATAAGGAAACTACCA  
169351 GTACCAATTTCCACAACCTTCCATTCCAAATCTTTCACCCaACTTGCATAT  
169401 CTGATCAGTGGCATTGACAGTGTCAATGATCAAATCATCTTCAGTGGCTT  
169451 TAAAGCGGGGAGTGTGGGGTATGatagTAGTAGTAGTAGTAGTAGTA  
169501 GTAGTAGTAGTAGTAGTAGTAGTACCAAAGACCAAGCACTTGCTTGATCA  
169551 ACAACAACTAGCTTAGATAGTAAAACGGGGTATAAGGATCTAGTGACCAA  
169601 CGACACGGGATTAAATGGTCCAATCAATGGGAGTTTTTCAATCCAAGACA  
169651 CCTTCTCATTCTGTTCTTCTTATTTCGGGGAATCATAGTAATCAAATTTCA  
169701 TCAGGAACCATTAAACTGCTTATCCTGTGAAAAAAGATCAAAAATCAAC  
169751 TGTCAAGATCAATTCCTTGATCAACGCTACGCCGTTGAATAGTTATGGGG  
169801 ATTTAAACATTAAATAAAGAGAATTCACCCAAATTATTTACTTATTTATT  
169851 AACTATTGTTACCCAATTTTTCTCTTTTTATTTGTTGTTTTTTTACTAAT  
169901 TAAATAAGCAGTCTTTTctTACAAAAAGaAAAATTCATATATAATCTTTG  
169951 cGCTGTTAACACCTTTGTAAcGCCAAAAATGTTCTTTCAAACTGGATG  
170001 CAATCTGTCAATTTTTTCTGAGAGTTTGATCCTGGCTCAGGATTAACGCT  
170051 GGCGGCATGCCTAATACATGCAAGTCGATCGGAAGTAGCAATACTTTAGA  
170101 GGCGAACGGGTGAGTAACACGTATCCAATCTACCTTATAATGGGGGATAA  
170151 CTAGTTGAAAACTAGCTAATACCGCATAAGAACTTTAGTTTCGCATGAAT  
170201 TAAAGTTGAAAGGACCTGCAAGGGTTCGTTATTTGATGAGGGTGCGCCAT  
170251 ATCAGCTAGTTGGTAGGGTAATGGCCTACCAAGGCAATGACGTGTAGCTA

170301 TGCTGAGAAGTAGAATAGCCACAATGGGACTGAGACACGGCCCATACTCC  
170351 TACGGGAGGCAGCAGTAGGGAATTTTTCACAATGAGCGAAAGCTTGATGG  
5 170401 AGCAATGCCGCGTGAACGATGAAGGTCTTTTTGATTGTAAAGTTCTTTTA  
170451 TTTGGGAAGAATGACTCTAGCAGGCAATGGCTGGAGTTTGACTGTACCAC  
170501 TTTGAATAAGTGACGACTAACTATGTGCCAGCAGTCGCGGTAATACATAG  
10 170551 GTCGCAAGCGTTATCCGGATTTATTGGGCGTAAAGCAAGCGCAGGCGGAT  
170601 TGAAAAGTCTGGTGTTAAAGGCAGCTGCTTAACAGTTGTATGCATTGGAA  
170651 ACTATCAGTCTAGAGTGTGGTAGGGAGTTTTGGAATTTTCATGTGGAGCGG  
170701 TGAAATGCGTAGATATATGAAGGAACACCAGTGGCGAAGGCGAAAACCTTA  
15 170751 GGCCATTACTGACGCTTAGGCTTGAAAGTGTGGGGAGCAAATAGGATTAG  
170801 ATACCTTAGTAGTCCACACCGTAAACGATAGATACTAGCTGTCGGAGCGA  
170851 TCCCTTCGGTAGTGAAGTTAACACATTAAGTATCTCGCCTGGGTAGTACA  
20 170901 TTCGCAAGAATGAAACTCAAACGGAATTGACGGGGACCCGCACAAGTGGT  
170951 GGAGCATGTTGCTTAATTCGACGGTACACGAAAACCTTACCTAGACTTG  
171001 ACATCCTTGGCAAAGTTATGGAAACATAATGGAGGTTAACCGAGTGACAG  
171051 GTGGTGCATGGTTGTCGTCAGCTCGTGTGAGATGTTGGGTAAAGTCC  
25 171101 CGCAACGAGCGCAACCCCTTATCGTTAGTTACATTGTTTAAACGAGACTGCT  
171151 AATGTAAATTGGAGGAAGGAAGGGATGACGTCAAATCATCATGCCCCCTTA  
171201 TGTCTAGGGCTGCAAACGTGCTACAATGGCCAATACAAACAGTAGCCAAC  
171251 TTGTAAAAGTGAGCAAATCTGAAAAGTTGGTCTCAGTTCGGATTGAGGGC  
30 171301 TGCAATTCGTCCTCATGAAGCTGGAATCACTAGTAATCGGAATCAGCTA  
171351 TGTGCGGTGAATACGTTCTCGGGTCTTGTACACACCGCCCGTCAAACCTA  
171401 TGAAAGCTGGTAATATTTAAAAACGTGTTGCTAACCTTTATTGGAAGCGC  
35 171451 ATGTCAAGGATAGCACCGGTGATTGGAGTTAAGTCGTAACAAGGTACCCC  
171501 TACGAGAACGTGGGGGTGGATCACCTCCTTTCAAATGGAGTTTATTTT  
171551 TTATTTATCTTAAACACCCATTAATTTTTTCGGTGTTAAAACCCAAATCA  
40 171601 ATGTTTGGTCTCACAACCTAACACATTTGGTCAGTTTGTATCCAGTTCTGA  
171651 AAGAATGTTTTTGAACAGTTCTTTCAAACCTGAAAACGACAATCTTTCTA  
171701 GTTCCAAAAATAAATACCAAAGGATCAATACAATAAGTTACTAAGGGCTT  
171751 ATGGTGGATGCCTTGGCACTAAAAGGCGATGAAGGACGTGTTAACCTGCG  
45 171801 ATAAGCTTCGGGGAGGTGGTAAAAACCTGAGATCCGGAGGTGTCCGAATG  
171851 GAGCAATCTGGTAGCTTGCAAAAGTTACCATTAAATTAATGAATTCATAGT  
171901 TAATTAAAGCGATACGTGGTGAAGTGAAACATCTCAGTAACCACAGGAAA  
50 171951 AGAAAACGAATGTGATTCCGTGTGTAGTGGCGAGCGAAAGCGGAACAGGC  
172001 CAAACCTATCTGAGGATAGGGGTTGTAGGGCTTGCAATTATGGAAGTTAAA  
172051 AGGATAGAAGAAGCTGTTGGAAAGCAGCGCCAAAGAGGGTGATAGCCCCG

172101 TATTTGAAATCTTTTAAATACCTAGCAAGAAACCTGAGTAGCTCGAAAAA  
172151 CGTTATTTTGTAGTGAATCTGCCCAGACCATTGGGTAAGCCTAAATACTAA  
172201 TTAGTGACCGATAGCGAAACAGTACCGTGAGGGAAAGGTGAAAAGAACC  
172251 AGAGATGGGAGTGAAATAGATTCTGAAACCATATGCCTACAACGTGTCAG  
172301 AGCACATTAATGTGTGATGGCGTGCGTTTGAAGTATGAGCCGGCGAGTT  
172351 ATGATAGCAAGCGTTAGTTAACCAGGAGATGGGGAGCTGTAGCGAAAGCG  
172401 AGTTTTAAGAGAGCGTTTGTGTTTATCATAGACCCGAAACGGGTTGAGC  
172451 TAGTCATGAGCAGGTTGAAGGTTGAGTAACATTAAGTGGAGGACCGAACC  
172501 GACTCTCGTTGAAACGATAGCGGATGACTTGTGATTAGGGGTGAAATTCC  
172551 AATCGAAATCCGTGATAGCTGGTTCTCGTCGAAATAGCTTTAAGGCTAGC  
172601 GTAAGATCACAAATAAGTGGAGGTAAAGCTACTGAATGTATGATGGCGCC  
172651 ACCTAGGCGTACTGAATACAATTAACTCTGAATGCCATTTATTTTATTC  
172701 TTGCAGTCAGACAGTGGGGGATAAGCTTCATTGTCAAGAGGGGAAGAGCC  
172751 CAGATCATTAAATAAGGTCCCAAAATATACTAAGTGGAAAAGGATGTGA  
172801 AAGTGCTAAAACAGCAAGGATGTTGGCTTAGAAGCAGCCATCGTTTAAAG  
172851 AGTGCGTAACAGCTCACTTGTGAGTGTTTTGCGCCGAAGATGTAACGG  
172901 GGCTAAGTATATTACCGAATTTATGGATAAGATATTTTATCTTGTGGTA  
172951 GACGAGCGTTGTATTGGAGTTGAAGTCAAAGCGTGAGCATTGGTGGATCC  
173001 AATACAAGTGAGAAATGCCGGCGTGAGTAACGCTTGGGAGTGAGAATCTCC  
173051 CAAACCGATTGACTAAGGTTTCCTGGACCAGGGTCGTCCTTCCAGGGTTA  
173101 GTCTGGACCTAAGCTGAGGCTGAAGAGCGTAGGCGATGGACAACAGGTTA  
173151 ATATTCCTGTACTTACAGTTAGACTGATGGAGTGACAAAGAAGGTTATCC  
173201 ACCCCCATTATTGGATTGTTGGGGATAAACCATAAGGTGGTACAATAGGCAA  
173251 ATCCGTTGTGCATAACACTGAGTGGTGATGTGAGTGAACGAGTGATCAA  
173301 GTAGCGAAGGTGGCAATTAATCATGCTTTCAAGAAAAGCTGCTAGGGCTA  
173351 ATTTAACTGTAACCAGTACCGAGAACGAACACACGTAGTCAAGGAGAGGA  
173401 TCCTAAGGTTAGCGAGTGAACCTATAGCCAAGGAACCTGCAAATTAACCC  
173451 CGTAAGTTAGCGAGAAGGGGTGCTTATCTAAAAGTAAGCCGAGTGAAGA  
173501 ACGAGGGGGGACTGTTTAACTAAAACACAACCTCTATGCCAAACCGTAAGG  
173551 TGATGTATATGGGGTGACACCTGCCAGTGCTGGAAGGTTAAAGAAGGAG  
173601 GTTAGCAATTTATTGCAAAGCTTTTAACTGAAGCCCCAGTGAACGGCGGC  
173651 CGTAACCTATAACGGTCCTAAGGTAGCGAAATTCCTAGTCGGGTAAATTCC  
173701 GTCCCGCTTGAATGGTGTAACCATCTCTTGAAGTGTCTCGGCTATAGACTC  
173751 GGTGAAATCCAGGTACGGGTGAAGACACCCGTTAGGCGCAACGGGACGGA  
173801 AAGACCCCGTGAAGCTTTACTGTAGCTTAATATTGATCAAAACACCACCA  
173851 TGTAGAGAATAGGTAGGAGCAATTGATGCAAGTTCGCAAGGATTTGTTGA

173901 TGTGAAATGTGGAATACTACCCTTGGTTATGTTTTGTTCTAATTGGTAAC  
173951 TGTGATCCAGTTTCAAGACAGTGTTAGGTGGGCAGTTTGAAGGGCGGT  
5 174001 CGCCTCCTAAAAGGTAACGGAGGCGCACAAAGGTACCTTCAGTACGGTTG  
174051 GAAATCGTATTTAGAGTGTAATGGTATAAGGGTGCTTGACTGTGAGACTT  
174101 ACAGGTCGAACAGGTGAGAAATCAGGTCATAGTGATCCGGTGGTTCAGTA  
174151 TGGAATGGCCATCGCTCAACGGATAAAAAGCTACTCCGGGGATAACAGGCT  
10 174201 GATACTGCCCCAAGAGTTCATATCGACGGCAGTGTTTGGCACCTCGATGTC  
174251 GACTCATCTCATCCTCGAGCTGAAGCAGGTTTGAAGGGTTCGGCTGTTTCG  
174301 CCGATTAAAGAGATACGTGAGTTGGGTTCAAACCGTCGTGAGACAGGTTG  
174351 GTCCCTATCTATTGTGCCCCACAGGAAGATTGAAGAGCTTTGCTTCTAGTA  
174401 CGAGAGGACCGGAGCGAGGACACCGCTTATGCTCCAGTTGTAGCGCCAGC  
174451 TGCACCGCTGGGTAGTAACGTGTCTATTAGATAAACGCTGAAAGCATCTA  
174501 AGTGTGAAACTATCTCAAAGATTAATCTTCCATTCTGTAAAGGAAAG  
20 174551 TAAGAGCCGTTATAGACCATGACGTTGATAGGTTACAGGTGTAAGCATAG  
174601 TGATATGTTGAGCTGAGTAATACTAATTGCTCGAGGACTTATTGGTTGAT  
174651 AAAAGGTATTTTCAACTAAAAGATTGTCGTTTTTGTGTTGGTGCTAATAT  
25 174701 CGCTGTGGAACACCTGGAACCATCCCGAACCCAGCAGTTAAGCACAGTG  
174751 GAGCTAAATGTAGGTAGTAATACTGAGAATAGGTAAGCACCAAGCAAAAA  
174801 TTAAGGACTATAGGTTTAAAAACCTATGGTCTTTTTTTATTTAATGAATA  
174851 GTTTTTATACTAATTTATCTAAAAAATCGAACAACCTTTGACTAAGTA  
30 174901 TACGCTCAATGGCAGTTTGGCCAAAGAGAAGGGCAAAGCCAGATAGAGG  
174951 TGCATCTGGGTAGTGGGCAAGCAACTAATTGATCCACTCAACGCGCCACT  
175001 CCATTGGTCTGAATGACAATCCCAGCCCAAATGCTTCAACTGGGTTTAAA  
175051 CTCCTACCAGGCAACGCTTATAGAAAATTGGATCAATCCTGACCAATTTA  
35 175101 TCAACTAATTGATGGGACCAAGCAGGGCAAAGGGAAGGATAGTAATGGGT  
175151 GGAATAGTGAAGAAAATACGGCAGCAGGGGATGCGCCTCTTGTTCACAA  
175201 AGTGGAGGTGGTCTTCTGGAACATTTAATAAATACCTCAACACCAACA  
40 175251 AGCGTTAGAAAGGATCGGCATCTTGTGTTGAAAGTAATGGAGAGGCGAGGA  
175301 ATGTGGTTAGCCTCCTTCCAACCTACCAACCCAACAAGGTGAAGGCTTA  
175351 CCAAACCACTAACACCTACAACAGGTTAATTGAACCTGACAAGTGACAAT  
175401 CAAGTAGTGATTTGAACAATATGACCAACTTGTAAAACTCCTAACAACT  
45 175451 AAAACATCAAAGCGAAATTGGGGAAGGACACCCAATCAATGGGAAATAA  
175501 TAATGGAGGGGGTGTAGTCAAACCTTTTCTTTGTGTTCTTATTCAA  
175551 TGAATCATACAAATACGGGAAGTGTGAACCAATTAAGGCTTATCCA  
50 175601 GTGAAAAAGATGAAGCTTCCCAAGTAGCGATCAATTCCTTGATCAACGC  
175651 TACGCCATTGAATAGTTAAAAACCTGATTTATTTTATAGAAACAGTTAC

175701 TTTGAAGATTCACTACTAATAATTTAAATTAAGCACTCATACTAATATAT  
175751 TAATCCCTTTAGATTGCTTAACTCTTTAAACTTCCCTTTATAATCAAAT  
175801 ATCGCCATGAACGACTGACAGTGACTGAAAAACAGACTTGTTAATTCCAA  
175851 AACCAAATCTGTTAGTTTCTGATTACCACAAACCTCAAGTAATATCATTG  
175901 ATATTGCTGAATTAATTAAGTGCTGTAGTGAGTTAAAAACACTTCTATT  
175951 AATGGTTTAATTGACTTTTTGAACCAACAGGATAAACTTGAATTTAACTT  
176001 AACAGATTAAAGGAGATAGATGTTGAAGATGGTAAGCAACTATTTGGGA  
176051 TAGAACTAGTGTTTATAAAACACTTTCAAATGAAATTGCTCGTTTTTAT  
176101 AAACAAGTAAACAAACACTTTTCGTGAAACAGGTAGTGAAAGTTTGTTTTT  
176151 AGCTTTACCAGTTATTGAAGGGATTAATGAGTTTAACGATATCTTTCGAG  
176201 CTCCATTACTTTATGTTGGAGTTAACTCAAAGTTTCCCCACGCTTTGAA  
176251 CGTTTCTGATTAGAAATTAACAAAGAAGAGATCTTTTTAAACCCACTAT  
176301 TATTGGAGTTGAAACCAACAAACGTAATAGTTTGTTTAAAAATAACTATG  
176351 ATACTACTAAGATAGATGTTAATGATGCTTTAAAGGTATTTAGTGAACCT  
176401 GAATATGAGTTTAGAATGCCTTTAACTTCTGAATTGAAGAGTTTGTAGTAA  
176451 AAAAGCAAAGAGTGATTTTAATACTGAAAAACGAACTAACTATCTTATTA  
176501 ACAACGTTCTTTTGGGGATCTTTGATGTTAAGGGTGATCAGCTGTTCCAA  
176551 AACTTTAATGAGATTCTAAACACTGATCCTGATGTATTAGATGAACTTCT  
176601 AAAAGATAGAAGAGATCTGTTGTTAGAAAACCGGAATTCCTGGAACAAT  
176651 TTGATTAAAAAGATACCTATCTCTTCAGTCACCTTGATATCTACCAACAG  
176701 TATGCAGTTAAGCAAGCTTTACTTGGTGATTTAATTATTGAAGGCCACC  
176751 TGGCACAGGGAAATCTGAAACAATTGTTAATATCTTAGTTAACCTTGTTT  
176801 TAAACAACAAAAAGTATTGTTTGTCTGAAAAAGTAACTGCACCTTGAT  
176851 GTTGTTTACAACCGTCTTGGTAGTTTTAAACACATCGCACTTTTCAACGC  
176901 TAGTGTGCTGCTGAAAAGAAACGCTTTTATAACCAGTTTGCTGAGTTTG  
176951 AAACTTATTTCACTACTTACTTTTCCAAGAAAGATTTGGATGCTACTTTA  
177001 CCAACATTTGAAGGTAAATGGGTGGATGATATTTAGGGGCATTTCAAGC  
177051 ATTACAAGCTCTTTATGACACCAAGATAAATTTCTGGTGAAAATCTGTTTA  
177101 GTTTCAAAGAGATTGTCAGTAGCTTTCAGATGTTGGATGCTAGTTACATC  
177151 AAGATTAAAGAATATGAACGTTTTGATGAGTGAGTGCGCGTCTTTTCAA  
177201 TCCATTGTGATTAGAAAAACACTTAAGTTACCAAGAGTTGAAAAAGAAC  
177251 TTAGTCAGCGCTGGAATGGTATTGATAATTTCTATCAGTTGCAATCGCTT  
177301 CTAAACCAAACCAAAAAACGAAAGGTCTTAACTATGTGTTGGAACACTT  
177351 TGAACAGTTTAATACAGTTATCAGTCCTAAGCATGTTTTGTTCTACAAGC  
177401 CTAGCAATAAATCACAATTGCTCTTAAACAACCTGAAACAGGATGTTGAA  
177451 CAATACACTAGTTTACAACGTTTCCAATCTCCTACTAAGTTTGAAACAAT

177501 CAAGTTGAATTTTCATCAACCAAGTTAATGAAAACCCAACCCCATGGTTCT  
177551 TTTCTTGATTTATCCAATTTTCATGCCAAGCCACTGTTGGAAAACTCGTT  
5 177601 AGTTTTGAGTCAAACATTATTAAAAACAAAACAAGCTTATCTTAATGGGAT  
177651 TGAAAGCTATGTAGCAAGTTGTAAGAACTGCTTAAAACAACATTTTTAA  
177701 ACAACTTTTTTTCAGCTTTATCAAACTAATAAAGATGAACTATTGGAGATC  
10 177751 TGCAGACAAGCAAAAAACCCAGTTTTTAAAAGAGATTACTTGGTGGTTTTAA  
177801 AAAACATTTTGAACCTCTTAAAAAACTCTTTCCAGTGCACATTATGACCC  
177851 TTGAGTCTGCAGCAACTCTAACCCTTAACCAACGTGGTTTGTATGACTAT  
177901 GTGGTTATTGATGAAGCTAGTCAAGTATTTCTAGAAAGAGCAATTCTCTAT  
15 177951 CTTATTTAGAGCTGATAAGTACATTATTGCAGGGGACACTAAACAGTTAA  
178001 AACCAGCTAACTTCTTCCAATCACGTGCTGAGTATGATGTTGATGAGGAG  
178051 TTTGAAGATGGCAATATAGAAGCTGCTGTTCACTCCAGTCTCTACTTCA  
178101 TTTTTTAAAGAACCGTTCAAGAATCTTAACCTTACTTAAGTTCCACTACC  
20 178151 GCAGTGATTAGCTGATCTGATTGCTTTTACTAATAACAGGATCTATGAC  
178201 AATGAATTAATCTTTATGAATAAAGCTAATGCTGATCAAAGGGTTTTTAT  
178251 TGTCCATGATGTAATAGATGGTATCTGAAAAACAACCGGAATCTCCAAG  
25 178301 AAGCACGTGATGTTGTGCAACGCTTAGAACAACTAACAACAACCAATGAT  
178351 TACAAAAAGTCACTTGGTGTAAATTTGTTTCAATAAAAACCAAGCAGATCT  
178401 AATTGAATATCTAATTGATAAAACAAAACAATCCATTACTTAACGAGTGAA  
178451 GAGAAAGACAAAATGATGTTGGTGAATATGAAGGATTATTTGTGAAAAAC  
30 178501 ATTGAAAATGTGCAGGGTGATGAAAGGGATATCATCATCTTTCTTTAGG  
178551 TTAGTATCGTTAGTAAATAGTTATGGTCCTATTAGTAAGCAAGGTGGAG  
178601 AAAACAGACTAAATGTAGCGATAACTAGAGCTAAACAAAGAATAGAACTG  
178651 TTTAAGACAAATAGAGGAGAAGACTACAATGGTTTAAGCTCCAGTTCCTT  
35 178701 GGGTAGTAACTGTTAGTTGAATATCTGCTTTATTGTGAAGCGATGGCTA  
178751 AAAACCAGGGTGAGAAAATCACTTTTCAAGCGGTAAAAAGAAAAGAAACA  
178801 AAAGCAAAGTATGAACTGGCAGTTGAAAATGATTTCTTCAACCAACTGCA  
40 178851 GGCAATTTTTGGTGGAGAGTTTGAGATTAAACGTAACGTAAATGAAGGGG  
178901 CTTACTTTTTCTCATTTGTCTTTTACTTTAATAATATCCCTTATCTTGCC  
178951 ATTGACTTTAACATCCCCATTCCCCTTCAAGAAAACAAGTTATGGAAGG  
45 179001 GATTTTATACCGTGAACAGTTTCTCAAAAAACGTCAATGGAACCTAATTA  
179051 ACATCTGGATTGATGAGTGAAAATTAAACCCAATTGGGGTGATTTCTAAA  
179101 ATCAGATCAAGTTTAGCAGTGCATCAAAACCAGCATGAAGAAATATAATT  
179151 AGATGAAGATAACTTTTCAATTTCTGGACAAGAAGTGTGCTTAGGCATTCT  
50 179201 TTTTTATTGTTTTCAAAAAAATAGTTATGAATGAATTAAACCAACCCCTT  
179251 ACTTGCTATTATTAAAAATGTTGCTAAAACCAAAAACCTTTCTATAGAAG



179301 AGGTGGTTTTTTGTTTGAAAACAGCTTTAGAACAAGCCTATAAAAAACAC  
179351 CTTAACTTTGTTAATGTTGAAGTTAACATTAACCTTTGATAAGGGGATTAT  
179401 TAATGTTGAACAACCTCTTTAATGTTGTTAGTGATGAAAATGAAGATTATG  
179451 ATGACTTTCTTGAAATCCCTTTACAAGCAGCTAACAAAATAAACAGTTCA  
179501 TTGCAATTAGGTGATGTGTTGCGAAAACCAATCCCCTTAAAAAACATTAG  
179551 TAGTGATCTTATCAATAAGATGATTGCTATCTTTAACCAAAAGATTAGTG  
179601 AAACAAACTTTAAAGCAGTAATGAGTGAGTTTAGTAGTGAGGTTGGGGAA  
179651 GTGATTGAAGCGAAAGTTGAAGATATTGATACTAACAAAGAAGGTGGTTT  
179701 AAAGGGTTATATTATTAACCTTGAACTACAAAGGGTTATATCTCCAAGC  
179751 GGGAAATTGTCAAAGGGGAGCGCTTAGAGATAGGTAAAAAATACCTCTTT  
179801 GTTATCAAAGAAATCCAACGGCAAGCATCGTTATGACCAATTACTTTATC  
179851 AAGAAGTGATACCCGCTTACTACAGTTTTTGTTAACTTCAAATACTCCAG  
179901 AAATTGAAAATGGTACGATTGTAATCAAAAAGATTGAACGTTCCCCAGGA  
179951 GTGAAATCAAAGATAGCAGTTATCTCCAATGATCCTGCAGTTGACCCAGT  
180001 TGCTGCTATCTTAGGACCTAAGGGTGAGAAGATTAGGGGGATTAGTGAGG  
180051 AATTTAATGGTGAGATTATTGACATTGTCTTTTGGAATGAAGACAAGTTA  
180101 AAGTTCCTAATTAATGCCATTTTACCTGCAGAAGTCATTGGTTATAACAT  
180151 CTTGCAGGATGATGAGCGTGATACTAGTATTGAAGTTGTTGTACCTGCAA  
180201 ACCAAATTGCTAATGTTTTTGTTTTAAAGGTGTAAACATTAGGTTAATT  
180251 AGTAATTTAACAGGTTGAAATAGTGTGATGTTTACAGTGAAAAAGATGC  
180301 AAGTGAAGCCAACATTAAATTCACGAGGTTAAGCTTTGAACCTGAAGGGT  
180351 TGTTTGCCATCAAAAAAGAAGGGAAAAGATCATTAGTAATGATGCTACT  
180401 GATAAAGTCTTTTACACCTCTAAAGACAATGTGATAGATGATGAGATTAT  
180451 TGTTGATTTAGCTAAAGATCTAATGGTTGATAATAAACAAAAACAACCTG  
180501 AGCAAGTTGCAAAGCAAGTTGTTGAAAAATCACAATTAGAAAAACAAGTT  
180551 ACTCCAAAAGAAAAAGAGAAAGTTCAACCAAAAGCTAAGGTCATTCTAA  
180601 TAGCCATTCCAAAAACCAGCTAAACCTAATCAGATTTTTTCTATCACTG  
180651 TTGATGCTAGTGATAAGAATCTTAAAAAGATCAAGTTGATAATAACCAA  
180701 ACAAACCCCCAAACAAAAACAACATTTGATAGCTTTGATGATCTTTAATG  
180751 CAACTAATAACAAGACTTTGTTTATTAACAAGAAAACATTTTGTTAAAAG  
180801 AGAAGTTTTACGTCCTTGTAATAATTAGACAACCAACTTGAAATTGATCTTA  
180851 ATCAAAATCTCAAGGGCAGGGGTTATTATTTGAGTGTTTTTGTTTAAAG  
180901 CTAGATAAAAAACACCTCAAAGCTGTAGTTGAAAAACACCTTAAGGTTAG  
180951 TTGTAATGATGCAAAGCTTACTGCAATGATTACCGCCTTACAACAATTAG  
181001 CACAAGATGAAAAAATAGAGCTTTCAATCAGGTTAAAAAACAAGTT  
181051 TGACGGTAGGATTAACCAGTGCCAAACACCAGTTACGTAATGTTAA

181101 CCGGGGTTAAAGATGGTGTCTTTTATCTATAAAGGTCCTTTAACTGTTAGT  
181151 GAGTTTGCAAGTAAACTAATATCGCTGTTGCTAACATTATCAAACACTT  
5 181201 TTTTTTAAATGGTTTGGCACTAACAGTTAATTGAGTTTAAACAAATGAAC  
181251 AGTTAGCAGATGCATGTGTTAACTTTGGGTTTGACTTTAAGATGGAAACT  
181301 GAAGTTACCCATGAAAAATATTGTAGCTAACATCCAGTTTGAAGATAGTGA  
10 181351 TGATTTATTGCAACCAAGACCACCTATTGTTACTATCATGGGTCATGTTG  
181401 ACCATGGTAAACTTCGCTTTTAGACACAATTAGAAAACTAATGTAAC  
181451 GCTAAGGAGTTTGGCGGAATTACCCAAAAAATTGGTGCTTATCAGGTGAA  
181501 AAATCACCAAAATAAAACGATTACTTTTATTGATACTCCTGGGCATGAAG  
15 181551 CATTTACTTTAATGCGTGCAAGGGGTGCAAAAGTAACTGATATTGTGGTG  
181601 TTGGTTGTGGCAGCGGATGATGGGATTAAAAAGCAAACAGAGGAAGCAAT  
181651 TAGCCATGCTAAGAGTGCTAACACTCCTATCATTGTTTTTATTAACAAGA  
20 181701 TGGATAAACCAACTGCTAACCTGATCTGGTGATCCAACAACCTCAATAAG  
181751 TTTGATTTAGTTCCTGAGGCTTGGGGTGGGAAAACTATCTTTGTAATGGG  
181801 TAGTGCTTTAACTGGTCAAGGGATTAATGAGTTGCTTGATAATATCTTGT  
181851 TGCTAGGGGAAGTGGAGGGTTATCAAGCTAACTATAATGCCCATTCATCT  
25 181901 GGTTATGCAATTGAAGTACAACTTCAAAGGGACTTGGCCCTATTGCCAA  
181951 TGTCATTGTAAAAAGGGGTACTTTAAAGTTAGGTGACATTGTGGTGTTAG  
182001 GGCCTGCATATGGAAGAGTTAGAACGATGCATGATGAAAATGGTAATAGC  
30 182051 TTAAAAACAAGCAACCCCTTCAAACCTGTGCAGATCTCAGGGTTTGACAT  
182101 TATGCCTGTTGCTGGGGAAAAAGTTCATTGTTTTTGATGATGAGAAGGATG  
182151 CAAAGTTAATTGCTAACAGTTTAAAGAACaACAAAAACAAAAAGCTAAC  
182201 AACTTAACAGTTAATCAAACCTTAAAGAACAGATTAAAAACAAGGAAAT  
35 182251 TAAGATATTAAATTTGATCTTTAAAGCAGATAGTGATGGTTCATTGCAAG  
182301 CTATTAAACAAGCAGTTGAAAACATTAATGTTGCTAAGATCTCACTTAGT  
182351 ATCATCCATGCTGCAGTGGGGCAGATATCAGAGAGTGATATTATGCTAGC  
40 182401 AAAAGCATCAGGGGCTTTATTGTTTAGTTTAACTTAGGTTTGAGTCAAA  
182451 CTGTAAAAAACATTGCTAGTTTACAAGGGTAAAATTAGAAGTTCACTAC  
182501 CATATCCCTAACTAGCAGAGGAGATTGAAAACATCTTAAAGGTCAATT  
182551 AGATCCTGTTTATGAAGAGATTGAAATAGGTAAAGCGGAAGTTTACAAC  
45 182601 TCTGGTTCCTCTAAAATCGGTAATATTGCAGGAACCATTGTTAAATCA  
182651 GGAAAGATAAAAAGAGGGAATTTATGTAAGTTATTCAGAGATAAAGAGAT  
182701 TATCTTTGAAGGCAGAATTGACTCTTTAAAAAATGAAAAACGCCTGTTA  
50 182751 ATTTAATAGAAACAGGGAAGAATTGTGGGATAGTTATTAATGGTTGCAAT  
182801 GATATTAAGATTGGTGATATCATTGTTGCTTATGAAAAGCAGATAGTTAA  
182851 AGATGGCAAGCTATAGAAAACAACGGATTGAAAATGATATCATCCGCTTA

182901 ATTAATCGCACGATTATTAATGAGATCTATGATCCTGTTGTTAAGTTAGG  
182951 TCATGTTAGCCATGTGAAGTTATCAGCTGATTTTTTTCATGCAGTAGTTT  
183001 ATCTTGATTGTTATGATCGTAGTCAGATTCAAAGTGTAGTTAATGCTTTT  
183051 AAAAAGGCTCAGGGCGTTTTTAGTCAAATGTTAGCACAAAATTTGTACCT  
183101 AGCTAAAAGTGTAAGTCCACTTTGTGAAGGATGATGCAATTGACAATG  
183151 CTTTGAAAATAGAACAGATAATTAAGTCTTTGAAAACTAACAGCTTGAA  
183201 GTAAAATTAATCCTAATGGACCCACAAAACAAGTCCCCAAAACCACAAGT  
183251 TAAATCAACTAGATTGGTTGTCAAAAAACAACAGCAGGTGTTGTTTTTC  
183301 CCAAATTGAGTATTCCTGTTAATGATTTTGAAAAACAGTTACTTTAACA  
183351 AGAGCACAAAAAAGGAAGCTAAAGTCTCAAAAAAGCCAAAGGAAAGC  
183401 TAATAAGCTTAATAATAACAAGATAGTACCTTTTTCAATTCTGCTTCAG  
183451 GTGAGACTAATAACACCATTCTTCCTCCTGGTGTAAAAATCAAGCTGAT  
183501 AATAAACTAACCCTTTTAGTAAATTTATTAGTTTTTCACTTCTTCAA  
183551 AAACAAACAACCAGATGAAATAACAGAAAGGTTAGTTGATGATCCTACTG  
183601 TAAAAACCGTTTTAGTGCTTTTAATAAGAAGCTTATTGAGTCTAAAG  
183651 GATAAAAACTAAGAGCAAGAGCGTGAAGATTGTTGGTTATACCAATTT  
183701 AGTTATTGTGGCATTTTTTGCTGGACTTTTAGCAGTGATGAATAAGTTCA  
183751 TCACCCTTTCCTCAGTTGAATATCCTGCTATTGCTTTACAACCTCCCTATT  
183801 AACAAATGCATTATGAGGGATTTCTATCTTTGTTATTAGCATTGTTACTTT  
183851 ACCGTTTTGAACAAATGTTTATCTTGTTTTTAATGGGAGTAAAGGATGTGA  
183901 GAAGTTCGCGTTCTATCCATTATTTTATCTGGATAGTGTTAATTATTAAT  
183951 GTAGTTTTATTACTAGTTAGTTGCTTGTGATGATTGCTGCTTATGCCCA  
184001 TCTTGATGGTTATAACATCTGAAGAACTTAGAATCACTTAACCCATAA  
184051 ACTAATGAAATCACTCTTTATTGGTTATTTTGATGGATTACATCAAGGTC  
184101 ATCTATTTTTAAAGCAGAACAGTAAGTTTGAACCAATGGTGTATTAAAT  
184151 GATAACCCACCTTTAAACAAACCAACTGGCTTTATGATTTACAACAACG  
184201 GGTGACACAAATAAAAACTTACTTGAAAGCAACTGTAGAAGTATTTGATG  
184251 TTGCCAAACATAACATGAATGCACTTAGTTTTTTTGAACAACAGATTAAA  
184301 AGATTGAATTGTGATGAAATTATTGTTGGTACAGATTGGCATTTTGGTAA  
184351 TGATCATAAGGATGGGATCTGGTTAAAGAACTGTTTAAAAATACTGTTA  
184401 TTGTTAATAAAACAAACCTATCAAGTAGTGTTATCCGTAACCTATCTAAGT  
184451 AATAATGAAGTTGAAAAAGCTAACCAACTTTTAGTGGAACCTTATTATAG  
184501 AGTGGGCACAGTAGTACATGGTTTAAAAAAGGCAAGGTTGCTTGGTTTTTC  
184551 CAACTGCTAACATTGTTATGGATAACCACTTATTGACTTTAAATAAGGGG  
184601 AGTTATATAGTAAGAGTTTTATTAAATAACCAAACTTTTTATGGGATTGG  
184651 TTTTATTAGCCAAAAGGATCAGGATTTGGTGTGTGAAACCCATATCTTTA

184701 ACTTTAATAATGAGATTTATGGTTCAGTGGTCAAATTTACACTGTTAAAG  
184751 TTCATTAGAACAATTAGTAAGTTTCCAGTCAAGCAGCTTTGCAAAAAGC  
5 184801 AATTCAAAGTGATGCTAACTTTGCTTTAAAGTGGTTGGAAAACCAAAT  
184851 TAGATAAAATTTAAATCATCCAAATATGGACAGTGCCCCCAGTGGTTTA  
184901 ACTTTAACTGTTATTATCCTTAGCATCATTCTGCTTGCTTTTATCAGCAC  
10 184951 AGTTGTATCAGCTTATGAAACAGCAATCACTTCTTTAAcCCCTTACAGGT  
185001 GAAAGAACTATATCAAGACTAACAACAAGCAAGATAAACTATCAACTAAG  
185051 ATAATAAACCACTTTCAAACCACTATTCAAGTTGTTAATTACTATCCT  
185101 AATTACTAACAACATAGTGGCCATTATGGTTTCTAACATCCTTTTTTTAG  
15 185151 CACTAGAACAAACAATTAAAAATGAGCTTTTATCAAGTGTTTTAAATTTG  
185201 GTAGTTAGTGGGGTTTTAATCGTCTCTTTTGTGAAATTCTACCCAAAAC  
185251 TTTGGGCAGAATTAATGTGATTAGAACCCTGGTTCTATTTGCTTATTGG  
185301 TTTATTTTATCTGATCTTTTGACCAATTACTAAGCTAACCAGTTTA  
20 185351 ATTCTCAAAAAGTATGAAAACCCCTTACCTGTTTCAAGGAAAGATGTTTA  
185401 TTATTTTATTGATGAAATTGAACAAAACGGTTATTTTCAAAGAAGATA  
185451 GTTTACTGATTAAAAAACCTTAATCTTTGACCAAGTACTAGTTAAAAAG  
25 185501 GTAATGATCAAGTGAAAAAAGTGGCTTATTGTTATCTTAATGACAGTAT  
185551 TAACCTGATTGCCAAGCAGTTTTTACAAAGGCAGTTTTCCAGAATGCCAG  
185601 TAGTAGATAAACTACTAATAAGATAGTTGGTTTTATCCATTTAAAGGAT  
185651 TTTTTTACAGCTAAAGAAGCAAACCCCTAAGTCACTTGATTAAACAGTT  
30 185701 GCTTTATCCAGTTGTTTTAGTTCAAGATTCCACCCCATCAAACAAGCAC  
185751 TAAGACAGATGCGTTTTAAACAGAGCACATTTAGCAGTTGTTAATGATAAA  
185801 CATGAAAAACAATAGGGATTGTTTCTATGGAGGATATTATTGAAGAGTT  
185851 GGTGGGTGAAATCTATGATGAACATGATGATATCCAACCGATCCAAGTAT  
35 185901 TGGATGAAAATGTTTGACTTGTTTTACCTAATGTAAAAGCAGCCTACTTT  
185951 TTTAATAAGTGAATTAAGCCAGATTTGGTAAAATCAAAAAATATTACTAT  
186001 CCAGCATTATCTCGCTTCACTAGATAATGATAGTTTGTGCTTGCCAAAATA  
40 186051 AGCTTGACACTCCCTTATTTAGTGTTGAAGTGATAGCTGATAGCGAAGAT  
186101 AAAACCAAAATCTTTACGAAATTAGAAAGAAGAGTGATGTTATTGCTTA  
186151 GAGCATTATTTTAGAGTTGAAAACCAACAAAAATTGTAAAGCTTTACTT  
45 186201 TTGTTATTAATCCCTTACTAGTTGGTTTAACTTGATAATCTATGGGAT  
186251 TGTCTTATTTTCCACTGAAGGGTAATTGACCATGGTGATCATAACCACT  
186301 TAAGAGCAAGGTTTCAACTCACTTTAGAGGAGATTATTGTTTTTGTGTT  
186351 GGTTAGTATTATCTTGTTTTTACTTTAGCTAGCTTTTGTGTGAGTTGCTT  
50 186401 TATGTTAATGAGAAGTCCTAAGCAAAAACAGCTAGAGGTTGATCATGCTA  
186451 ATAAACTAATTTAAACCAAAAGCAATAGTTAATTGTGATCTTTTTCAG

186501 TTGGGTGATTACTGTGTGTTTACATTTAAAAAACTTAGCTTTAAACAACG  
186551 GTTTAAGCAAGATTTTTTTGCTAGAAAGTAAGTTTTCGTTTCGCAGTGAAC  
186601 TGTATCGTCTTTGTTTGGTGGGAGTGTTAATTGCTCTCAATTTAGCGTTA  
186651 AGTTTGATTGAAATTCCTGGGATAGTTTACCTTGGGGTAGTTCGATCCA  
186701 ATTCCGTTTTTTTAATACGGCTATCTTGTTTATTGCTGTTAGGTTGGTGG  
186751 GATTATTATCTACTTCTTTAGTGGCTTTAATCACCCCCTGATTACACCTG  
186801 TTAATCCATCCTATTCACACCCCCATTAGTAGTTTGTTTTACATGGTTAA  
186851 TGACTTTTTTGGTGTCTGTGGATCTTTTATTTCTTTTTTTCCATCTCTTTA  
186901 AAGCAGAGGTGAACCAAATACTACTGTAGTTGACAACAAACCTTTTAGT  
186951 CAGTTAGTTAATACTAAAAAGACGAAGTGAACAAAGTTTTTTTCTTACT  
187001 TGTAATTAGCTTTTTGTGTGGCTTTATTGAGGGGTTAGGTTMTTACTTTG  
187051 GTTATTTTTTAATCCTTGGTAATGTTTCTAGTTTAGGATTGAAGATCTAT  
187101 TATGATGGGTTACAACAACGTGATCTGATTAACAGTAGTAATGTTTTGTT  
187151 CTTTTTAATGACAACAACGCTATCTTCAGTATTAAATACATCTTTGAGA  
187201 TGTTATTTTTCTTTAGTGTGAAAAGAATGTAGTTAATATTGCTAACCAC  
187251 TTTGGTTTGTATTAATCTAAACTTTTTGCAACTAATTAATTAGTTAACTA  
187301 ATAATGAAGTATGTAAAAGTACAGATCATCAATAAATCAACTATTGAACT  
187351 GTTAGAGGATGCTAAAAAAGGGGAAAAAATTAATTTAGATTTAATTAACC  
187401 AAGTTGATCAGACCAACATCCTCAATACGATCACTACTAACCACAAAATTA  
187451 GCATGAGAAAAGGAGTTAAGTGCTCAATTTATCAATCAGCAGAATGAGTT  
187501 AATTAAAAACTTTGAAATTGAGATCATTAAGTTAAAACTATGCTTAATG  
187551 ACAAAGAGCAAGCATTGTTGTTAAAAACCAAATTAGAATTACAAAACCAG  
187601 TTTCAAAAGCAGATAGAGAACTATATCAATGAGATTAACAAGCTCAAGTT  
187651 AACCAATAAAGAGCTTGAAATTACTAACCAAAAAACAAGTAAAGCTCAC  
187701 TTAAACTACAGCGAAACGAATTTGAAGAGAAAATCAACCAGCAAAACTTA  
187751 ACGATTGAAAAACTGAAAATTCAACAAGCAAGAAGTAGTATCTGAGCAGT  
187801 TGCTAAAAAAGGGAATGAACTTGAAAAGTGGTGTGAAAACCAGTATGAGT  
187851 CTTATGCAGATAGCTTTGAAAAGTGTGAGTTTACTAGGTATAAACTGAA  
187901 ATTAAGTTATTAGATGAAAATGATTTTCTAATGAAAAGCAGATTACAT  
187951 CTTTAGTTTCTTTGGTGAACCAATAAAATCCGTTTTTATCAATTT  
188001 GCTGTGAGATGAAAAGTGAGTTTAAATGATAGTAAGCATAAATCAAAAAAC  
188051 AAAGATCATATTAGCAAACCTGGTCAGGGATGCTAAACGTGCTAACTGCAA  
188101 GTATGCTTTTTTAATTAGTGAACCTGAACTGGAGACTGAAAATGACATCC  
188151 AAGTGCCTTAATGCCAACATTGGAAAAGTGGTGTGAAAGTCTATCTAGTT  
188201 AGACCAATGTTTTTATCTTAATGCTTAACTTTTCTATAAGTTAGCTAA  
188251 GAAGTTGTTTGCCCTTAACCGTTTTCAATCAGTTGAACTAATTGATAAAA

188301 ATAAGTTAAATGAACAGTTTAAACAGTTGAAAGATAATTTTTTAACCAA  
188351 ACCTTTTTAGAGATTGAAAAAGTGTGTAAAAGTAACTTAGTTGATATTGA  
188401 AACACTTGAAAAAGCAGTGGTGAAACTAAGGGTTAGAAACGAACGCGTTT  
188451 TAGATCAGTTACTTAATAAATGAACTAAGAAATTGATAGCTTTGATTTA  
188501 CAGTTAACTAAGAAATTACTAATAACTACTAGGGTTTAATTTGTTAGCT  
188551 TATTTAGAAAAATTCAAAATAAGCAAATTATAATTaGGTGTCTTCTTTA  
188601 CTAAAAATATGAAATTATACCGATCTTTAAAAGCAGCCCTGTTACCAGGG  
188651 ATATGCACTAGCATTTTACTTGCTAGTTGTGCTTCAACAAATACTTATCA  
188701 AGACCAAAGGAATGCCCTTGATTAGTTTGGCTTCTAATCGTGATACTTAA  
188751 TTGCGAATGCTAAAAATCCAAAGAAGAAGTGCAAAAAGAAGTTACCAA  
188801 ATGAATAGTAGTACTTCATCAATGATGACAGCTACCCAAAGTGTGCAAT  
188851 TACAACACATCAAATACTGAAAAAACAATAATTCTAAGTATGATCTAG  
188901 ACAAGCTTTTTAAGGATTACATCCTTTATGTTGTTGATAATTTTTCAGGA  
188951 CTTGTTTTTAAAGAAGTGGCGGTCATAGGATCCAGTTAATCGATAAGGA  
189001 TAAAGAGATTTTGGATGGTGGTAATCTAACTAAACATACCCACCACGATC  
189051 ATAACCATATGCATAATCATGAACATGAACATGAAGAACACCATGATGAG  
189101 GAAGAGACAGAAGTAGTTGGCAGAGCACTATCTTTTACTAATGGCATCTT  
189151 TCTAGTGATTGACTATAAAAAAGACTCTGAAAGAAAAAATATGAGTGGTT  
189201 CAACTACTATGATGCACCAACACCACCATGAAGCTGAAGAACATAAAGAG  
189251 GAACGTAAGCTCTCTTTAAACTTAAAGCATACAAATTTAATACCCCTTT  
189301 TAACATTAGTGAGTTTATTAGTGCTTGACATCATAAAGAATCTCATAATA  
189351 GTGACACAGAGTTCAATAACCTTCACAATAAGTATGACAAGGAAGAATTG  
189401 GATATTATTGACTATAACTTTGAAGAAAAAGCTGTTGATGAAACAATTGC  
189451 TTACTAAAAAAGATAGTTATTAACCTTAATTTAGAATTAATAATGACAG  
189501 TGTACACTTACACTGTTTTTTTTATTTAATTGAGAAAATATTGGGTTGATG  
189551 GAACAACAAAACCCTGATCGTTTAAAAAAGATAGGGAACCTATTTATGC  
189601 AATTGTTACAGCTAAAGGTATCATTAGCCGTTTCTTTTGATCAATCCTTA  
189651 GTTTTTTAATTACTAACCTTATCTTCTTTTTTGAGCTTTTGTAGCGCTC  
189701 TTAATTTATCTGTTAGCAAGTGTGATAATCAGTTTGCATTTGTTTTTAT  
189751 TGCTGCAATTATCTTCATTATTTTTTACAACATCTTCTTTTAAGTTACC  
189801 TGTGTTTTATCTATTTTAAGGGCCAGAAAGCAATTGAAACAACTGTAAG  
189851 TACCTGTTAACAATCCTTGATATTAAGAGTGATGAACTGTTACCTTTTTTC  
189901 GCTTTTAGGTAGTTTAAGAAAAGGTTATATGCTAGATGAAATGCTCTTAG  
189951 AACAGTAAATATTTGCTACAATCATAACGCTTTAGTTTTTGTGATACA  
190001 CCAAAATCCGTAGTCAATTTATTAATACTAGTGAAGTATGATTTTGATG  
190051 AATAGCGCTGTAAATATCCTGAGCTGAAGATCAAACTTGAGTCTTATGA

190101 TAGCACCCCTTTTAGATCTCACTATTTAAAAAGATAGTTGAGGTTGTAAAGG  
190151 GTGTGAACATTAAAGATTAAAGGTCCTTTACCTTTGCCTACTAAAAAGGAA  
190201 GTGATCACCATTATCCGCTCTCCCATGTTGATAAAGCATCCAGAGAGCA  
190251 GTTTGAAAAAATACCCACAAGCGCTTAATGATTCTTGTTGATGTTAATC  
190301 AAGGAGGGATTGATAGTTTAAAAAAGATTAAAGATCCCAGTTGGGGTTACA  
190351 CTGCGTTTTTCAAATAGGTTATGGATGTAAGGGGAATATTTGGTGTTAA  
190401 AGTAGGGATGAGTCAGATCTTTACTGAGCAAAATGAGTGCTTACCTATCA  
190451 CCATTGTTTTATTGTGAAGCTAATCAGGTGGCTGGGATTAAACGATTGCT  
190501 AAAGATAATTACAACGCCACTCTATTAAGCTTTCAAACGTTGATGAAAA  
190551 ACAACTTAACAAACCTAAACAAGGGTTCTTTTCCAACTTAACTAGAAC  
190601 CTCATAAATATCTGAGGGAAATCAGAAAGATGCAAGGGTTTGAGTTAGGT  
190651 AAGAAGATCACCCCCAGGAGTTGTTTAAAGATAGGTGAATATGTTGATGT  
190701 CACTTCACTCACCAAAGGTAGGGGTTTTACAGGAGCGATTAAAGGTGAA  
190751 ACTTTAAGATAGGTCTTTGGGTCATGGGGCGGGTTATCCCCACCGCTTT  
190801 CAGGGTTCTGTGCAAGCAGGTAGAGGTGGTAGTAGTGCAGCGTGTTTT  
190851 TAAGGTAAGAAGATGTCTGGGCATTATGGTCATGAACAAGTTACGATCC  
190901 AAAACCTCTTTATTGTTGGCTTTGATGAAATCAATAAGTTAGTGTTAGTT  
190951 TCAGGCGCAATTGCTGGTCCTGAGGGTGGGATTGTTTTAATTAAAACTGC  
191001 AAAAAAGAAAACCTGGCAAGATAAAAGATATAAAGTTAGCAGTACAACTG  
191051 TTAAAGCCCCACAACATAAAGCACCAAAAAGCAGAAAACCTAAGGTTGAA  
191101 ACCAACCAGGTTAACCCEAAAATTGAAGAAGAGAAAACCTAAGTAATGGCT  
191151 AAACCTAAAGTAATCCAGTTTGATGGTAGTTTTAAAGGTGAGATCCAACC  
191201 TGCTAACCACCTCCTTTTAAAAAAGCAGTGATCCAACCAGTGTGTTGATG  
191251 CTATCTTATTAGAACAAGCAGCATGTAGACAAGGCACTCACTCTACTTTA  
191301 ACTAAGGGTGAAGTTAGTGGTGGGGGTAAAAAACCATATAAACAAAAGCA  
191351 CACTGGTAAAGCTAGACAGGGTTCAATAAGAAACCCCATTTATGTGGGGG  
191401 GTGGTGTTGTTTTTGGTCCTAAACCCAACCGTAACTACAACTAAAACTA  
191451 AACAAAAAGGCTTATCAACTTGCTTTAACTAGTGCCTTTGCACAAAAGCT  
191501 TAACAACAACCAAGTGATAGTTGCTGAAGCCAAGTTGTTTGAACAAAACCA  
191551 ATGCCAAAACTAAAAAGATGCTGACGTTTCTCAAGAATGCCAAACTAAT  
191601 GAGCAAAAACTCTGTTTGTGATTGATACTATCTCAAAACCACTGTTGTT  
191651 GAGTACTAACAACCTAAAGCAGATAGTAGTCAAACAGTTTAAATAAGTAT  
191701 CAGTAAGAGATCTACTTTTAGCTAAACTATCATCATTGAAAAAGCTGCT  
191751 TTTACAAAACCTGGAGGAACGACTTAAATAGGCTATGGATGTAACCAACAT  
191801 ACTCTTAAACAGCTCTTAACTGAAAAGAGTTATCTCAACCAGATGGGGG  
191851 AATTGAAAAAATATGTCTTTGCAATTAACCCTAAAGCTACTAAAAACCAA

191901 GTAAACTAGCGTTTGAAATTATCTATGGGGTTAAACCTTTAAAGATTAA  
191951 CACGCTAATTAGAAAACCAGTGACCATTAGAAATGGCACTAAATACCCGTG  
5 192001 GGTTTAGTAAGCTAGCAAACTAGCAGTAATCACCTTACCTAAGGGAATG  
192051 GATATTGCCATTACTGGTGAGAAAACAACCAAGAAAGAAACAAAGGATCA  
192101 ATAATGGCAATTAAAAAGATTATTAGTCGTTCTAACAGTGGGATTACAA  
192151 CGCCACTGTCATTGACTTTAAAAAACTCCTTACCAATTCCAAACCCGAAA  
10 192201 AGTCGCTTTTAGTTACTTTAAAAAAACATGCAGGAAGAAACAACCAGGGC  
192251 AAGATCACTGTTCCGCCACCACGGTGGGAGACATAAACGTAAGTACCGTTT  
192301 AATTGATTTTAAGCGTTACCACTATGACAAATTAAAAAGCAACTGTTAAAT  
15 192351 CGATTGAATATGATCCTAACCGCAGTTGTTTTATCTCCCTTTTACACTAT  
192401 CAGAATGGGGTTAAACCTTACATCATTAGTCCTGATGGGATTAAGGTTGG  
192451 TGATCAAGTTTATTCATCTGATCATGCCATTGATATCAAACCTAGGTTATT  
192501 GTATGCCCCCTTGCTTTTATCCCTGAAGGAACCCAAGTTCATAACATTGAA  
20 192551 CTTAACCCCTAAGGGTGGGGTAAGATAGCAAGAAGTGCTGGAAGTTATGC  
192601 GAGGATCTTGGGTCAAGATGAGACTGGTAAATACATCATTCTCCAGTTAA  
192651 TCTCAGGGGAACTAGGAAGTTTTTAAAGGAGGTAGAGCTACAGTTGGT  
25 192701 GTTGTCTCTAACTTAGATCATAACCTTGTTGTAATTGGTAAAGCAGGGAG  
192751 AAGTCGTCATAAGGGAATCAGACCAACGGTTAGAGGTTGAGCAATGAACC  
192801 CTAATGACCACCCGCATGGGGTGGGGAAGGGAGAAGCCCAGTTGGCAGA  
192851 GATGCACCAAGAACCCCTTGGGGCAAACGCCATATGGGTGTGAAAACACG  
30 192901 TAACATGAAAAACATTCAACTAACCTGATTATTAGAAACAGAAAAGGAG  
192951 AACAACTAATGTCAAGAAGTAGTAAAAAGGGCGCATTTGTTGATGCTC  
193001 ACCTCTTAAAAAAGTGATTGAAATGAACAAACAAGCCAAGAAAAACCA  
35 193051 ATTAAGACTTGGTCAAGAAGAAGTACTATCTTCCCTGAGTTTGTGGGTAA  
193101 CACCTTCAGTGTGCATAACGGTAAAACCTTTATTAATGTTTATGTTACTG  
193151 ATGATATGGTAGGTCATAAGTTGGGTGAGTTTTCCCAACTAGAACTTT  
193201 AAACAACACACTGCTAACCGTTAGTTATGATTGCTTTTGCTAAACAATAC  
40 193251 AGAGTTCACATCTCCCCCAAAGACCGGTTAGTGTGCCAGTTAATTGT  
193301 GGGTAAGAAGATTAATGATGCGCAAAACATCCTTTTAAATACGCCAAAGA  
193351 AAGCTGCTTACTTTTTAACTAAGTTACTAAATAGTGCGATTAGTAATGCC  
45 193401 ACTAATAACCACGGGATGAGCGGGATCTTTGTATGTATTTGAATGTGT  
193451 TGCTAACCAAGGACCTAGCATGAAAAGAACAATCGCTAGAGCCAAAGGTT  
193501 CAGGGAGTGTTTTAACCAAGCGTTCTTCAAACCTAGTTATTAAGTTATCT  
193551 GATAATCCCAATGAAAGAAAATTACTCTTAACCCAACAAAAGGAACTGGT  
50 193601 GAAAAAAGAACAATGGGTGATAAAAAAGAGAAAGCAAAGCAAAGCAA  
193651 AACACAATAACTATGGGACAAAAAGTAAATTCAAACGGCTTAAGGTTTG



193701 GCATTAATAAGAACTGGATCTCACGGTGAAGTCCAGTTCCAACCAACAA  
193751 ACAGCAACCTGATTAGTACAAGATGAGAAGATCCGTAACCTCTTTTTTAT  
193801 CAACTATCGCAACGCTCAGGTGTCTAATGTTGAGATAGAAAGAACCCAA  
193851 CGACTGTTGATGTTTATGTCTATGCAGCTCAACCTGCTTTATTGATAGGC  
193901 AGTGAAAACAAAACATCCAAAAGATTACCAAAATGATCCAAATCATTGT  
193951 GGGCAGAAAGATTAAACTTGATCTTACTATCAATGAGATCGGCTCTCCGA  
194001 TGTATCAAGTAGGATCATTGCCCCGTGATATTGCTAATGCGATTGAAAAC  
194051 AGAGTACCACTCCGTTTCAGCAATGCGCCAAGCTCTAACCAAGGTTTTAAA  
194101 AGCAGGTGCTAATGGGATTAAGGTATTGGTATCAGGCAGATTAAATGGGG  
194151 CGGAAATTGCCCCGTGACAAGATGTATATTGAGGGCAATATGCCTCTTTCA  
194201 ACTTTAAGAGCAGATATTGACTATGCCTTTGAAAAAGCAAAAACCACCTA  
194251 TGGCATTATTGGGGTGAAAGTATGGATTAAACAGGGGGATGATCTATGCaa  
194301 AGGGTTTAAACAGAACCCCGACACACATCCTCCATCCCCAAAAGAAACAG  
194351 CTAAAAACCCCACTATCAAAAAACCAATTGAGTAATAGCAAAACAAA  
194401 ACTCACTGGTAGTGATATTGAACTGCTAGTTTAAAAGCACTTACTGATA  
194451 ATAATCAAAACCACGAATAGTTAAGATGTTACAACCAAAAAGAACCAAT  
194501 ACAGAAAACCACATAACGTCAGTTATGAAGGACACACTAAGGGCAATGGT  
194551 TATGTTGCTTTTGGTGAGTATGGAATTGTTGCTACTAAGGGTAATTGGAT  
194601 CGATGCGAGAGCAATTGAATCAGCGCGGGTTGCTATCTCAAAGTGCTTGG  
194651 GTAAAACTGGAAAGATGTGAATCAGGATCTTCCCCCACATGTCAAAAACC  
194701 AAAAAACCCCTTAGAAGTGAGGATGGGTTGAGGAAAGGTAACCCTGAATT  
194751 TTGGGTTGCTGTGTTTAAAAAGGGGACAGTGATGTTTGAAGTTGCTAACA  
194801 TCCCTGAACAACAGATGATCAAAGCCTTAACAAGAGCAGGCCATAAACTC  
194851 CCTGTACCTGAAAACCTAATGAAAAGAGAGGAGAACAGTTAATGACAATC  
194901 GCTAAGGAGCTGAAGCAAAAGAGCAACGAAGAGTTAGTGAAACTAGTAAT  
194951 TAAGCTTAAGGGTGAACCTCTTAGAATACCGCTTTAACTTGCCCATGGTG  
195001 AACTTGACAAACCCCATCTGATTGCCAAGGTGAGAAAGTTATTAGCAGTT  
195051 GTACTTACTATTCTCACTGAACGCAAACTCAACTGACAAGTTGAAAAAGA  
195101 TAAGTACAAGTTACTTTCAAGAAAAACCAATGAACCTTATTGTTAACAGTT  
195151 GAAAGCAAAAACCTATCAACTAAACCTGAATCCAAACAAGAACTAAAAAG  
195201 GCTGAAGTTAAACCTAAGGTTGAATCAAAGCCTGAATCCAAACAAGAAAC  
195251 TAAAAAGGCTGAAGTTAAACCTTTAAAAACAAGAACTAAAAAGTTGAAG  
195301 TTAAACCTAAAGTTGAACCAAAACCTTTAAAAACAAGAACTAAAAAGGTT  
195351 GAAGCTAGGATTGAAACTAAGACTAAAGTTGAATCAAAACCTTTAAAAACA  
195401 AGAAGTTAAAAAGGTTGAAGCTAAAAAATCTGTTTCAAAACCCCAAAAAAC  
195451 CAGTTAAAGCCAAAATGATTAAAAACAAGGAGAAAAACAATAATGAAGC

195501 GCAACCAACGTAAGCAGTTAATTGGCACAGTTGTTAGCACCAAAAATGCT  
195551 AAAACAGCAACTGTCAAAGTAACATCACGCTTTAAACATCCTTTGTATCA  
195601 CAAATCAGTTATTCGCCATAAAAAGTACCATGTCCATAACTTTGGTGAAC  
195651 TTGTTGCTAATGATGGTGATAGGGTACAAATTATTGAAACAAGACCCCTT  
195701 TCCGCTTTAAAGCGGTGAAGGATTGTCAAAATCATTGAAAGAGCAAAATA  
195751 GTTTATGGTTAGTTTATGACAAGATTAAATGTAGCTGATAATACAGGCG  
195801 CTAAGCAAGTAGGTATTATCAAAGTTTTAGGTGCTACATACAAACGTTAT  
195851 GCATTCCTTGGTGATGTTGTTGTTGTATCAGTTAAAGATGCAATCCCTAA  
195901 TGGCATGGTTAAAAAGGGTCAAGTGTTAAGAGCAGTCATTGTTAGAACCA  
195951 AAAAGGGACAACAACGCCAAGATGGTACCCACCTAAAGTTCCATGACAAT  
196001 GCTTGTGTGCTTATCAAAGAAGATAAATCCCCAAGGGGAACAAGAATCTT  
196051 TGGACCAGTTGCTAGAGAGTTGAGAGAAAAAGGTTACAACAAGATTTTAA  
196101 GCTTGGCGGTGGAGGTTGTTTAAATGCAAAGGATTAGAAAAGGTGATAAGG  
196151 TAGTTGTGATCACTGGTAAAAACAAGGGTGGTAGTGGGATAGTGCTTAAG  
196201 GTATTAACCAAGCAAAACAAAGCGATTGTTGAGGGGATCAATAAGGTTAC  
196251 TGTTCAAAAAAGAACAAGTCAACAAGCGCAGCAAAACAAACCCCAA  
196301 CTACTAAGAAGCCCCCTTACCATTAAATAAACTTGCTTTATTTGATCAG  
196351 AAGGCCAAACAGCAACAATTGGCAAGATCAAATACCAATTGATCCTAA  
196401 AACCAAACAAAAACAAGAGTCTTTAAGAAGACTAATAATGCCATTTAAC  
196451 TGTTATGAATAACCTTGAAAAACCTATAAACTGAGTTAGTTAATCAAC  
196501 TCCAACAACAGTTGGGCTTTTCTTCCATTATGCAAGTCCCTAAGTTAACA  
196551 AAAATCGTTGTTAACATGGGAGTTGGGGATGCAATTAGAGACAACAAGTT  
196601 CCTTGAATCAGCACTAAATGAACTGCACCTGATTACTGGTCAAAAACCCG  
196651 TTGCTACTAAAGCTAAGAATGCTATCTCAACTTACAAGTTACGTGCTGGC  
196701 CAATTAATTGGTTGTAAAGTTACTCTAAGAAATAAAAAGATGTGATCCTT  
196751 TCTGGAATAATTAATCTATATTGCTCTGCCCAGAGTAAGGGACTTTCGCG  
196801 GTTTATCACTGCGCTCTTTTGATGGGAAAGGTAAGTATACGATTGGCATT  
196851 AAAGAACAGATTATCTCCCTGAAATTGTCTATGATGATATCAAAGAAT  
196901 TAGGGGTTTTGACATCACTATTGTCACTTCCACCAACAAAGATAGTGAAG  
196951 CACTTGCTTTACTGAGAGCACTAAAGATGCCGTTTGTAAGAATAGATA  
197001 TGGCTAAAAATCATTAAAAAGTAAAACAATCCCGTCCCAATAAGTTTAGT  
197051 GTACGCGACTACACCAGGTGTTTAAAGGTGTGGGCGTGCTAGAGCAGTGTT  
197101 AAGCCACTTTGGTGTGTGTAGGTTGTGTTCCGTGAACTTGCTTATGCAG  
197151 GAGCAATCCCAGGAGTTAAAAAGCATCATGATAATCAATAAAGTTCCCA  
197201 AAGCCCATTTTGATCCAGTTTCTGATCTTTTCACTAAGATCAACAATGCT  
197251 AGAAAAGCTAAGCTTTTAACTGTTACCACCATCGCTTCTAAGTTAAAGAT

197301 AGCTATCTTAGAGATTTTGATTAAAGAGGGCTATTTAGCTAACTATCAGG  
197351 TGTTGGAAAATAAACTAAAACCAAAAACTAGTTAGTTTCACATTAATA  
197401 TACACCCAAAGAAGGATATGTTCTATTAATGGGGTGAAACAGATCTCAAA  
197451 ACCAGGATTAAGAATCTATCGTTCCCTTTGAAAACTTCCCCTTGTTTTAA  
197501 ATGGTCTTGGTATTGCAATTATCTCCACTAGTGATGGAGTGATGACTGAT  
197551 AAAGTAGCAAGGTTAAAGAAGATTGGTGGGGAGATTTTAGCTTACGTTTG  
197601 GTAAAAAATTATGTCAAAAAATAGGAAATAGATCAATCAAAATTGATCCTA  
197651 GTAAAGTGAGTTTAAATGCAAAACAACAACACTGCTTACTATTAAAGGACCA  
197701 TTAGGGGAAAACACCATTAAACTACCCAAAACTTACCCTTAAAGTTTGT  
197751 TGTTGAAAATGACACTATTAAAGTAATAATAACAACAACCTTAAACAAA  
197801 CTAAGATCTTACACGGTACTTTCAATGCGTTAGTTAACAACGCAGTTATT  
197851 GGGGTTACCAAGGGTTTGTAAAAGAACTCATCCTAGTTGGGGTTGGTTA  
197901 TCGTGCTAATGTGGAAGGGCAATTTCTCAACTTACAATTGGGCTATTCCC  
197951 ATCCTATTAAGGAGTTGATCCCAAACCACTTACTGTTAAAGTAGAGAAG  
198001 AACACTGAAATCACCATTAGTGGAATAAAAAAGAGTTAGTAGGTCAGTT  
198051 TGCCACTGAAATCAGAAAGTGAAGAAAACCTGAGCCTTATAAGGGTAAAG  
198101 GGGTACTTTACTTTAACGAAGTAATTGTTAGAAAACAAGGTAAAACCTGCA  
198151 GAGGGCAAGAAATAAGATGACAAGAAACGATAAAAGAAGGATTAGACACA  
198201 AACGGATTGTCAAAAAGATTAGGTTAACTAACCTTAACAACAGGGTTGTA  
198251 CTAATTGTTATCAAGAGTTTAAAAACATCTCGGTTCAAGCTTGGGACTT  
198301 TAGTAAGAAaCGTTGTTTAAACATCAAGTTCTCTCACTTCACTAAAATTAA  
198351 AAAATGGCAACAAGGAGAATGCTAAACTAGTGGGAATGGATATTGCAACC  
198401 AAACCTCATCAAACTAAACCAAAAGGATGTGGTTTTTGATACTGGGGGTAG  
198451 TAAGTACCATGGTAGGATTGCTGCTTTAGCAGAAGGAGCGCGAgCTAAGG  
198501 GTTTAAATTTTTTAAAGCTATGAATGATCAAAAACTACTAACACTGGCTT  
198551 GTTAACTTCCACTCTTAAACCAAGCCCAACACAACCTTAAACCTTCCA  
198601 GTGAAGCCATTAAAAAGCAGTGTCAAAAAGGAAGGTCAATTACAAAAAC  
198651 AAGCGCTTTCAAAAACATAACTTTAATAACAAAAGTGAGTTGAAGAGAG  
198701 GATTGTCAAACTCAAACGGATCTCCAAAACCACAAAAGGTGGGAGAAACA  
198751 TGCGCTTTAGTGTCTTGTGTTGTTGGTAACAAAAGGGCAAGGTTGGT  
198801 TATGGGATTGCTAAGGCATTGGAAGTACCACTTGCCATTAAAAAGCGAT  
198851 TAAAAAGCCATAACTCCATTATACAGTAGAGATCCATAAGGGTTCAA  
198901 TCTACCACGAAGTGATTGGTAGAAAAGGTGCATCTAAGGTGTTGTTAAAA  
198951 CCTGCACCTTTAGGAACTGGGATCATTGCTGGGGGAGCGATCCGTGCAAT  
199001 TGTAGAGTTAGCTGGTTTGTAGTGATATCTATACCAAGAACTTGGGAAGAA  
199051 ACACCCCCATTAAATGATCCATGCCACTATGGATGGGATCTTAAAGCAA

199101 CTCTCACCCAAAAAAGTGGCATTATTAAGAAATAAACCAATTAGTGATCT  
199151 ATAAAAACAATGGAACTACACCAATTAAGGTGTCTCTAAAAGCCGTAA  
5 199201 CCACAAGTCCAAAGTGGTAGGTAGGGGCCATGGCTCGGGATTAGGTAAAA  
199251 CATCATCAGTGGTCAAAAGGGACAAAAGCAAGAAAATCAGGTTTAACT  
199301 AGGTTAGGTTTTGAAGGGGGACAAACACCCCTTTACCGCCGGTTGCCTAA  
10 199351 GTATGGGGTTGCTAACAAAGGGATCTTAAAAAAGGTGGGTGTTTTAA  
199401 ATTTGAACAAAGTTGCTAAACTCAATCTCAAAACAGTTACTAGAGCAACT  
199451 TTGATTGAAAAAAGGTAATTAGTAAAAAATAACCTCCCTTTGAAGTT  
199501 AATTGGGAACACAAAACCTCACTACTCCCATCCACTTTGAAGTGCAAAAAA  
15 199551 TCTCCAAAAATGCTTTAAATGCAGTGCAAACTAGCAAAGGTAGTGTGAAA  
199601 ATTATCACCTAATGCAAACTGTTTCTTCACCCAAACAAAACCTTAACCTT  
199651 GGTCAAAGGTTACTAACTCTATTACAGAACCGTGACTTTATGGTGTGCGCT  
20 199701 GGTTTTAACAGTGGTACTTTTAATCTTGTTTAGGGTGTTAGCAATTATCC  
199751 CCTTACCAGGGATTAGGATTAATGAGAGTGTCTTGGATAGAAATTCCAAT  
199801 GACTTTTTTTCACTTTTTAACTTACTTGGGGGTGGGGGATTAAACCAGCT  
199851 ATCGTTGTTTGCAGTTGGGATCAGTCCTTATATCTCAGCCCAAATCATCA  
25 199901 TGCAACTGCTTTCAACTGATCTAATTCCTCCACTTTCAAAGCTAGTTAAC  
199951 AGTGGGGAAGTGGGGCGAAGAAAGATTGAGATGATCACAAGAATTATCAC  
200001 CTTACCCTTTGCTTTAGTGCAAGCATTGCTGTGATCCAAATTGCTACTA  
30 200051 ATGCAGGCACTGGTTCAAGTCCGATTAGTTTAGCTAATAGTGGCAGTGAG  
200101 TTTATTGCTTTTTATATTATTGCTATGACTGCAGGGACTTATATGGCAGT  
200151 GTTTTTGGGTGATACTATCTCCAAAAAGGGGTGGTAATGGGATTACTT  
200201 TGTTAATTCTCTCAGGGATTTTATCCCAACTCCCCAGGGCTTTATTGCT  
35 200251 GCTTACAATGTTTTGAGTGGGATAGTAATTACTCTAACCACAGTTAAC  
200301 TGCAGCAATTAGCTTCTTTATCTATTTCTTAGCATTCTTAGTTTTACTGT  
200351 TTGCCACTACCTTTATCACCAGCGACCAGAAAGATTCCCATCCAACAA  
200401 TCAGGACAAGGGTTGGTTAGTGAAGTCAAAACCTTACCTTATTTGCCTAT  
40 200451 TAAGGTGAATGCTGCTGGGGTGATCCCTGTCTATTTGCATCCAGTATTA  
200501 TGTCTATCCCTGTGACCATTGCCCAGTTTCAACCCCAAAGTGTGACGG  
200551 TGGTTTGTGGAGGATTACCTATCACTTTCAACACCCGTAGGGATCTTTTT  
45 200601 ATATGCAGTTTTGGTTATCCTTTTTTCTTTTTTTACAGTTACATCCAGA  
200651 TTAACCCAGAACGGTTAGCTAAGAACTTTGAAAAATCTGGCAGATTTATC  
200701 CCAGGGATTGACCGGGCAATGATACAGAGAAACACATTGCGCGGGTGTT  
200751 AATAAGGATTAACCTTTATAGGTGCTCCTTTTTTAACTGTTATTGCTATTA  
50 200801 TCCCTTACATTGTTTCTTATTTTATTAGGTACCTAACTCCTTGAGTTTA  
200851 GGGGGGACGGGGATTATTATTATTGTTACTGCTGTAGTTGAATTTATCAG

200901 TGCACTGCGTTTCAGCTGCTACTGCTACTAACTACCAACAACCTAAGGAGAA  
200951 ACTTAGCAATTGAAGTGCAACAAACAGCTAAACAAGATAGTCTAGAGCAG  
201001 CTTCAAAAAGAAGCACCAGGGATTGGTAACCTATGGTAGCACAGTTTAAT  
201051 AAGTTCATTATCTTAGGACCCCCAGGGGCAGGAAAAGGTACAGTTTGTA  
201101 ACTGCTTAGCAAAAACAACCTAAGTTAGTCCATATTGCTAGTGGTGATCTGT  
201151 TTAGAGAAGCCATTAAAAACCAGAGTGTTATTGGTAGAAAGATTGCAGCA  
201201 ATTATCAGTCAGGGTGGTTATGTTGATGATGCCACTACTAACCAGCTTGT  
201251 TTATGAATATATCACTACCAATCCATTACCAATGGTTTTATCTTAGATG  
201301 GTTATCCAAGAACAGAGAACCAGCTTGATTTTCTAAATATTAACTAACC  
201351 ATTGACATGGTCTTTGAACTAGTTGTTAGTGATCTGAATAAACTGATTAC  
201401 ACGGATTGATAACAGGGTTATTTGTAACAACGTAAACAGTGTTTATAACT  
201451 TGCTTTTTTCAAAAACCACTAGTTGAAAATAGTTGTGATCAGTGTTTCAGCT  
201501 AAAGTAGTGAAAAGGAGTGATGATAACAAAGCAGTGGTCAAAGCAAGAAT  
201551 GGAGTTATATCAACAAACAATTCAACCAATCCACACTTACTTTTTCAACA  
201601 AACAACTTTTAGTACAAATTGATTGCTTTTTTACCACTAGAAGAACAACCTC  
201651 AAGACAATCAACAATTTATTAGATAAAGATGATCTATCTCAAATCTGCA  
201701 AATGAAGTTGCAGGGATTAAAAAAGCATGTGCAATCTTCAAAGCAGTTAA  
201751 GGCATATTTTACAATTGAAAAGTTACTTGGCAAAAAGTTGGTTACCATTG  
201801 ATCGTTTTAATCAACAATTCATTGAACAAAAACAAGCTAAATGTGCGTTT  
201851 CATGGTTATCTAGGTTTCCCTGGTTTAACTGTCTATCGTTAAACCAAAC  
201901 GGTTATCCATGGAGTTGCCGATCAAACGTGTTTTTAAAGATAGTGATAAAC  
201951 TAACGCTTGACATTGGGATAGACTATCATGGTTATCTTTGTGATGCAGCT  
202001 TTCACTTTACTTGGTAATAAAGCTGATCCAAAGGCAGTAAACTGTGTTAA  
202051 TGATGTTGAACAAGCATTTAGTAAGGTAATTGAACCTGAGCTATTTGTTA  
202101 ACAATCCGATTGGTAATTTATCCAATGCGATCCAACTTACTTTGAAAAC  
202151 AAGGGCTATTTTCTTGTCAAAGAGTTTGGGGTCATGGTTGTGGGATTAA  
202201 GATCCATGAAGATCCTTTAATCTTAACTGGGGAGAGAAAAACCAGGGCG  
202251 TTAGGTTACAAGAGGGGATGGTAATCTGTATTGAACCGATGGTTATGACT  
202301 GATAGTAGTGAGATAACAATGGCAGCTAACAACCTGGAATGTACTAATTT  
202351 AAAGAGTAAGTTTAACTGTCTGTGGAACAGATGTATCACATCACAAACA  
202401 ACGGCTTTGAATGTTTAACTAACTAATGAAAAACGATAAACTCTTTCTAA  
202451 CAGGTAAGATACTGGAAATTATCCATGGTGATAAGTACCGGGTGATGCTT  
202501 GAAAACAATGTTGAGGTTGATGCACATCTAGCAGGTAAAATGAAGATGAA  
202551 AAGAACCAAGATTCTCCCTGGGGATGTTGTTGAGGTGGAATTTTCTCCCT  
202601 ATGATTTGAACTAGGTAGGATAACCCAAAGAAAATAATTAAATATTAT  
202651 GAAGGTTAGAGCAAGCGTAAACCAATTTGTAAAGATTGTAAGATCATCA

202701 AACGTCACCGCATCTTAAGGGTGATCTGCAAAACCAAAAAACAAGCAA  
202751 AGGCAAGGATAATGGCACGAATCTTAGGGATTGATATCCCCAACCAAAAA  
5 202801 CGGATCGAGATAGCTTTAACATACATCTTTGGGATTGGTTTGTCAAGTGC  
202851 AAAACAATCTTAAAAAAGCAAAGATTAACCCCTGATAAACGCGTTAAAG  
202901 ATCTGAGTGAAGAGGAACTTGTTGCGATTAGAAACGCAGCAAGCGGTTAC  
10 202951 AAGATTGAGGGTGATTTGAGAAGAGAGATTGCTTTAAACATCAAACACCT  
203001 AACAGAGATCGGTTCTTGAAAAGGGATTAGACACAGAAAAAACCTGCCAG  
203051 TAAGAGGACAACGCACTAGAACCAACGCAAGAACCAGAAAAGGCCCTAGA  
203101 AAAACAGTGGCTAACAAAGAAAATTGAAAGTAAGTAATGGCTAAGAAAAAA  
15 203151 AAGATTAATGTTCCAGTGTTTGTATCCATGTCTCCTGTTACCTAACAA  
203201 TACCATAGTATCAGCCACTGATCCCAGTGGTAATGTCTTGTGCTGAGCGA  
203251 GCAGTGGTACAGTAGGATTCAAAGGTTTTAGAAAGAAAACCCCTTACTCA  
203301 GCAGGGGTAGCAGCTGATAAGGTGGCTAAACTGTGAAAGAGATGGGAAT  
20 203351 GGGGAGTGTTAAGATGTATCTGAAGGGAACAGGTAGAGGAAAAGACACCA  
203401 CGATTAGAAGCTTTGCTAATGCTGGGATTACGATCACAGAAATCAATGAA  
203451 AAAACCCCTATTCCCCACAATGGCTGCAAGCTCCTAAGCGTCCGCGCTAA  
25 203501 TCAAAACAACAACCTTATGGAAAAATTTTTAAAGTACGAAATTAAGGTAA  
203551 CAACAACCAACCAACCAACACTAACCTAACTATGGGATCTTTGAAGTAG  
203601 CACCGTTAGAATCAGGATTTGGGATTACCATTGGTAATGCGATGCGCCGA  
203651 GTGTTACTTAGTTGTATCCCAGGCGCTAGTGTGTTTGCCATTGCCATTAG  
30 203701 TGGGGTAAACAAGAGTTTAGTAATGTGGAGGGTGTGTTGGAAGATGTGA  
203751 CTGAAATGGTGTTAAACTTCAAGCAACTAGTGGTGAGAATCTCTGATCTT  
203801 TTGTTTGAAGATGGGAGATGATCGAACCACCCTTAGAAAGGTGACCAGT  
35 203851 TTTAAAGTTACTGCTGAAAAAAGGGTGCAATATGCAAAGGATCTTG  
203901 AGTGTCCAGCTGGTTTTGAAGTGATTAATAAGGACCTTTATCTCTTCTCT  
203951 TTACAAAAGGACATGAAACTAACAGTCAGTGTATGTTAAACAGGGTAG  
204001 GGGCTTTACTAGCTTTCTTGAAAACAGAGAATTGATCAATTCGCTTGGCA  
40 204051 TTATTGCTACAGATGCTAACTTTTCCCCGGTTTTTACACTGTGGTTATGAA  
204101 GTTCAAGAGGTGAAAACCTCCAAACAAAAGTTAACTGACCATCTCACCTT  
204151 TAAGATTGCTACTAACGGTGCAATTAAAGCAGTGGATGCGTTTGTCTATGG  
45 204201 CAGCAAAGATCCTAATTGAACACTTAAACCCAATTGTAAGTGTCAATGAG  
204251 TCAATTAAGAATTTAACAATTATCCAAGAGAAAGCAGAGGAAAGAAAGGT  
204301 GAAATCATTTGCCAAGCAAATTGAAGAACTTGACTTTACTGTTAGAACCT  
204351 TTAAGTGTGTTGAAAAGAAGTGGGATCCACACACTCCAAGAGTTACTATCA  
50 204401 AAGTCATTAACTGACATTAGAGAGATTAGAAACCTAGGTAAGAAATCAGA  
204451 ACGGGAGATTATCAAAAAGGTGCAAGAGTTAGGTTTAAAATTCGGTTCTT

204501 AATAAAATAGAGCTATGTCATACATTAATAAAGAGGGGAAAACCACAGCT  
204551 TGAAGAGTGATGACAGTGCCTCAGCAAGTGAGTGCAAGTTAAGTTATGG  
5 204601 AAAGATTCAAACCACTTTAAAAAAGCTAAGAACACCCAAAAAAGGTTAG  
204651 AGAAGATTATTACCATGCTAAAGTTGATAACTTTAACAACCGCAGGGCT  
204701 GTTAAAAAGTGGTTATTAAATACCAATTCATTAGATGTAGATCAACTCAC  
10 204751 AAACCACCTTTTTAAAAAAGTAGCACCACGTTTTTTAAAGCGTAATGGTG  
204801 GTTATAGTAGAGTGTTAAAGTTGGGAGTTAGAAGGGGTGATAGTACTGAA  
204851 ATGGCGATCTTACAGCTGATAGATGCTACCAACTAAACAAGCTGCTTGTA  
204901 GTTTTATTAATGTTGCTTTTTCTATAATGAACTGCCATTAATTAGGGAA  
15 204951 CTATCTTTTAGTGTTTATGAGGGGGAATATGTTTGTATTGTTGGTCATAA  
205001 TGGCAGTGGTAAATCAACCATTTCCAACTGTAAACAGGGTTATTAAAGC  
205051 CCCAGGCAGGTGAGATTAAGATCTTTGGTAAAAACAGTTGATTTTGATAAT  
205101 GTTAGTTACTTGAGAAATAACATTGGGATCATCTTTCAAACCCCTGATAA  
20 205151 CCAGTTTATTGGGATCACTGTTGAAGATGACATTGCCTTTGGGCTTGAAA  
205201 ACAAGTGTTTTTCAAGACAGAAGATAAAAGCCATTATTGATGAAGTTACC  
205251 CTACAAACCCAAACTGATGGGTTTATTAAACAAGAACCCATAACCTATC  
25 205301 AGGGGGACAAAAACAACGGGTAGCAATTGCATCTGTTTTAGCACTAAATC  
205351 CTGCTATTATCATCTTTGATGAATCAACTGCGATGTTAGATCCTAAAGCT  
205401 AAAAAACGATTAAGCAGTTTATGGTTAACTAGCCAAACAGGGCAAGTG  
205451 TGTGATCTCAATTACCCATGATATGGAAGAAGTTACTAAAGCTGATAAGG  
30 205501 TGTTAGTAATGAATGAGGGCAAACCTGATCAAACAAGGTAAACCTGTTGAA  
205551 GTTTTCACTAGTGAACAAGAGTTACAAAAATCCGTTTAGACATCCCTTT  
205601 TTCCTCAGTCTTTCAACCAAGATAAGAGGGATCACTAGTACAATTGATT  
35 205651 ACCAAACCCCTGATTAAATCAATTGCCAAGCTGTGAAAAAAGATAGTCC  
205701 CAATTAAACCTTTAAAGCAGATGAGATTTTAGCAGTTAGTCACTTATCA  
205751 TGTGTTTTTAACAGTAAACTAACAATCCCATTAAGGTGATTGATGATTT  
205801 TTCCTATACCTTTCAAAGAACCAAATTTACTGTATTATTGGTGATAGTG  
40 205851 GCAGTGGTAAATCAACCCTTGTTAACCCTTCAATGGGTTGATAAAACCC  
205901 AACCAGGTGATATTTGGGTTAAAGATATCTATATTGGTGCTAAACAACG  
205951 CAAGATTAAGAACCTTTAAAAAAGTGCAGAAAACTATCTCAATTGTTTTCC  
45 206001 AGTTTCCTGAGTACCAATTGTTTAAAGATACCGTGAAAAAGACATTATG  
206051 TTTGGTCCAGTAGCATTAGGTCAATCCAAGTATGATGCGCGCCAAAAAGC  
206101 GGCTTATTATCTGGAGATGATGGGGTTAAATAACCTTTTTTAGAACGTA  
206151 ATCCCTTTGAATTGAGTGGGGGGCAGAAAAGAAGGGTAGCGATTGCTGGT  
50 206201 ATACTTGCAATTGAACCAGAAATCTAATCTTTGATGAACCAACTGCTGG  
206251 GCTTGATCCTGAAGGGGAAAGGGAGATGATGCAGTTAATTAAACTGCCA

206301 AACACAACAAAGAACGGTATTTATGATCACCCACCAGATGGAAAATGTC  
206351 CTTGAGGTGGCTGATGTGGTTTTGGTTTTAGCTAAGGGTAAACTAGTAAA  
5 206401 AGCTGCTAGTCCATATGAAGTGTTTATGGACCAAACCTTCCTTGAAAAAA  
206451 CAACGATTGTTCTCCCCCTGTGATCCAAGTGATCAAAGATCTAATTGCG  
206501 ATTAATGCTCACTTTAATAAGTTAATTGAGTTGCAACCAAAGAACCTAGA  
10 206551 ACAGCTTGCAATCAGCAATTAACAAGACTATAGCAAACCATGGATAACTTT  
206601 ATTAATGGCTATATCCCAAGAAACAGCTTTGTTTACAAGCTGCATCCAAC  
206651 TACTAACTAGTAATCTTTTACTGTTAGTTATCTTGGTATTTGTACCAA  
206701 TTGGCTTTGTTTTTCAAAGTGTTATCTTCTTTTTTGTACCTTTGTTTTT  
15 206751 TTTATTGCTAAACTCCCGGGGCGGTTTTACAGTTCAGCAATTAAGTCAAT  
206801 TACGCTGTTATTTCTCTTGTGTTATTTGTAACTGGTTTACCTTTCTGTG  
206851 ATCCAGGGTTTTATCTTACTAGTGATCAACTTAACAGTTTACCAGCCATT  
206901 GATAACAGCAAGTTTAGCTTTTGAAACATTAGTTTGTTTAACTATCAAGA  
20 206951 TAATGTTTTTTCCAGGTTTTTGCTTTTAAACAGGGGTAATTTAACCAACT  
207001 TAAATCAACTTGATTTTTTCTATAAAGCTAACAATGCTGATAGTTACACC  
207051 AAAGTAAAGGCATTGATAGTTTAGCAAGTATGCTAGCAAACAATGGCAA  
25 207101 TGGTTTAAGCAAAGACAAAATTCTGAGTGCTTTTTTAGATCACAATTTAA  
207151 ACCTTTATTTAGCGAGAAGTTGGGGGGCAAATTTTGCTGGGTTTGTGTTT  
207201 GATTTTAACCCAACAACCAACTCTTTAACTCACCCCTTTTCTAGCAAA  
207251 TGCTAGTTATGTTTTAACGTTAAGAGCAGTTATCTTAGCATTCTATGTCA  
30 207301 CCCAAAAGATCCTAATTATGATCTTATTTGCAACTGTACTCACTTCCACT  
207351 TCAAGTTCAGTTGAAGTAGCATATGGGATTGAAAGGTTATTATGACCTTT  
207401 AAAACTCATTAAAAATACCTGTTAATGTCTTTGCAATGACCATTGCCATTG  
35 207451 CCATTAGGTTTGTCCCTTCCTTGTTACTAGAAATCACAACGGATCTTAAAT  
207501 GCCCAAGCCTCCAGGGGTTTAGACTTTGAAATGGGGGATTTTTAGTGAA  
207551 GATGCGTTCACCTCTCTTCGTTAGTAGTGCCAATGGTTTCCATTGCCTTTC  
40 207601 GCAATGCCTCTGAACTTGCTAGTGCAATGGAAGCAAGGGGTTATCACCTT  
207651 GCAAAGAAGCGCAGTAGTTATAGACAATACAAAATCACTTGGATTGATAT  
207701 TTTAGCGTTATTTTGGTTTTTGGCTTGGTTTGTGTGATTATCTTTTTAA  
207751 CTATTAGAGGAGCGGTCTTTTTGGATCTAGGTACACCAGAATGGTTATTA  
45 207801 ACAGGAAAGATTAATGAACAGGTAATCAGGGATCTGAAGGTAAGTGGCTA  
207851 GGTACTTGGGGATTGTTAGTTATGATGGCAGTTACTTTAAAGGGTGAGCG  
207901 ATTCAACCAAACCTAGCTACTATCCAAGGTTTATTGGAGCAAAGTTTTTC  
207951 ATTAATCATTGGCAGAAAGATAAAGGTAATTGGTTCAGGTAGAACTGATA  
50 208001 AAGGGGTACATGCCATCAACCAAACCTTTCATGTTGATATTAATGGTGAA  
208051 ATTAATCTCAATTTGTTAATTAGAAAAATTAACCAGTTGATTAAGCCCCA



208101 CTGTATAGTTAAAAACCTTGGTATTGGTTAACGATAGCTTTCATGCGCGGT  
208151 TTCAAGTTAAAAACCAAGGTGTATGAATATCTGATTAACTGTGGGAATTTA  
208201 AATCCGTTGCAATTTAACTATGTTTGGCAGTTAAACCAGCAATTGGATCT  
208251 TGAAAAACTCAAAGCTGATGCCACTTTATTTTTAGGTAAGAAAAACTTTC  
208301 TTAGCTTCAGTAGTTTCGATTCACTGATTCAATTCCGACAATTAGTAAA  
208351 ATTACCATACAAAAAGAACTAACCAACTAGTTAGACTAACTTTTTTTGG  
208401 CAGTGGTTTTCTCAGGAGTCAAGTGAGGATGATAGTTGCTTGTTTAGTGA  
208451 ATTTAAACACTAATAAAATGGCACTTGAAACAGTTGCAAAATTGTTTGAA  
208501 CACCCCAAGAAAGGGAGTTGTGTTGTTAAAGCCCCTAGTTGTGGTTTTGTA  
208551 TCTGAAAACAGTGGTATATGAAAAATAGTTACAAGTGGGATCTATCAGTT  
208601 TTATTAAACAACCAAAGCTTACAAGCAAATTTTTTAAAAATTCAAACAGT  
208651 TAGTGAAGCGTTAATTAAAGCTTATAACAACGGGTTGTGTTTTACAAATA  
208701 AAAGTAGCTTTGAACAGTTTTTAGCAATCGATGATAAGTTCACTGAAGTT  
208751 GAAAATCGTTACACTAACTACCTTTATAACAAGCAGAATGAAAATAACTT  
208801 GGATAAGGAGGTTAATGATGCAATTTTTGCATACCAGAGTTTTAAAAATA  
208851 ACCATAACCTTGCTTTTCAGTACACTGCAACAGGAGTTATATAACCATGAA  
208901 AAAGTCATTAAGGATTATTTAACTGATCCAAAGCTAGCGGTTTACAAGCG  
208951 CAACTTAATGTTAGTTTTTCGCGATAAAACCCACCAACTATCTAGTCAA  
209001 CCCAGAGTTTATTGAGTCAAATTAACCCCTGTTTTTAACCAAGCAGAACGG  
209051 ATTTTTAACATCCTTTCAACTGCTGATTTAACTTGCAACCTGTTGTTTA  
209101 TCAAAACAAaAAATATCCGATTAACAGTGTGAGTGATTATCAGTCCTTAC  
209151 TTGAAAACACTAACAGGGGATTAGAAAAGCTTGTTATGAGAAGTGGATT  
209201 GAAATTTATTGAACTAATAGAAACAGCTTAAGTTTAAGTTTGGTGGAATA  
209251 TTACATCCAAGTAGAGAACTTCGCTAAACTAAAGAACCATCCTAGTTACA  
209301 TTGCCCAAAGTCTTTTAATGATGAGATTGAAGTTGGTTTTATTGATTTT  
209351 GTTTACCAACAAGTAGCTCAGTTTGCCAAACCTTTCAAGCATTTATTCG  
209401 CTTAAAAAACAGATTTTATAAACATGTTTTAAAAGTCAATAAAGTTGAAC  
209451 CATATGATCTTACCCTAACACTTTTTTAAACTAAAAATCATACACGATT  
209501 GAACAAGCTAAACAAGATGCACTAAAAGTTTTAGATCTACTTGGTGACAA  
209551 CTACATCAAGATAGTTAAAAAGGCTTTTAATGAAAAGTGGATTGATTGAC  
209601 TAGCAGATAAAAAACAGTACACAGGGGCATATTCAATCTCCAATGTTAAG  
209651 GGCTTAGAGCACTTTTTTATCTTAATGAACTTTGATAAAACCAAATCATC  
209701 ACTAAATACGTTGGTACATGAAGTTGGTCATTCAAGTTCACTCTTGGTATG  
209751 CATCACAACCAATCCCAAAACATCGATCCTACTATCTTTTATGCTGAG  
209801 ATTGCTTCTATTGCCAATgAACTGTTGTTGTGTTATTATGAGCTGCAACT  
209851 TTATAAAAAATAACCACAAGCAGTTAATTGCTAGTTTATTGAGTCAAATCA

209901 ACCATTTTTTTGGCGCTACTACAAGACAAATAATGTTTTTCACAATTTGAA  
209951 AAAGATACGCTTTTATTTAATCAGAGTTAACCAGAAACCTGACTTTAAAAAC  
5 210001 TTTGATTAAAATTTATGCAAATACTGCGGTTAAATACCAAGGTTTTAAAC  
210051 CTGAAGTAGTTGCTAATAAACTAAAAAGACCCAGTATCAAAAATCATTG  
210101 TCACACATCATTTGCTATCCCCCATTTTTATGCAGGTAACCTCTATGTTTA  
10 210151 CAAGTATGCCATTGGCCAAGTTGCAGGTATTTTAGTAGCTAAAAAATTA  
210201 ATAGTGGTGATAAAAAGATGAAAGATAATTACTTTAAATTCCTCAGTTCA  
210251 GGTTC TAGTTTAGCGCCACTTGAAACCATTAAACTCTTAGGGATTGACCT  
210301 TACTTCACCCCAACCCTGACAAGAAGCACATAACGAAGTAAAGCGTTGGC  
15 210351 TTAAAATTGTGAAACAAAGCTTTAAAAAACTCCAAAAATAAGTGCACCAT  
210401 TTTAACCGCGCTAAAAAGGCCAAGAATAACGAGTTTTTTACTTTAATTGA  
210451 TGAGATTGAAAACGAAGTAATTAAC TACCAAAAGCAGTTTGCAAAATAAA  
210501 CCATTTTTTTGTAACGTGAATGATGGTAAAAATTCCCATTTTTTTTCAGTTT  
20 210551 TTTCAAATAACTTTAACCAGTTACAATAAAAAAACTCATTGGGTTTAG  
210601 TTTTAATAATCTCTCACAAGCTGACAAGTTCAC TTTTGATGGAAATAAAG  
210651 TAACTAAAACCAAATTAAGGGTAATGGTGATTTTAGTTCTGATGAATCG  
25 210701 ATTGAAGTGTTAAAACAAGCAGATATAGTTGTAACAAATCCACCCTTTAG  
210751 TTTGTTTTCAAAGTTTCATTGATCTGTTAATACAACAACAAGCAGTTTC  
210801 TGGTTTTAGGGTTAAATGCAGCAGTTAGCTATAACCATATTTTTACCTAC  
210851 TTTAAAATAACAAGTTGTGGTTTGGCTATACCGTTAATAAAAACAATGAG  
30 210901 TTTTTCAGTTAACAGTGACTATCAACTTTTATAACCCCAAACTAGTAACT  
210951 TTTTACAAAAAATGGCAAGTGTTTCCAAAAGATAGCAGGTATCTCTTGG  
211001 TTTACTAATTTAGGAAAACCAATTATAACCCCTTTTAAATACCAACTG  
35 211051 TTTTTATAAAAACAACGAAAAAACTATCCCAAGTTTGATTGGTATGATG  
211101 CTATTTATGTCAACAAGATTAAAAACATCCCTATGGATTGAAATGGATTG  
211151 ATGGGAGTTCCTTTAACCTTTTTTAACTGTTACAACCCCAAGCAGTTTGA  
211201 ATTAGTTGATTGTCTTGCTAACCCCTTATGCTACCTTAGATACATTAAAAA  
40 211251 CAAATGCCTTTGTGAAATTAAATCAGGGTGATGTGAGAAATGTTAATGgT  
211301 AAAAGAAGGTATGTAAGGGTAATAATTAAAAAACACAAATTTAGTTTTT  
211351 TCAACATTTAACAACCTCTGTTTTTACAAAAGTTAGCTTAATTTTGCTAAA  
45 211401 TTGTTTTTTGATAGCACACTGCTGTCAACGAACCATGTTGATAAATGAAA  
211451 TTCAACTATTTTTTTTATCAAGCAGTGTTGGGTCCAATTGCCCTATT  
211501 TACAAC T GCTTG TAGTGCTGTTTATAGGTTTGATCAAGTTGATGATGGCA  
211551 AGATTAACTAGCAACTGTAACTTCAGCTTCCGCTAGTGGCTCGCTTACT  
50 211601 ACTATCATCAGTAAATATAATTCACAAAAAGATCCTAATGATTATCCAGT  
211651 GGAAC TGGTTTCAC TTGATAGTAGGGGCAGTTATTCTAATGGCAAAAAGG

211701 ATCTGCAAGCTAAACTGCTAGCTAAGGATAAAAAATAACTTTTATAACCTT  
211751 ACTTTTAACTATAGTGATGTAGTTTCAATCCTCTCAAGAAGCCAGATGGA  
5 211801 GTTGAGCTTTGATACGGTTGATACTAGTAATTTTGATCCTAGTTTCTTA  
211851 GTTTTAACAATAATATTTCCAATGTTAATCCAAATAGCATCTATGCTTTA  
211901 CCTGCTACTGTATCAGGTGAAGTTTTAGTTTTAAATGGACCGGTGTTACA  
10 211951 TTACATTTTAAAGTAGTGCTAAAAAAGATAGTAACACCACCCTTTCAACCC  
212001 ATTCAGCTAGCAATAATAGCAATAAGGGAACAATGGTTGTTGCTAGTGAT  
212051 AGTGAACATCAAGTTTATGAACTAAATTAGAAGCTGCAGCAAAAATGAA  
212101 TGCTCAAATAATGAAACCCAAGTTTTAAAAAGTAATTCATCAGAATCTA  
15 212151 ACCAAACCCAAGCTAGTGATACAGAGATTAAAAAGATTTGGGGTGATTAT  
212201 CAAGAAGTTGATGGAGGGTTGAAAAATTACACCTTTAAAGCTAGTGTTTT  
212251 TAACAATTGAAAAGACCTAAATGACTTTGCCACCAGGATTGCAAAATCCT  
212301 TTACAAAACCTGCAAACTACCACTAAAAAAGGGGAGGAAGTACAAGCTGTA  
20 212351 TTTGGGATTGGTAGTTTGGAAAATGCCTTATATACTGCTTTATTTGCTTC  
212401 TGGAAAAGCTGATTACAATAACTTTCTTTTAAACATCAAAAACCAGCGAA  
212451 TTAATTTCAAGTAACCTTTTTTAATAAATCCTCAACTGCATTTCAAACCTT  
25 212501 AAAACTATCTTTAACAGCTTCAAATCCTTAATTGATCAAAACGGTTTAAT  
212551 CTCAAATGCACACTTTAACACCCCAGTTAATGACTATGCTAAGTTTAAAC  
212601 AATTAGCTTTTTACACCTCTTCAACTGCACGCTTCCCTATTCAATTGCA  
212651 AGTGATAGTGTAAGCGTTTTAATAGTTAATGACAAGACAATTGAAAACAA  
30 212701 AAACAATAAGAGTGTTTTTGAGGTTAATTTAAGTAGTGATAGTGATAACA  
212751 ACAGTAACCTAATTGGTACTGTATCACTGGAAAATAGTAAACAAGTTTCA  
212801 CTCTATGAAAAGCAAGTGGATAGTAATAACAAATTTGGTGTGATGCTTT  
35 212851 GTTAATCAAAGATGAAACTTTAATCAACCATCTTAAGAGTTTAAATCGC  
212901 AAGTTAGTGCAAAAAGTGCTAGTGAACTTCCCAAACAAAACAAAACAAA  
212951 ACCTTTTATGACATTTACAACCTGTGAATGCAGATCAAAAAGCAATCTTTGA  
40 213001 TGTTGGTAAACTTAATGGCAAAACTGCCAAAATCATTATTAATGCTACTG  
213051 AAACAATAATGCTAAGATTAGCACCTTACAAGAAAAAGAGGCAATAGTT  
213101 CTAAGAGCACCCCCAACGCTTTGAGAGCACTGATCCATTTCTATTGCTTT  
213151 AGTGCAAGGTCCTAGTTTAAATAGGGATCCATGCAAATGAAAGAGAGGATA  
45 213201 TTGAAACCAAAAAGTTTGTGAATTGGTATCTGAATACTAAAGTCCAATGG  
213251 GAAGAAAATCTATTAAAACTCCTGCAGAATATGTAGCTGATAAAGCTTC  
213301 TTATCTTTTACCTTTTAAAAATAGGCTAAATAATACTAACAGTTACAATG  
213351 AGTTTGTAAAACTGCAGTTAGTCAGTTTGCTGATAAAAATGTAACTAAA  
50 213401 TTTGCAGAACCTGCTGATTTTTTATCCAACAAAGTACGTGATGGTGTTAA  
213451 GAGTAATTTAAATGCTGCAATTAACAACCACAGCATTGATTTTGATAGTT

213501 TTATCAATGATTTAACAGACTATCTTGGTAGTGATGTTAAAAACATCTAA  
213551 TAATTTATTCCCCAACCTCTATTTTCTGTACTAGTGCCTAAGGTGGTA  
5 213601 GTGGAGTATCACAACTGAATAACCAAGTAGTCAAAGAGAGTTTGGAAGT  
213651 GGAATCTTCTTCTCTTTCAACCCCCACCCAAAGGTTGCAAAAAGATAGTC  
213701 CGGTGAAGGATTCAAACAAAGACAGTGAGAACTCGAAACAAGTCTTCA  
10 213751 TCGATGAGTAGTGGGGCTACATCTCCTCGCAAGGCCCTTAAGATAGAGGT  
213801 GGAGAAAGGCAGTAATGTCAATCAAGGCGAACTAGCAAAAAACGACTTTG  
213851 CTAAAAAGCCACTGAAACATAAGAACAGTAGTGGGACAGAGGTGAAGTTA  
213901 GCTGCGAATGGGGAGTTTGCAGGAGACAAGGCCTGAAAACCATTGTTGAC  
15 213951 TACCGAGCAAATAAAAGATAATAGGGGGATGGGGGCTTTCTCCAACCTCCC  
214001 CCTCCCCCTTCAACTTCCGCTTCTCAACCCCCCTCCCCACTTTTTCTAAC  
214051 ATCAATGTTGGGGTTAAATCAATGATCACTCAACATTTAAATCAGCAAAA  
20 214101 CACCCGGTGGGTGTTTATACCTAACTTTTACCTGACATCTGAACAGGAG  
214151 CAGGTTATAGAAAAGCTAATAACAACAATAACGGCATTCTTTTGAACAG  
214201 GTGAAACCTAGCAATAGTAGTCAACAGTTTAAATCCCAATTCAGATGATAA  
214251 TAAAGTCACTCAAGGTGGTGGCTCCCCAGCCAAAAAACACGTATGACA  
25 214301 ATTTACCAAACCTCCATCAGTCCCACCAGTGACTGGATCAACGCATTGACT  
214351 TTTACTAATAAGAATAACCCGCAGCGCAATCAACTGTTGCTCAGAAGCTT  
214401 ACTAGGAACCTATCCCGGTCTTGATCAATAAGAGTGGAGGAAGTGGGAATG  
214451 AGTTTACCCATACGAGTGAGCAGAAGTGGGATAAAACGAATGAAAAAGAT  
30 214501 GGGAAATTTACCTGGGTTTGGGGAGGTGAATGGTGGTTTTATTATGTTTTT  
214551 ATCAAATCTTTATTTACTTTAATAGTTAAAAAAGTTTTGAATTTTTCTTA  
214601 GTTTTTTATTTGTTTAATATTTAAGAAAGTCTCAAATTTTTATCAGTTTA  
35 214651 TTGGTCAAAGAAGTCGCAAATTTCTTAATTTATTTATTCAATAGTTAAA  
214701 AAAGCGTTAGGTTTTTCTTAGTTTTTTTATTTGTTTAATATTTAAAAAATT  
214751 TCTTGATTTTTATCCTTAATTTAATTAATAAAACCTTTACCCCTATTATC  
214801 ACAAACCATCCATAACACCAACCTGTTTGTGTTGTTCAAGTCTAGGGATG  
40 214851 TAAAAGTTAAGTATGAGTCAAGTGGCAGTAACAACATTAGTTTTGATTCA  
214901 ACTAGTCAAGGTGAAAAACCATCCTATGTGGTCGAGTTTACTAACTCTAC  
214951 CAACATTGGCATCAAGTGAAGCGTGGTGAAAAAGTATCAGTTAGATCTAC  
45 215001 CAAATGTTACCAATGAGATGAACCAAGTGTGCAAGAATTGATCCTAGAA  
215051 CAACCCCTTACCAAGTATACCTTAAACAGTAGTTTGGCTAAACAAAAGGG  
215101 TAAACCCAAAGGGAGGTGCATCTCTCAAATTCAAATCAGTGACAATCGA  
215151 TGCGTAATCAACATGACCTAAACAACAATCCAGCCCCAATGCTTCAACT  
50 215201 GGATTTAAATTAGACAAAGGCAATGCATATAGAAAATAAGTGAATCCTG  
215251 ACCAATTTACCAACCAATTGATGGGACCAAGCAGGGCAAAGGGAAGGATA

215301 GTAGTGGGTGGAGTTCAACAGAAGCAACAACGGCAAAAAATGATGCGCCC  
215351 AGTGTTTCTGGAAGTGGAACATCAGACACCGCTTCAAAATTCAAAAGTTA  
5 215401 CCTCAACACCAAGCAAGCGTTAGAGAGCATCGGCATTTTGTGTGATGGAA  
215451 CAACGGCGAGGAATGTGGTTACCCTCCTTCTACTTTCAACCCAACAA  
215501 GGTGAAAAGTGGTCAATATCAACAAAATAACACCTACAACAAGTTAATTG  
10 215551 AACCGGAAAGTGCAACAAGTGCAGCGAGCAGCATGACCAACTTGTAAAC  
215601 ATGTTGTCTAGTAAAAACATCAACAGAAGTTGGGGAAGGGGGAACAGC  
215651 AATGCAGGGAAGTTTCAGTGTCCAAGACACCTTCAGCTTTGTGTTCCTT  
215701 ATTCGGGAATCATACAAATAGTGAACAACTGGACCCATTAAACTGCT  
15 215751 TATCCGGTGAAAAAGATCAAAAATCAACTGTCAAGATCAATTCCTTGAT  
215801 CAACGCTACGCCGTTGAATAGTTATGGGGATTTAAATAATCACCCAAGT  
215851 TAATTTACCCAAATTATTTACTTATTTATTAACCATTGTTACCCAATTTT  
20 215901 TCAACCACTTCCCCACTCTATAAATTGTTATTTTTTAACAATTTGAACAA  
215951 TTAAATTGCAAAAAATAACTATATTAATGTAAATTTAGCTAACAAGCTTA  
216001 ACTGGTTGTTTTTGAGATGAAAGGGTTTTTAAAACCAAATTTCTCGCTCG  
216051 GTGCTTTGTTTTTAACTTTAAGCCCCATAGCCACTGCATGCATTGCTGAA  
25 216101 AAACCAGTTAACAACCGCTTTAACTTTAATAGCGAGCAATTAGCTAGGCT  
216151 AAGAAAAGCAAGGGTTAACCACTGAAGAGATGGGGATACTTTGGAAGTTA  
216201 GCTTTGCAAATAACCACCAAAAACCGATCCGTATCTATGCCATTGATACC  
216251 CCTGAAAAAGCAGTTTTATCTATACAACGCAAATCAGAGATAGAACTTAA  
30 216301 AGAAGCTAATAAAGCAACTGAGTTTGCCAAAAGCTTAATCCCATTGGTA  
216351 GTGAGGTGTGGATCTGACCACTAAATAGCTATAGCTATGATCGTGAAGTA  
216401 GCTGCAGTGTTTTTCAAACCAATCCATTGCAACTGCACTTTGAATCGTT  
35 216451 TGCAGTTGAAATGGTAGCAAATGGTCATGCTTTACCTATTGCTGGTAATG  
216501 ACTTTGATTTTGTTTTTAGTGATTTGGACCCATTTAATCCCCTAAAAATA  
216551 GTAGGGATTGAACTAGCTAATGGTTTTAAACAATGCTTTTAAACAACAGAAA  
40 216601 AAACATCTTTAGTTATTTAGAAAACAGTTTTCAATCAATAACAATGGTCT  
216651 ATCAACAACGCGGTGTTGACCAAAGTTGAACAAGGTATTTAGCTCCTAGT  
216701 AATGATTTTTCTCTACTAAACTGGGGTTGGGATTAACCATCTATGAATT  
216751 GAACTAAACAATGGCTAACAATAAGAGTGCAATTGAGTTGAAAAACATC  
45 216801 GTTGTGATTTTGGTGAATCAGTTGCGATTGACAACATTAACCTTAGTGT  
216851 TGAAAAACACCAACTAGTTAGCTTACTTGGTCCTAGTGGTTGTGGTAAAA  
216901 CCACTACACTTGCACTTATTGCAGGACTTATTAAACCAACTAGTGGTCAG  
216951 GTGTTATTTAATGGTTATGATGTCACCAAAAAACACCCCAAGAACGTAA  
50 217001 ACTAGGGCTAGTTTTTCAAACTATGCACCTTTATCCGCACATGAATGTGT  
217051 TTGAAAACATTGTTTTCCCCTCTACAGTGATAACTCGTGAAAACAAGCA

217101 GTTTTGGAAAAAACAGTGTTGCAAACCATGAGATTAAGTGTGTTACT  
217151 TACTAGCAACGGTGCATCAGTTCAAGAGATTGATCAGCTCAATAAGTTAT  
5 217201 TTCATGATAGTATTGAAAAACCCAAACAGATCCAATACCAAATTAATGAC  
217251 CTTAATGTTAGTGTGTTTTAAAAACTTAAATGAACTAACTGCAAACCTTAA  
217301 GTTAATACCAAGTAAGCACCAGTTTGCTATTACCAATCTCAACAAACAAA  
10 217351 CTCTAAACAGATTAATGAACTGGAAGCTGAGTTTAAACAAAGTGAAAG  
217401 TTACAAAAACAAACCCCAATTAAGAGTGGGGTTGAACACAATGCCAACT  
217451 CCAAGCAATTAAACAACACTTTAGTTATGAAAAACAACGGTTAAAAAAC  
217501 ACTATTTCAAACTAAAGTGGAATAAAACAAACCTTGTGAAAACCTT  
15 217551 AAGTTAGTTAAAAAAGCGATTAGTGAACAACTAAGTTAATTAAACAGAG  
217601 TAGTGATTACACTAAGTTAAAGCAATTAAACGGTTAATTAAAGTTGAAC  
217651 CTAACCAACTCAAAAAACAATATAAGGTTTTCTCAATCAGTTAATTAAA  
20 217701 AACTATTCACCTTAAACTGATAAGTTAACTGATACTCACTTAATGAAAT  
217751 TGAACAGATTAAACCAGAAATTGTTTCAATAAAACAGTTTATCAACAAAA  
217801 CTGCACTTGAAGTAGCTAACAACTAGCGATTACCAAGATTTTAACCAAA  
217851 CGCCCTGATAAGATTTCTGGTGGACAACAACAACGCGTAGCAATTGCTAG  
25 217901 AGCAATTGTCAGAAGACCTAACTATTGTTAATGGATGAACCACTCTCTA  
217951 ACTTAGATGCAAAGCTAAGGGTACAGACAAGACAGTGGATCAGACAGTTT  
218001 CAACAGGAGTTACAAATTACCACTGTTTTTGTCACCCATGACCAGGAAGA  
218051 AGCGATGAGTATTAGTGATGTCAATTGTTTGTATGTCAACTGGAAAAGTGC  
30 218101 AGCAAATCGGCACACCCAGTGAACCTTTATTTAAACCTGCTAATGAGTTT  
218151 GTTGCGCGCTTTTAGGCACCCCTGAGATGAACATCATTGAATGTAGTGT  
218201 CAAAAACAACCAAGTTGTTTTGAAACAACCATCTGTTAGTTACTGAGAGTT  
35 218251 TTAAGCTTAATGTAGAGAACTCTTAGTTGGGTTTAGGTATGAACAATA  
218301 GTGGTCACTACTAACAAAAGTAGTTTGCAAGCTAACTAATTAACATTGA  
218351 AAACCTTAGGTAAACACTTAGTTGCTACCATTAGTTTGTGTTGATACCACCT  
218401 TATCAATGCGCTTAGAATTGAATAGCCACTTAAAGTAGGTGATAGTTTA  
40 218451 AATTTCAATTATTAAAGCTAACAACCTCCATTTTTTGTATATTGATACAAA  
218501 ACAACGATTGAGATTAAACAATGTTTAAAGTGGTTATTAACATCATAA  
218551 TCAACCTCATAGCCTCCAGTTAGGGTTACTAGACCAACCATTACCGTTCT  
45 218601 GAAAGCCCTTTTTGTTGTTCCCTCCCTGCGCTTTTAAACAACATTTTGT  
218651 ACCATTATCCCCTTCTTTTAAAGCTTACAGAAGGGTTTGTAGTCTAACAG  
218701 TGATCTGTATGATCTCTCCTCCCAATCCTTTAGTTTACGAACCTTTCAGG  
218751 ATCTGTTAGTGAATCTAACTTTGTGTTGGGCTTACGCAATAGTTTTCTC  
50 218801 TATTCATAATCTCTTTACCCTTTAGCATTATCATTGCTATTGTTATTGC  
218851 CAGTGCCATAGTATTTGTGTACAAAAAATGTTAAGAGGGTTTTGACAGA

218901 CCGTGTTTTTTTTACCCATATGTAACCTTCAGGGGTGGCAATCTCGATTGCC  
218951 TTTGTATATATCTTTGATTCTGCCCTCTGGTATTTTAAACACGGTGTTTAA  
219001 TGTCACACCAAGTGGCTTGATTACAGGTTACAGTGATACATTTAATGCCT  
219051 TGTGGGCTATCTTAATCTTTGGGGTGTGGAAAACTTGGCATTTAATGTG  
219101 TTGATTATCTCAACAGCAATGTTAAGTGTTAATCCCCAAGTTTACAAGGT  
219151 AGCAAGTTTAGATAGTGCCAATCTGTAAAGACAGTTCTTTAAGATTACTC  
219201 TTCCCTCCATCCGTCCTACTTTAATCTTTCTTACTACCCTTTTAATCTTA  
219251 GGGGGGATGCAAGTCTTTCCGCTGGCTTTGTTTTGAAAAACAACTGAAGA  
219301 AGCGGTTGCTAATGGGGGAATAGTATCTTGCTTTACATCTTTCAACAGA  
219351 TCCAAAGTGGCAATACTAAGCTTAGCAGGTGCTGCTACTTTAGTGTTGTTT  
219401 GTGTTGGGAGTTTGTATAGGGTAGTGTTACGTAATGGCTTTTTATCTGAT  
219451 TGAATGGTTGCAGTGAAAAATTAAACAGCTTTATGTTCAAAAACAACCTTA  
219501 CGCTTTACTAGTTGAATTAATCAACACAAGTTTACCAACTTGATCTGAG  
219551 CTTAAAAACCCGCTCGATCAACAAAAATTGTTTTAACGTTGGTTTTCAAAA  
219601 CATTGGTATTGGGGTTTTTTGGGTAAATTGTCATCTTCCCTTTTATCTG  
219651 ATGGTTGTGGTTAGTTTTGCTAGTGATGAAAGAGCATTAGACACAAGAAC  
219701 CCCAATCCTTTGACCTGATAGTTGAAACTTTGATAACTTTAGTAGGGTGT  
219751 TAAGTGATGGGAAATATCTCAATGCAATAGTTGTCAATACTTTAGTAACG  
219801 GTACTTTCAGTGTTACTAACATTGTTTTTTACCATTGTCATGGGTTATAG  
219851 TTTTCACTACGGAAGTGAAAATACAAAAAACTGGTGTGGTTTTTCTTTC  
219901 TTAGTGTTAATACTGCCTGAGTCTGCGCTTTAATTGGTCAGTATCGG  
219951 ATTGTAATAGTTGCTAACTGAAATAACCCCAACAGTCCCTTGATTGTTCT  
220001 GGGACTCATTATGCCCTTTGTTAGCAGTGTTTTTAGTGGGTTTATGTACC  
220051 GTACTAGCTTTGAAGCCATTCCATCTCAATTAAGAGAGTCAGCACTCATT  
220101 GATGGGTGTAATGGCTTTAACTACTTTTTGAAGATTGCTTTACCAATGGT  
220151 GAAATCTACCAGTTGAACAGTGGGGATTTTAACTGCATTTAGTGCTTGAA  
220201 ATTCCATTTTATGACCATTACTGTTGTTGGGCAACAGGGTGGATTTAAAC  
220251 ATTAAGTTGTGGGTGTTACAACAAGGGATCTTGGATGCTAACAGTAGTGA  
220301 TGAACAGATCAGAACGCTGTTAAATCTCAAGATGAGTGCAGCGATTCTAG  
220351 CTATCCTTCCGATGTTTATTATCTACTTTTTGTCCATAAAAGGATTATG  
220401 AATGCCATTAAAAACAGAGCCAACACCATTAAAGGGTTAATATGCAAAAGT  
220451 TTAACAAGCTGGTTGGTGCAATGCACAGATGGGTAAAACTAGCACTATTA  
220501 GTAATCATTGTGTTATTAGGGATTATCTTTTGTCTGTTTGCCATCTATGA  
220551 CATTGCGCAAGTGATCATTACCATTATCAATGAAGGGGCACTTTTATAAT  
220601 CTTGTATTGAAAAAAGGATCAATAACTGAAGCAATTAATGCCATTAAAC  
220651 AATTTGATAAGATTGTTATCTTTCACCATGTGCGCCCTGATGGGGATTG

55

220701 TTAGGAGCACAACAAGGCTTGTTTCACCTCATTAAAGCTAACTTTAAAAA  
220751 TAAGGAGGTGAAGTGTGTTGGTAATAACAACAACCTGTTTAGCTTTATCA  
5 220801 ACATGACATTTACCAACCAAATTGATGAGAGCTTTTAAAAGAAGCACTT  
220851 GCCATTGTGGTCGATGCTAATTACAAAAACAGGATTGAATTGAGAGAACT  
220901 GTTAGATAAAAAACCTGTTTAAAGCAGTGTTAAGGATTGATCACCATCCCA  
10 220951 ATGAAGATGATCTAAACACTAGCTTTAACTTTGTTGAAGAAAGCTATGTA  
221001 GCTTGTGTGAGCAGATAGTGGAGATGGCCACAGTGGCGAAGTGGACCAT  
221051 ACCACCAGTGGCTGCTACTTTACTATATATAGGTATCTATACGGATAGTA  
221101 ATAGATTTCTATATAGTAATACATCATATAGAACACTATACTTAGCAGCA  
15 221151 ATACTATATAAAGCTAAAGCTGATATAAGGATAGTACATGATCATTTAAA  
221201 CCATACTAGTTTAGCAGATCTTAAGTTTAAAAAGTATGTTTATAACCACT  
221251 TTAAAACCCAAGGACAAGTGATCTATTTTATCTGTACTAAAAAGATCCAA  
20 221301 AAGAGACTAAGAATGACTGCAGATCAATGTGCTAGAGTTAACTTGTTAAG  
221351 TAACATAGCAGATTACAAGATCTGACTTTTCTTTATTGAACAAGCTAATA  
221401 ATGAGATCAGGATAGACCTGAGGAGTAATGGGATTAATGTCAGAGATATA  
221451 GCCATTAAGTATGGTGGGGAGGACATAATAATGCAAGTGGAGCGATCAT  
25 221501 TACTAACAAAAACAAATTAGTGATGTTGTTAGTGATTGTGTGAAAAAA  
221551 TTGTTTATAATTAAGTTTGTATGCACCAACCAAAGAAAAGACTGGCTAAG  
221601 AAGTCTTGAGCCTTTCTAACCGCTGCACTTACCCCTGGGGTTATAACAGG  
30 221651 TGTAGGTGGTTATTTTCTCTTTAACCAAAATAAGCAACGTAGTAGCGTGA  
221701 GCAACTTTGCTTACCAACCCAAGCAGTTAAGTGTTAAACACCAACAAGCA  
221751 GTTGATGAAACCTTAACCCCTTGGACTTGAAACAATAACAACCTTCTCTTC  
221801 ACTAAAGATTACTGGAGAGAACCCAGGATCATTTGGATTAGTAAGAAGCC  
35 221851 AAAATGACAACTTAAATATTTCAAGTGTTACAAAGAATTCTAGTGATGAT  
221901 AATCTCAAGTATCTCAATGCTGTTGAGAAATACCTTGATGGTCAGCAAAA  
221951 CTTTGCAATCAGAAGGTATGATAACAACGGTAGAGCTTTATATGATATTA  
40 222001 ACTTAGCAAAAATGGAAAACCCCTCAACGGTGCAAAGGGGTTTAAATGGC  
222051 GAGCCTATCTTTGATCCTTTTAAAGGCTTTGGTTTAACTGGTAATGCCCC  
222101 TACTGATTGGAATGAGATCAAAGGTAAAGTTCAGTAGAAGTAGTTCAAT  
222151 CCCCCATTCCCCAACCTCTATTTTGTGTTACTAGTGCCTAAGGTGGCA  
45 222201 TTAGAGTATCACAACCTGAATAACCAAGTAGTCAAAGAGAGTTTGGAAGT  
222251 GAAAGCAACCCAATCATCCTTCAACCCACCCAAAGGTTGCAAAAAGATA  
222301 GTCCAGTGAAGGATTCAAGTAAACAAGGGGAGAACTCAGTGAAACAACCT  
222351 GCTTCATCCATGAGTAGTGGTATGGCTACATCCACTCGAGCCAAGGCCCT  
50 222401 CAAAGTGGAGGTGGAAAGGGGGAGTCAAAGTGATTCACTTTTAAAAAACG  
222451 ACTTTGCTAAAAAGCCACTAAAGCATAAGAACAGTAGTGGGGAGGTGAAG  
55



222501 TTAGAGGCAGAGAAGGAGTTTACTGAGGCCTGAAAACCATTGTTGACTAC  
222551 TGATCAAATAGCAAGAGAGAAGGGGATGGGGGCGACGGTGGTTAGTTTCT  
5 222601 ATGATGCACCCTACAGTGAAAACCATACTGCCTTTGGACTTGTGATCAC  
222651 ATCGATCCTAAAAAGATGGTTGAAAAC TACCACCAAGTTGAAAGACCCC  
222701 GAAGTGAAACCACCATGGGATCTGGGATTACAACGCAAGAAACCTCTTGT  
10 222751 TACAAACAACAGGGTTCTTTAACCCAAGAAGACACCCGGAGTGGTTTGAT  
222801 GAAGGACAAGCTAAGGCAGATAACACTAGCCCTGGCTTTAAGGTAGGGGA  
222851 TACTGATCACA AAAAGACGGGTTTAAAAAAACTCTTCTCTCCAATAG  
222901 CTTTACCATTGTAAGCATACTTTGCTAACATTGGTAACATGGTTGCTATT  
15 222951 GGTAAC TCGGTATTTATCTTTGGTGGTAATGGTCATGCTACTAAGATGTT  
223001 TACCACCAATCCCTTAAGTATTGGGGTATTTAGGATTAATAACACTGATA  
223051 ACTTTAGTAAGTCATCAGTAACAGGTTGACCATATGCAGTGTTATTTGGG  
20 223101 GGATTAATTAATCCCCAAACCAATGGCTTGAAAGATCTTCCCCTTGGTAC  
223151 CAACAGGTGGTTTGAATATGTACCAAGAATGGCAGTTAGTGGGGTGAAAT  
223201 GGGTTGGTAATCAACTAGTGTTAGCAGGAACACTAACAAATGGGTGATACA  
223251 GCTACTGTACCTAGGTTAAAGTATGATCAACTAGAAAAACACTTAAACCT  
25 223301 AGTTGCTCAAGGCCAGGGACTATTGAGAGAAGACTTGCAGATCTTCACTC  
223351 CCTATGGGTGAGCTAATCGTCCTGATATTCCTGTAGGAGCATGACTCCAA  
223401 GATGAAATGGGCAGTAAATTTGGTCCCCATTACTTCTTAAATAACCCCTGA  
223451 TATCCAGGACAATGTTAATAATGATACGGTTGAAGCATTAATCAGTAGTT  
30 223501 ACAAAAACACTGATAAGTTAAAACACGTTTATCCTTATCGATACAGTGGT  
223551 TTGTATGCTTGACAGTTATTTAACTGGTCTAACAACTAACCAACACTCC  
223601 CCTATCAGCTAACTTTGTTAATGAAAACAGTTATGCACCAAACAGTTTGT  
35 223651 TTGCTGCTATCTTAAATGAAGATCTGTTAACAGGGCTAAGTGATAAGATT  
223701 TTCTATGGTAAGGAGAATGAGTTTGCTGAAAATGAAGCAGATAGGTTTAA  
223751 CCAACTTTTAAGTTTAAATCCTAATCCTAACACTAACTGAGCTAGGTATT  
223801 TAAACGTAGTACAACGTTTTACTACCGGACCTAACCTTGATAGTTCTACC  
40 223851 TTCGATCAGTTCCTTAGACTTTCTCCCCTGAATCGGCAATGGTAAACCCTT  
223901 TTCCAAC TCCCCCTCCCCCTTCAACTTCCGCTTCCTCTTCTACCCCCCTCC  
223951 CCACTTTTTCTAACATCAATGTTGGGGTTAAATCAATGATCACTCAACAT  
45 224001 TTAAATAAAGAAAACACCCGGTGGGTGTTTATACCTAACTTTTCACCTGA  
224051 CATCTGAACAGGAGCAGGGTATCGCGTTCAAAGTGCTAATCAGAAAAACG  
224101 GCATTCTTTTGAACAGGTGAAACCTAGCAATAATAGTACCCCTTTTGAT  
224151 CCCAATT CAGATGATAATAAAGTCACACCATCAGGTGGCTCCTCCAAACC  
50 224201 AACCACCTATCCTGCTTTACCCAACAGTATCAGTCCCACCAGTGACTGGA  
224251 TCAATGCATTGACTTTC ACTAATAAGAATAACCCGAGCGCAATCAACTG

224301 TTGCTCAGAAGCTTACTAGGAACTATTCCGGTCTTGATCAATAAGAGTGG  
224351 GGATAGTAATGATCAATTTAACAAGGATAGTGAGCAGAAATGGGATAAAA  
5 224401 CTGAGACAAATGAGGGTAATTTACCTGGGTTTGGGGAGGTGAATGGGTTG  
224451 TATAATGCCGCATTACTCCATACCTATGGTTTTTTTGGCACCAATACCAA  
224501 CTCTACTGATCCTAAGATAGGTTTTAAAGCTGATAGTAGTAGTAGTA  
10 224551 GTAGTACACTAGTAGGTAGTGGGTAAACTGAACTAGTCAGGATGTAGGT  
224601 AATCTTGTTGTAATCAATGACACCAGCTTTGGGTTTCAACTTGGTGGTTG  
224651 GTTTATTACCTTCACTGACTTTATCAGACCAAGAACTGGTTATCTAGGGA  
224701 TTACCTTAAGTAGCTTACAAGATCAAACCATTATCTGAGCAGATCAGCCT  
15 224751 TGAAGTAGTTTCAAAGGCAGTTATCTAGACAGTGATGGTACCCCTAAATC  
224801 ACTGTGAGATCCAAGTCTTTAAAATCCCTTCCAAATAGTTCAACTACCT  
224851 ATGATACCAATCCTACCCTCTCACCTCCTTCCAAGTCTACCAACCCAAC  
224901 AAGGTGAAGGCTTACCAAACCACTAACACCTACAACAAGTTAATTGAACC  
20 224951 AGTTGATGCAACAAGTGCAGCAACTAACATGACCAGTTTGTTAAACTCC  
225001 TAACAACTAAAAACATCAAAGCGAAATTGGGGAAGGGAACAGCTTCTTCG  
225051 CAGGGAAATAATAATGGAGGGGTGTTAGTCAAACGATTAACACCATCAC  
25 225101 CACTACGGGAAATATTAGTGAAGGTCTAAAAGAAGAACTAGTATTCAAG  
225151 CAGAAACACTTAAAAAGTTCTTTGATAGTAAACAAAACAATAAGAGTGAA  
225201 ATAGGGATAGGTGATAGTACATTTACCAAGATGGATGGTAAACTAACTGG  
225251 CGTAGTATCTACTCCCCCTTGTTAACCTTATCAATGGCCAGGGAGCAACTA  
30 225301 GTGATAGTGATACTGAAAAAATTAGCTTTAAACCTGGTAACCAGATTGAC  
225351 TTTAATAGGTTATTCACCTTACCAGTAACTGAACTATTTGATCCTAACAC  
225401 GATGTTTGTCTATGACCAGTATGTACCACTATTGGTTAACTTACCTAGTG  
35 225451 GCTTTGATCAAGCTTCAATCCGCTTAAAGGTAATTAGTTACTCAGTAGAA  
225501 AACCAAACCTTAGGAGTTAGATTAGAGTTCAAAGATCCTCAAACCCAACA  
225551 GTTTATCCCGGTACTAAATGCATCAAGTACAGGTCCCCAACTGTCTTTC  
225601 AACCTTTAACCAGTGGGCAGACTATGTCTTACCTTTGATTGTAAGTGT  
40 225651 CCTATAGTAGTGATTATCCTTAGTGTTACTTTGGGATTAACGATTGGAAT  
225701 TCCAATGCACAGAAACAAAAAGGCATTACAAGCAGGGTTTGATCTTTCTA  
225751 ACAAAAAGGTTGATGTCTTGACCAAAGCAGTTGGTAGTGCTTTAAAGAG  
45 225801 ATCATTAACAGAACAGGGATCTCTAACGCTCCTAAGAAGTTAAACAAGC  
225851 TACCCCAACCAACCAACTCCTAAAACCCACCAAAACCTCCAGTAAAC  
225901 AATAAGATGAAAACAATGAGAAAACAGATTTATAAAAAAGCATACTGGTT  
225951 ACTATTACCCTTTCTACCATTAGCACTAGCCAATACCTTCCTTGTCAAAG  
50 226001 AGGATAGTAAGAAaTGTTACTGCTTACACCCCTTCGCCACCCCATCACC  
226051 GATTCTAAAAGTGATCTGGTTAGTTTGGCACAACTTGATTCTTCTTATCA

226101 AATCGCTGACCAAACCATCCATAACACCAACCTGTTTGTGTTGTTCAAGT  
226151 CTAGGGATGTAAAAGTTAAGTATGAGTCAAGTGGCAGTAACAACATTAGT  
5 226201 TTTGATTCAACTAGTCAAGGTGAAAAACCTCCTATGTGGTCGAGTTTAC  
226251 TAACTCTACCAACATTGGCATCAAGTGAACGATGGTGAAAAAGTATCAGT  
226301 TAGATGTACCGAATGTAAGTAGTGACATGAACCAAGTACTGAAAAATTTA  
10 226351 ATTCTTGAACAACCTTTGACTAAGTATACCTTAAACAGTAGTTTGGCCAA  
226401 AGAGAAGGGCAAAACGCAAAGGGAGGTACATCTGGGTAGTGGGCAAGCAA  
226451 ATCAGTGAACCAGTCAACGCAACCAACATGACCTAAACAACAATCCCAGT  
226501 CCCAATGCTTCAACTGGGTTTAACTCACTACCGGCAATGCATATAGAAA  
15 226551 ACTAAGTGAGTCCTGACCAATTTATGAACCAATTGATGGGACCAAGCAGG  
226601 GCAAAGGGAAGGATAGTAGTGGGTGGAGTTCAACTGAAGAAAACGAAGCT  
226651 AAAAATGATGCGCCCAGTGTTTCTGGAGGGGGATCATCTTCTGGAACATT  
226701 TAATAAATACCTCAACACCAAGCAAGCGTTAGAGAGCATCGGTATCTTGT  
20 226751 TTGATGATCAAACCCCAAGAAATGTTATCACCCAACCTCTATTATGCTTCT  
226801 ACTAGCAAGCTAGCAGTCACCAACAACCACATTGTCGTGATGGGTAACAG  
226851 CTTTCTACCCAGCATGTGGTACTGGTGGTGGAGCGGAGTGCACAGGAAA  
25 226901 ATGCAAGTAACAAACCCACCTGGTTTGCTAATACCAATTTAGACTGAGGA  
226951 GAAGACAAACAAAAACAATTTGTTGAGAACCAAGTTGGGGTATAAGGAAAC  
227001 TACCAGTACCAATTCACCAACTTCCATTCCAAATCTTTCACCCAACCTG  
227051 CATATCTGATCAGTGGCATTGACAGTGTCAATGATCAAATCATCTTCAGT  
30 227101 GGCTTTAAAGCGGGGAGTGTGGGGTATGATAGTAGTAGTAGTAGTAG  
227151 TAGTAGTAGTAGTACCAAAGACCAAGCACTTGCTTGATCAACAACAATA  
227201 GCTTAGATAGTAAACCGGGTATAAGGATCTAGTGACCAACGACACGGGG  
35 227251 CTAAATGGTCCGATCAATGGGAGTTTTTCAATCCAAGACACCTTCAGCTT  
227301 TGTGTTCCTTATTTCGGGGAATCATACAAATAATGGAACAACCTGGACCCA  
227351 TTAAAACTGCTTATCCAGTGAAAAAGATCAAAAATCAACTGTCAAGATC  
227401 AATTCTTTGATTAAACGCTACGCCCTTGAATAGTTATGGGGATGAGGGGAT  
40 227451 TGGGGTGTTTGATGCGTTAGGTTTAACTATAACTTTAAATCTAACCAAG  
227501 AACGTTTACCTTCCAGAACTGATCAGATCTTTGTTTATGGGATTGTCTCC  
227551 CCTAATGAATTGCGAAGTGCTAAAAGTTCTGCTGATTCAACTGGTAGTGA  
45 227601 TACAAAGGTAACTGATCAAACACCCAATCACGTTACCTCCCTGTTCCCT  
227651 ATAACATTTCAGAAAGGATCATTGATGCAGATGGATTTAAGCGTCCTGAA  
227701 AACAGGGGTGCTAGTGTAACCTTCTCAGGGCTTAAATCAATTGCCCC  
227751 TGATGGTTTTTGCTAACTCAATAGCTAATTCTCAGTTGGGTTAAAGCAG  
50 227801 GAATTGATCCTAACCCAGTGATGAGTGGTAAGAAAGCTAACTATGGAGCG  
227851 GTTGTGTTAACACGGGGGGGTGTTGTTAGATTAACTTTAACCTGGTAA

227901 TGATTCATTGCTTTCAACAACTGATAACAATATAGCACCTATCTCCTTCT  
227951 CATTTACTCCGTTCCACAGCTGCTGAGAGTGCAGGTGGATCTCACTACCTTC  
5 228001 AAAGAAGTTACCTATAACCAAGAATCAGGGTTATGGAGTTATATCTTTGA  
228051 CAGCTCCTTAAAACCAAGCCATGATGGTAAACAACTCCTGTCACTGATA  
228101 ACATGGGCTTTAGTGTTATCACTGTCTCAAGaACTGGCATTGAACTAAAC  
228151 CAAGACCAAGCTACTACAACCTCTTGATGTAGCACCTAGTGCACTAGCAGT  
10 228201 GCAATCAGGGATCCAATCTACCACCCAAACCCTAACTGGAGTACTCCAC  
228251 TTAGTGAGGAATTCAGTGCAGTTATTGCTAAAGATAGTGATCAAAATAAG  
228301 ATTGATATCTATAAAAACAACAACGGGTTGTTTGAAATTGATACCCAACT  
15 228351 AAGTAATAGTGTTGCCACCAACAACGGTGGGTTAGCACCTAGTTACACAG  
228401 AAAACAGGGTTGATGCATGGGGTAAAGTTGAGTTTGCTGATAACAGTGTA  
228451 TTGCAAGCAAGAAACCTAGTTGATAAAACTGTTGATGAGATCATCAATAC  
228501 CCCTGAAATCTTAACTCCTTCTTTAGATTACCCCTGCTTTTGAAGATC  
20 228551 AAAAAGCTACCCTTGTTGCTACTAAGCAAAGTGATACATCACTTAGTGTC  
228601 TCACCAAGGATCCAGtCTTAGATGGTAATTTCTATGATCTTAACTCTAC  
228651 CATCGCTGGGGTACCTTTAAACATTGGTTTCCCTTCAAGAGTGTTTGCTG  
25 228701 GGTTTGACAGCACTCCCTGCATGGGTGATCCCTGTATCAGTAGGTTCTTCA  
228751 GTTGGGATCTTGTTTATCTTGTTAGTCTTAGGACTTGGGATTGGGATCCC  
228801 AATGTACAGGGTAAGAAAACCTCAAGATGCATCGTTTGTTAATGTCTTTA  
228851 AAAAGGTTGATACACTCACAACCTGCTGTGCGTAGTGTGTACAAAAAGATT  
30 228901 ATTACCCAACTGGTGTGGTGAAAAAGCACCTAGTGCATTGAAAGCTGC  
228951 TAATCCTAGTGTTAAAAAACCTGCTGCTTTTTTAAAAACCACCTGTTCAAC  
229001 CACCAAGTAAACCTGAAGGGGAACAAAAAGCTGTTGAAGTTAAGTCAGAA  
35 229051 GAAACCAAAAGTTAGTTTTTAACTTTCAATAACCTAAAACACAATCTTT  
229101 AAAACAAGGTTGTGTTTTTTTGTTTTTTGTCACTTTTCACTAACTTGCA  
229151 ATTTAGAGAGTGGATATGAAAAGAACAGTTAAAAAATAAAACCTGACCA  
229201 CTTGTTTAATAAAAAGCAGTGGCACTTACTGAGTGAAGAGATCAGTGATA  
40 229251 ACCCAATGATTAAAGCGTTATTGACTCAAACAACAAAAGCGTCAGCTTGCC  
229301 AAACTAAAAAACGCCGTTATTTTAAAAATTAATATGTATTCTACTTTA  
229351 AGACAATATAAACCATTGAAAAGAAAGAAATGGTTAAACAAGATCTCAAA  
45 229401 ACGGAAGTTAAACAACCTTTATAACAAAGCTTATTAGTTTTGTTTTTTAT  
229451 TTTTACTAGTGCCTAAGGTGGTATTAGAGTACCACAAGCTCAGTAAGGAT  
229501 GTAGTCAAAGAGAGTTTGGAAGTGAAGCAACTGATTCTTTTGATCCAC  
229551 CCAAAGGTTGCAAAAAGATAGTCCAATGAAGGATTCAAGTAAACAAGGGG  
50 229601 AGAAACTCAGTGAAACAACCTGCTTCATCCATGAGTGGTATGGCTACATCT  
229651 CCTCGCAAGGCCCTTAAGATAGAGGTGGAGAAAGGTTCTTCAGGGTCTGA

229701 CACCCTCACCAAATCCGACTTTGCTAAAAAGCCACTGAAACATAAAGAAA  
229751 ATAGTGGGACAGAGGTGAAGTTGGATGCACAGAAGGATTTTGCCGGAGAG  
5 229801 AAGGCCTGAAAGCCATTGTTGACTACTGATCAAATAGCAAGAGAGAAGGG  
229851 GATGGGGGCGACTTAGACTTTCTCCCCTGAATCGGCAACAACAAACCCTT  
229901 CTCCAACCTCCCACACTGCTTCCCTTTCTGTTAGTTCAAATACCCCCCTCC  
10 229951 CCACCTTTTCTAACATCAATGTTGGGGTTAAATCAATGATCACTCAACAC  
230001 TTAAACAAAGAGAACACCCGGTGGGTGTTTACCCCTAACTCTTCACCTGA  
230051 CATCTGAACCTGGGGCTGGGTATCGCAAACAAGGTAACAATAATGGCATCC  
230101 CTTTTGATAATGTGAACCTAGCAATAGTAGTACCCCTTTAATCCCAAT  
15 230151 TCAGATGATAATAAAGTCACTTCAGGTGGCTCCTCCAAACCAACCACCTA  
230201 CACCCATTTACCCAACAGTATCAGTCCCACCAGTGAAGCAATGCAT  
230251 TGACTTTCATAATAAGAATAACCCGCAACGAAATCAACTGTTGCTCAGA  
230301 AGCTTACTAGGAACCTATCCCGGTATTGATCAATAAGAGTGGAAACGGGAGA  
20 230351 TCAATTTAACAAGGATAGTGAGCAAAAATGAAACGAAACAGATAAATTAG  
230401 GAGGCAACCTCCCGGGGCTTGGGGAGGTGAATGGCGGTTTTTATCAACTA  
230451 AATAAAAACTTATTAGCTTATTTTTATTAGGTTTTTACTTATTTAATAGT  
25 230501 TAAAAAAGTTTTGAATTTTTCTTAGTTTTTTATTTGTTTAATAGTTAAAA  
230551 AACACTAGGCTTTACCTTTATTTAATTAATAAAACCTTTACCCCTATTAC  
230601 CAAACCATCCATAACACCAACTTGTTTTGTGTTGTTCAAGTCCAAGGATGT  
230651 GAAGCTTACATATAGTTCAAGTGGCAGTAACAACATTAGTTTTGATTCAA  
30 230701 CTAACAACAAACCCTCCTATGTGGTCAATTTACTAATCCACCAATGTT  
230751 GGCATCAAGTGAACGATGGTGAAAAAGTATCAGTTAGATGTACCGAATGT  
230801 TTCTAGCAACATGAACGATGTACTGAAAAATTTAATTTCTTGAACAACCCC  
35 230851 TTACCAAGTATACGCTTAATAGTAGTTTGGCTAAAGAGAAGGGTAAGACA  
230901 CAAGTAGCGGTACATCTGGGTAGTGGGCAAGCAACTAATTGACGATCGAT  
230951 GCGCAACTCCATCAGTCTAAACAACAATCCCAGCCCCAATGCTTCAACTG  
40 231001 GGTTTAAATTAGACAAAGGCAATGCATATAGAAAATAAGTGAATCCTGA  
231051 CCAATTTACCAACCAATTGATGGGACCAAGCAGGGCAAAGGGAAGGATCA  
231101 AGCGAATTGGAGTTCAACAGAAGAATCAACGGCAGCTAGTGATGCGCCCC  
231151 TAAGTACAGGAGGGGGATCATCTTCTGGAACATTTAATAAATACCTCAAC  
45 231201 ACCAAGCAAGCGTTGGAAAGCATCGGTATCTTGTTTGATGGGGATGGAAT  
231251 GAGGAATGTGGTTAGCCTCCTTCCTCTACTTTCAACCCAACAAGGTGAAA  
231301 AGTGGTCAATACCAAACCACCAACACCTACAACAGGTTAATTGAACCTGA  
231351 CAAGTGACAATCAAATAGTGATTTGACTAACATGACCAGCTTGTTAAAAAC  
50 231401 TCCTAACAACTAAAAACATCAAAGCGAAATTGGGGAAGGGAACAGCAATG  
231451 CAGGGAAGCAAGACACCTTTTCCTTCGTTGTCCCTTATTCAGATAGTCAT

231501 AGTAATCAAAC TTCATCAGGAACCATTAAAAACGGCTTATCCTGTGAAAAG  
231551 TGATCAAAAATCATCAGTAGCGATCAATTCCTTGATCAACGCTACGCCGT  
5 231601 TGAATAGTTATGGGACAATAAAAAAACTACCTGTCAACAAAAACAGGTA  
231651 GTTAATTATTTATCCAATTAGTAAGTTGCCTATGGGTAAACAAAGAGATG  
231701 CACTTAATATACGACCAACCTAATTTATTTGAAAGCGTATCTTTTATTAA  
10 231751 TGAATGTGGAAC TAAGCAACTATTATTTAAACACAGCAAAAGCGTGTAA  
231801 TTTTATTATAAAGCGATT TAGTGGAACAGAAATAAAAGATTAAACATGAC  
231851 TTTATACAAC TCTGTTC CATCTACTAAATGCACAAAAAAGCTTTTT  
231901 GACAAAAAATAGTTATTTTTTGTAATTGCTTAATTTAATAACAACTAA  
15 231951 ACTATTATTGTTACTTAATGATTTTTTGATCTATATAGCACAATTAATAT  
232001 AACTTCATGATTGATCAAAACAAGTTAATTACTAAGTGAAAAAAGCATT  
232051 TGCAAAAGCTAAGAATTTAACTACTTTAGTTAATCTTAAGAACACTTTAC  
20 232101 ACAACAGTGATTTAAAGCCATTACTCCAAAAGATTAAACCGCTACAAAA  
232151 CTAAGTGAAAAAAGTAGTTTAGGTAAGCTTTATCAATCACTTGATATTCA  
232201 ACTAAGTGATCTGTAACTAGTTACAAAAAACCTTTGAAATAAATAACC  
232251 AAGTTAGTCAAAAACCTTCACTTGATGTGATGCTACCAGCAACAGAGTTT  
25 232301 ACCAATGGTTCTAATAACGCACTATATCAGGTTATTGATAATTTAGTTGA  
232351 ATACTTTAAAAGCTTTTTATTCACAATTAATTTTGATAGTGAAC TGACCA  
232401 GTATTAGTGACTGTTTTGATCTTTTAAATATCCCTAAAGATCATTCCAGT  
232451 AGGAATGAATCTGATTCTTTTATATCGATAAAACAGTTTATTGAGAAC  
30 232501 CCATTGTACTGCTACCACGCTAAAAGCAGTCAGAACTTCTAAAAAACTA  
232551 ATAATCCTGATATCAGGGTTGTCTCTTTAGGAGCGGTTTTTCGTAATGAT  
232601 AGTGATGATGCCACCCACTCCCATCAGTTTACCCAAC TTGATTTTATGTG  
35 232651 GATTAAAAAAGGCGTTTTCATTAGCTAATTTAAAGTGGTTTATTAACAATA  
232701 TGATCACCCATTCTTTGGGGAAAACTTTTACTAGGTTTAGACTATCC  
232751 CACTTCCCATTCACTGAACCCTCGTTTGAAATTGACATTAGGTGTTGGTT  
232801 ATGTCAAAATGGTTGTTCTATTGTGAAGCAAACCAAGTGAATTGAGATCT  
40 232851 TAGGGGCGGGGATCATCCATCCCCAGGTGATGAATAACATGGGAATTGGG  
232901 GATACTGAAAATATTACTGGGATAGCAGCAGGAATTGGGATTGAACGCTT  
232951 AGCAATGTTAAAGTATGGGATTGATGATATCCGTGATTTTTATGATAACA  
45 233001 ACTTTAAGTTTTTAACCCAGTTTACTGACTAAAAATGTTGATATCAAAA  
233051 AAAACACTTGGCGTTTTAATCCCTGACATCTTTAGTTTTTCTAATGATCA  
233101 AATTGCCCAAAAGTTAGAACAAATGGGGATTGAAGTGAATCAATTAAGC  
233151 AGTTTAACAGCCCTGATTACCTCCAAC TTGCAAAGGTTGTATCAATCCAA  
50 233201 CCCCATCCCCATGACAACAAGCTTTTTATCTGTGAATTACAAATTGATAA  
233251 AAACAAGTTTATTAATGTTGTTTCCAATGCTAATAACATTAAACAATCCTG  
55

233301 ATAATATCAACAAGTTTGTTCATTGTTGCAAAAAAAGGAACTGAGTTACTC  
233351 AACGGGTTAATTGTTAAAAACCCAAAATATTAAAGGGATCATTTCAGAAGG  
233401 GATTTTATGTAGCTATATTGACATTAACCCCTTCAGTAGACAGATCATTG  
233451 AAAAAACAGAAGTTGCTGATGCGATTATCATTGATCATGTTAGCAATGAT  
233501 CATGACTGAAACCAATACCTCTCGTTTTTAAGTTTGGATGATGTGATCTT  
233551 TGATGTTAAAAACCCCAACTAACAGAGCAGATCTTCATAGCTTAATCTTTT  
233601 TAGCAAAAGAACTTGGGGTACTTTTGAAAACCAAAACCTTTTAAAACAA  
233651 AAAAGTAGTGTTGTTAACCATGACTTTTTTAAGTTTCCCTTAAATTTAA  
233701 AAACAAGTTAAAGCGAATTATTTTGGCGGTTTGTTCTTAAGACAAATTA  
233751 ACCAACATAGTTCACCTTGAACAGTTAAAGGACTGTTAATTAACCAATG  
233801 ATCAAACCAGTTAACTATTATGTTGATAAAGCTAACTTAGTAACAGTGTT  
233851 CACCGCTCAGCCAATCCATTGTCATGATGCAGATAGAATTGTTGGTAACA  
233901 TTGAACCTAAACAAGCAACCCATAATGAACTTTTGTGGACTTGATGAC  
233951 AAGCAATATGAGATTGAACCAGGGGATATTGTTGTTTGTGATGAGAAGGG  
234001 CATTATTGCACTGGTAGGGATCATTGGTTCAAAGCGCACAAATGGTCCAAC  
234051 CTACAACAATAACATCTTTTTTGAAGTTGTTAACTGTAAACAGTGAAACC  
234101 ATTAAACAACTGCCAAGCGCTTTTTTGATCAATAACTTTGCCAGTAAGTT  
234151 TATGGTTAAACCGATTAGCTTATTAGCTACTGATAACTGTTTAAACTACT  
234201 TACAAAAACAGTTTACTAACCCTGATAACATTGGCAAAATTAGCCACTTT  
234251 TCAAGTTCGCTTAAAGTTGAACCATTTAGTAAAAAGCTCACAGTGAATTT  
234301 CCATAAGATACGCCAACTAATTGGCATTGAAAAAAGGAACTAACTGATC  
234351 AAACCATTAAAAAAGCCTCAGTCAACTAGGGTTTAAAGTTGACAACCAA  
234401 CTTCTCAAAATCCCCAGTTACAGACAAGACATTAATACCTGACAAGACAT  
234451 TAGTGAAGAGATTGTGAAGTTAATTGATATCAATAAGTTAAAACCAATTG  
234501 GGATCACTAGTAGTTTAACTTTGAAAAGTCCAGTTACTTTAACACTTTT  
234551 AATGCTTTAACAAAATAAGAAAAAGCTACAAACACTTGGTTTTTCACAA  
234601 CGTTATTACCTACCAGTTAACTGATCAAAAAAGTGCAAAAACCTTTTAATT  
234651 TGTTTAACTTAGAAAATTTTCATCACCATTAAAAACCCAGTGTCCTAAAAC  
234701 CATTCTGTAATGCGTGTTAGCTTAATTGATTCACTGTTAAAAGTGCTAAA  
234751 AACCAATAACAATAAAGAATGAACTGGTGAACATCTTTGAGTTTTCTT  
234801 TTATTA AAAACCCAAAACAATAGTGAAGTGCACCTGGCAGTATTATGAGTT  
234851 GAAAAACTGTTTACTTCTAGTTTCAATCCTATGCAAGGGATAAGCAATGA  
234901 TGTTTTTACTATGAAGGGATTAGCAAACTCATTGTTGCTAACTTAGGGT  
234951 TTAGTTGTGACTTTGAACCACTTGATGATAGTGAAGTATTTTGTTAATAAT  
235001 CAAAGTTTAAAAATAGTAGTTTTTAACGAACAGATCGGTTTTATTGGGCT  
235051 AATTAAAGAATCATTGTTAAATAACTATGATCTGAACAATAAACCCATT

235101 ATTGCTTGAAATCAACTTAGATAGGATGCTCTCTCTCTAAACAGGATT  
235151 GAAAAAACTACCTTGGTTACAGTAACTACAACCTGTTTGCAAGGaTCT  
5 235201 TACCTTTAGTTTTACCAACCCTGCTAGTCACCTTGATCAGTTTGCTAACA  
235251 TGATCAAAAGGATAACTGGCATTGAAAGTTGAAAGTTAATTAGTGTCTTT  
235301 GAAACTATGCAAAACAACCACTGATCACTAAGTACACCGTTCGTTATTT  
235351 TCTGAAAAATGATGCTAACAACCACTAACTAACCACCAATTGAACTTA  
10 235401 TCACATAAATCTTAAACTCCAGTGTGAAAACTAAAAATTAAATTAGAT  
235451 ATTTAGAATTACTTATTACTATCAAGATAGTTACCAACTATTTTGTTAGT  
235501 AAACTTAATACAATTGGCACAAAACGCAAAACACCTTCTAAAAAAGAA  
15 235551 CAAAAACCACTCGTTAATGAACAGATTGCTTTCAATCAGTTCACTTTAAT  
235601 TGATGAAAACAGTACTAATTTAGGGATAGTTAAGATGGAAAACGCTTTAA  
235651 AGTTAGCACAGAAGAAAACAGTTAGATCTAGTTCTAATTGCTCCAAACCCA  
235701 ACCAAACCGATCGTTAAGTTGTTGGACTTTGGCAGATATACCTATGATTT  
20 235751 AAAGCGTAAGAAAAGACAAGCCAAGAAAAACCAACAATCATCCAACCA  
235801 AAGAAGTTGTTGTCAAACCAACGATTGCTAAACATGATTTAGAATTTAGA  
235851 GCAAAACAGAGTAAGAATTGGATAGAAAAGGTCATCATGTCAAGTTTAT  
25 235901 AGTCCGTGCCCTTTGGCAGGGTTAGCACCAGGATAGAGTTAATTGAAAAGG  
235951 TGTTTGATGACTTTTACCAGTTAGTTAAAGATGTAGTTGAGATCCAAAA  
236001 CCTTTAACCGCTTCTTCCAAAACGATGTACGCTGCTCTATTAGTACCTTT  
236051 AAAAAGATAGTTATGAAAACCAAAAGTGCTGCAGTAAAACGCTTTAACT  
30 236101 CACCAAATCAGGACAAATTAAGCGCAAACACGCTTATACTTCCACCTCG  
236151 CGCCCCACAAATCAACCAACAAAAGCGCCATTTGCGCAAGCAAGCTACT  
236201 GTGAGCAACAGTGAATTGAAAAGAATTGGTATTTTAATTTAGTTATGCGT  
35 236251 GTTAAGGGAACAAATACAACCAGGATTAGAAGAAAAAATGGTTAAACA  
236301 AGCTAGTGGTAGCTTTTGGGACAAGAAAAGCTTCTTTTAAGGCAGCTAAAC  
236351 AAAGTGTATCCAAGCAAGCAAGTATGCTTACCGTGATAGGAGACAGAAA  
236401 AAACGTGAGTTTCGTTTCGTTGTGGATCTTAAGGTAAATGCTGCACTGCG  
40 236451 TGCACAAGGGATGACTTATTCAGTGTATCAATGAATTGAAAAAAGCCA  
236501 AGATAGTCATTAAACAGAAAGGTACTTTCTGAACTAGCAATTAAAGAACCT  
236551 AATAAGTTAAATCTGATTATCAATACCATCAAAAAACCACTAATAAACC  
45 236601 AACTGTTGCAAAAACCTTAGTAACGTTTTTAAAGTTAAGTTTGCCACCTG  
236651 TTTAACTGTTCAATTTGACTAAAACCGCGTTGTTGGTTAAGAAATAACA  
236701 ACGCTTGTTCAATGCCATGACTACTGCCTTTGGGTAAATCATAGTTTACC  
236751 TTTTGGTTGAGTAATTGCAGCTGATTAAATAAGCTATCTCTTGCTAAGAT  
50 236801 AGATGCAGCTGCAATCACCAGTGACTTAGTTTCACCATTAATTAGAACT  
236851 GATCAGGTAATAACACTGTTTTATCAGTGAAATTAGTTAGCTTATTAGA



236901 TAGTTAACAAATAACTCTTGATTGGCAAACCTGGTCAATGCTAATTGTTAC  
236951 TGTTTGTCTTAATAACTGATTTTTTTCCAGTAACTTTTGGTAAAGCTGAC  
237001 AGTGTAATTTGGTCAAAAGTAAATTGGTATTTTTTCAGTGATTTTGTCAA  
237051 TCATTATACTGCTTGGGATCTAATGTAATTGTATGGTGATCCATTACTGT  
237101 TGTTTGGATCGATTTAGCTAACAGTTTGACAGTGTGATCACTGAGTTTTT  
237151 TTGAATCAGTTACTTGTAATTTTcCAAGATTAATAAGCTGTTTTTTTTT  
237201 AATTA AACAGCACTAACACAAATCCCACCAAACCTATCACCCCTTGCCAG  
237251 ATTCATCACTGCCAATTAAATAAAAATCAGCTGGTTTGTAATGTTGCAAC  
237301 TATCTAGTTAATTAATAAAATTATACTTACTCTGATTGATTCTTAATGGC  
237351 TGAACAGAAACGTGATTATTATGAAGTGTTAGGAATAACCCCTGATGCTG  
237401 ATCAATCAGAGATTAAAAAGCCTTTTCGTAAGCTGGCTAAAAAGTACCAT  
237451 CCTGATCGTAACAACGCGCCTGATGCTGCTAAGATTTTGTCTGAAATTAA  
237501 TGAAGCAAATGATGTTTTATCAAACCCCAAAAAAGAGCTAACTATGATA  
237551 AGTATGGTTTTGATGGGGTTGATGGTGAACCTGCTTTTAACCTCCAAGCA  
237601 GATGTTTTTCAATCCTTTTTTGAAGAGATAGCAAAATCAGGGGTTTTTAA  
237651 CAACCAAACCAATCCTGAACAAAAAGAAAAAAGAAACGTTACCACTGGT  
237701 TCTCCAAAAACCTAAGCAAGAACAACCTGAAATTAACCTAGATCACGTT  
237751 GTTGAGCAAACCATTA AAAAGGTGCAACAAAACCAAACCAAACAAAGA  
237801 CCCAGATGAATTACGTTCTAAGGTCCCTGGAGAGGTTACTGCTAGTGATT  
237851 GGG AAGCATTGGTTGGTGATACTAGGTATGGGTATTTTGATGAAACAGGG  
237901 GATTGGAGTTGAAAGGGTTACTTTGATGAACAGGGCAAATGGGTTTGAAA  
237951 CGAACCAGTTGATTCTGAAACCAGTGAGGTATCAGTTGAACCTGAACCAA  
238001 CCCAGTTGCCCTGAAGCTAGTTTTGAAGAAGCTCAACCTGAAATTAAT  
238051 GCTGAACCAGAAGCTAGTTTTGAATCAACTCCAACCTCAGAACCAGTTGC  
238101 CCCAGAAGCTAGTTTTGAAGAAGCTCAACCTGAACCAACTCCAATTCCTG  
238151 AACCAATCCCAACCCAGTTCAAGTTCAACCCCTGTTGTTAGATCTCAAC  
238201 CTCTTTACTATCCCAACTAAAGCTACTAAGGATGATCTTTTGTGTTGACAA  
238251 CATTAACTCACTACCTATGAACAAGTTGTTGATTATCTCAACAGTCAAG  
238301 CAACCCCTAATTTAGCTAAAACCGATGGTGAATTGCAAACGATTGATGGT  
238351 ACCAACCATTGTTATTAGAACAGTGCAAAAAGATCAAAAAACAAGCAGA  
238401 ACAACTCTTTAAAAAACTCTTTTAAAAAAAACAACTCCCTTCATCACCC  
238451 AACCTGAAGTTGTTGAGGAAAGTAAAACAGTTTGTGATGAGAACAACGTT  
238501 AACCTTGTTTACTTTGAAAAGGTCCCTGAAATCCTTTTCATTAAACCAACA  
238551 ACCTAAGGAGGTAAAATACACCCGTCAAGTCTTTGATGGGTTGACAAACA  
238601 AAACAACCTAGTGAAACGATTACACTAGAGATCCAACCTCCTCAAACCCCA  
238651 AAAGAGACTGTTAGTGCCATTTTTAAAGGCTTTGGTAATGACCATGGCAA

238701 GGGCTGTGGGGATTAAAGATTGTTTTTGAAAAGATTAAAAGCCCCTTTT  
238751 TTCAAGTCAATGAGGATGGCTTGCACTCTGCTTGCACTATTGACCCCTTA  
5 238801 GTTGCTTACAACGGCGGGATTATCGATGTGTTTGGGCCCTACACTAAGCTT  
238851 CCAAGTTAAGGTAGATGGGAGATAGACATCAATGCCATTATGAAGTTTG  
238901 AAAAAGTGGCATTGCTAAAACCAAGCGCAAGGGCGATCTTTTGTCCAT  
10 238951 CTCTATTACAGTAGTGTCCCTAAAAGAACTCACCCTAACCCCAAGT  
239001 TCAACAGTTCTTAGAAGCTTTTACAAGCTGAATATGAAGTGTGCAAGACA  
239051 ACATCAAGAGCTTAAAGTACTTTAAAAATAACCTAGTTATCCCCAAAAAG  
239101 CCACCTTGATCAACAAAGCTATCAATACCTCTCCCAAGAAGCCATTAGTTA  
15 239151 GAATTTGTTAATATGTGTGAAAAATCACAACAATTAAGAGCTTTTAAA  
239201 CGCCATTAGAAGCTTAGTTGTCAAGAACAATAAGCTAAGGTTAGTATGA  
239251 TTGAAAAGGAACTGTTAGCTTTTGTAGTGAAGTGTGACAAAAAGTTCAAA  
239301 CAACAAGTCAACAAGCTTCAATGAAGTACAACAAAAGATCCCACTACTCCA  
20 239351 AAAAGCTAACGAAGAGTTTGCTTTAAAGTTTGAAAGGATGCAACGCGAAG  
239401 CACAAAACAGATCCAAGCCAACTAGATGAGTTGAATCTTAAAAATAAA  
239451 AAGGAGTTAGAACAAGCCAAGAAATATGCGATTGCCAAAACCTTGACCA  
25 239501 ACCCTTAAACATCATCGATCAGTTTGAAATCGCGCTTTCATATGCCCAA  
239551 AAGACCTCAAGTAAAAAACTATACCACTGGTTTTACCATGGTACTTGAT  
239601 GCTTTTTCAAGGTGATTGGAAGCAAATGGGGTTACCAAGATTAAGATTGA  
239651 ACCAGGGATGGAATTTGATGAAAAGATTATGTCTGCATTGGAAGTATG  
30 239701 ATTCTAACCTTGCTAAAAACAAGGTAGTAAGAGTCTCAAATCTGGCTAT  
239751 AAAGTCTATGACAAAGTGATCCGCTTTGCATCAGTATTTGTCAGCAAAGG  
239801 TAATAAAAAATCATAATAACAAGTATGAGTGAACAAAAAGAAAGACAA  
35 239851 TCCAAATTGCGATAAGTGAAGACCACTATGAAGAGTTACAAAAGGCATTG  
239901 GAAGTACTTAAAGGACCCAAATTACCTTTTTCAAGCACTGTTGAAGAGTT  
239951 TGTGGAGTTAATCTTATCTAAGTATGAGTACTTCAATAAGATTAGTA  
40 240001 GTTTAGCTAAGAGTGGTTTTGATGTAGCTTCATTGCAGCAAGAACTGAG  
240051 AAGATAGGTAACCTTAGTGGGGTTGATGATAACCTCAAGGGTTTTCTCTC  
240101 AGAAGTGTGAAAACCTCAAGGAATGGGTTTAGTAACCCCAATAAGATG  
240151 GCAAAAAAATGATGACGATAATAACTCGTCATCAAAATCATAGTTATAT  
45 240201 AAAAGTTAAGTGGTGGCGAATAACAGAGTGAAGTGTCTCTGATCCTT  
240251 ACCATGGATCTGTTTTGCCCTAAACCAATTCGGCAGCAAAGCTAATTC  
240301 AATTTTAAATTCAAAGTTAGATGAAAAGTAACTACAGTGCAAGTAACT  
240351 CAAGATCTTAAAGGGTTTGGATGCAGTTAAAAAGCGTCCGGGGATGTACA  
50 240401 TTGGTTCTACTGATAGTAAGGGTCTGCACCACATGCTATGGGAAATCTT  
240451 GCTAACAGTGTGATGAAGTTTTAGCTGGTTATGCAACCAATATTACTGT

240501 TACTTTAGATCTCAACAACACCATTACTGTTAGTGATGATGGCAGGGGTA  
240551 TTCCCTATGAGATCCACCAAGACAGTAACATCTCTACGATCGATACAGTT  
240601 TTCACCTTTCTCCATGCAGGGGGGAAGTTTGATGATCAGTCATACAACT  
240651 AGCAGGGGGATTACATGGGGTTGGTGCATCAGTGGTCAATGCCTTAAGTG  
240701 ATCATTTAGAAAGTAACAGTGAAAAGAAATGGTCAGATCTACCAATCAGTT  
240751 TATCAAGCTGGGGGTAAAGATCATCCAAAAAGCCAAAAAGATTGGTGATAC  
240801 AACTAGCCATGGTACCACTGTTAGTTTCCATGCTGACCCTAAGGTCTTTA  
240851 AAAAGGCTCAATTTGATAGCAACATTATTTAAAGCAGGTTAAAAGAGCTA  
240901 AGCTTTCTGTTTGCTAAACTAAAGCTCACTTTTACTGATCAAAAACTAA  
240951 TAAAACCACTGTTTTTTTTAGTACCTCAGGACTAGTTCAGTTCCTTGATG  
241001 AAATTAATAATACTGTAGAAACACTTGGCCAAAAAACACTGATTAAAGGT  
241051 GAGAAGGATGGGATTGAAGTGGAAGTGGTTTTCCAGTTTAACCAATCAGA  
241101 TCAAGAGACAATCTTATCATTGCTAACTCGATTAAAACCTTTGAAGGAG  
241151 GGAGTCATGAAAATGGGTTTTGTCTTGCCATTAGTGATGTGATCAACAGC  
241201 TATTGCAGAAAGTACAACTTACTAAAAGAAAAAGATAAAAACTTTCAACT  
241251 TAGTGAGATCAGACAAGGGTTGAATGCTATTATCAAAGTTAACTTACCTG  
241301 AAAAAACATCGCTTTTGAAGGACAACTAAGAGTAAGTTGTTTTCAAAG  
241351 GAAGTGAAAACGTTGTTTATGAATTGGTCCAACAACACTATTTCCAGTT  
241401 TCTGGAAAGAAACAACAATGATGCTAAATTGATCATTGATAAACTACTCA  
241451 ATGCTAGAAAGATTAAAGAGCAAATCAAACAACAACGTGAGTTGAAAAAA  
241501 AGTTTATCAAGTCCCCAAAAAGAGAAGATCTTATTTGGGAAGTTAGCACC  
241551 TTGTCAAACCAAAAAAACCAAGTGAAAAAGAGTTGTTTATTGTTGAAGGTG  
241601 ATAGTGCTGGTGGCACTGCTAAATGGGCCGTGATAGAATTTTTCAAGCT  
241651 ATCTTACCTTTGCGCGGCAAGGTGTTAAATGTTGAAAAAATTAACAATAA  
241701 GAAGGAAGCGATCACTAACGAAGAGATCCTCACTTTAATCTTTTGATTG  
241751 GTACAGGGATTTTAACTAACTTCAACATCAAGGACTTAAAGTACGGAAAG  
241801 ATCATCATTATGACTGATGCAGATAATGATGGCGCACACATCCAAATCCT  
241851 CTTACTTACCTTCTTTTATAGGTACATGCAACCCTTAATTGAACTGGGCC  
241901 ATGTCTATCTAGCTCTTCTCCTTTATATAAACTGGAAACCAAAGATAGA  
241951 AAAACAGTTAAATACCTCTGGAGTGATTTGGAGTTGGAATCAGTCAAAC  
242001 AAAGCTTAATAACTTCACTTTACAACGATACAAAGGACTTGGAGAGATGA  
242051 ATGCTGATCAGTTGTGAGATACTACTATGAATCCAACCTACCAGAAAGCTA  
242101 GTGCAAGTAAAGCTTGATGATCTAATTAACGCTGAAAAGCAAATCAACAT  
242151 CTTTATGGGTGAAAAGAGTGATTGCGCAAACACTGGATTGAAGCCAACA  
242201 TTAACTTTAGTGTGAAAACTAATGGATCAAAAAACAACAACCTCTTTC  
242251 AAAAGGCAATTGAAGAAGTCTTTCAGTTAGCTTTAGTAAGTATGCTAAA

242301 TACATCATCCAAGATAGAGCTTTACCTGATCTAAGAGATGGGTAAAAACC  
242351 AGTACAAAGACGGATCTTATATGGGATGTTTCAAATGGGCTTAAAAACCA  
5 242401 CCACTCCCTATAAAAAATCAGCCCGTGCTGTTGGGGAGATCATGGGGAAA  
242451 TACCACCCCCATGGTGATAGTTCCATTTATGATGCAATTATCAGAATGTC  
242501 CCAAAGCTGAAAGAACAACCTGAACAACCTGTTTCTATCCATGGTAACAATG  
10 242551 GTTCAGTGGATGGGGATAATGCTGCAGCAATGCGTTACACAGAAACCCGC  
242601 TTAAGCTTGTATGGATTTGAACTATTAAAAGACATTGATAAAAAGTTAGT  
242651 TAGTTTTATCAATAACTTTGATGATAGTAAAAAGAACCAACGGTTTTAC  
242701 CAACCTTACTGCCTAACCTCTTTATCAATGGTGCGAGTGGGATAGCTGCT  
15 242751 GGATATGCAACTAATATTGCTCCCCATAACACTAATGAACTATTAGATAG  
242801 TCTTTGCTTGCGAATAGACCAACCTAATTGTGAACCTAAACAAATTTTAA  
242851 AAATTGTTAAAGGTCCTGATTTTCCAACAGGGGGTAATGTTTATTTTGAA  
242901 AAGAGTTTAAAGTGATATTTATCAAGCAGGCAAAGGTAAATTTATTATCCA  
20 242951 AGCTAAGTATGAAGTTAACAAGAACTTAAACCAGATTGAAATTACCCAAA  
243001 TCCCTTATGAAACACTGAAAGCTAACATTGTCAAACAAATTGAAGAGATT  
243051 ATCTTTGACAATAAACTATCTGCTATTGAAAGTGTCAATTGATAGTTCAGA  
25 243101 TCGCAACGGCATTAGGATCATTATTAAACACAAGGACTTTTTGCCTGCTG  
243151 AGAAGATCATGGCCTTTTTGTTTAAACACACCCAACTCCAAGTGAACTTT  
243201 AACCTTAATAACACCGTGATTGCTAACCGCTTTCCCATCCAAATTGGTTT  
243251 ACTAAGTTACCTCGATCATTTTTTAAAGTTTTGTCATGAACTAATTATTA  
30 243301 ATAAAGCTAAGTATGAACTTGAGCTTGCAAGCAAGCGCTTGGAATATT  
243351 TTAGGACTAATTAAAGCGATTAGTATCATTGATAAAATCATCAAATTAAT  
243401 TAGATCAGCAGTTGACAAAAGTGATGCAAGAGAAAAGTTAATTGATAACT  
243451 TTAAATTTACTTTTAAACCAAGCAGAGGCAATTGTTAGTTTGCAGCTTTAC  
35 243501 CAACTAACTAACCTGATATTTTTGAACTTAACCAAGAACAAAATGAACT  
243551 TGAAAAAAGTGTGATTAGTTCAGAGCAACTAATTGCTAGTGAAGAAAGCAA  
243601 GAAACAACTCCTAAAAAACAGTTTGAAGGTTATAAAAGCAGTTTCAC  
40 243651 CAGCAACGAAGGTCACAAATATGTGGCTTTATTAACCAAAAAAGGTGGA  
243701 GGAAAGTGAGCTAATTGAAAACAAAACCTATGGGGTTTTAATCACTAAAG  
243751 CTGGTAACTACCATAAGTTTGAATCTAACCAACTATTAAAAAGCACCCT  
45 243801 GATTTTAAAGTGAGAGTGACACAATTATCTTGCACAACTATTGCTAA  
243851 TACCGACCAAATTTTTATTGTCACTTCACTAGGTAACATTATTAATATCC  
243901 CTGTTTATAAATTAGCTTTCAATTCAAAAATAAAGTAGCAAGTTTAGTT  
243951 AGTAAAAACCAATCCTTTTGGAGTATGAAACGATTGTTTTGTTGGAAC  
50 244001 AATGAACAGTGTAACCAACCAATCCTTGTTTTAACTTCCAACTAGGAA  
244051 TGGTTAAACGATTGATTAAACCAACTTAACATTAAAGCCACTTAAAGCT

244101 ACTTTGTGTATCTCACTCCGTGATAAAGACCATTTAGTAAGTGCATTTTTT  
244151 ACAACAAGATGATAAACTGATCTGTTTAGTGTCTGATCACAACATTACA  
5 244201 CTGTTTTTTCACACCAATGAGATCCCATTAATTAGTAGTAAGGGGATGGGA  
244251 GTGAAGGGGATGAAGTTAAAACTAGAGGATCAAATTAAGTTTGTGTGTC  
244301 TTTTGAAGCTAATGAACCGTTAGTGATGATATGTAGTGATGGTAGTGCA  
10 244351 TTTAACTTAAACAACTGAACTAGTTGTAGTTAGCAGGATGGCAACTGCA  
244401 AAAAACTGCCTGTTAAGAAAGCAATTAACATTGTTTTAGTGATGCAAC  
244451 TAACACCCAGTTAATTAATTTTCAGGGTAAGAACGGTAGTAAATTAATTA  
15 244501 CAACTAGTGAACCTGAACCAGATGAGTAAACTGCAATTAGTCAAACCAGG  
244551 TTAAACAACTTAATTAGGTTTGGTTGTGGATCTTTTTATCATATTTTTTC  
244601 TATCTCTTCTTTTAGAGTAGTTAATAAGGCTTTAATCTTTTGGTAGTCCA  
244651 TTCTGGTTGGTCTTACTATAGCAAGTTGGTGCTTGGCTTCACTGGTGGTA  
20 244701 TTGATTAAAGTAGAAGCAACTGATATCTCTTTAAACCCAATTGATCACC  
244751 AAAGACAATGTTGGTCTTTTGGTTGGTTTGGTTTATGAATGCCATCTGTT  
244801 GTCAAACACTAGTATCTTCAAGCAGATTTAAGATTTTAGTGAGTTTCTCT  
244851 TGGTTAGCAAACCTCGGGTTGTTTAGCAAGGTATTGGATCCCATAGATCTT  
25 244901 TTTATTTGCCTCAATTTGATCTAAATCAAATAACTTAAATAAGATCTCAT  
244951 CAATTACATACTGATACTCATGAACCTTGGTTCTAATGATCTCTTTTAAA  
245001 ACTTCTAGTTGGTTGTTAATCTCTGAAAAGCGGGTATCAATGATGCGATC  
245051 ATTAAAGATCCTTACACAAATAACAATGTCTTCAAACCTGCCTTTGGTTAG  
30 245101 CATAGCTAATGGTTTTTTTAAAGACTTTACCACTAGCGGAGACCAATAAA  
245151 AATAAGGCAAATGACTTATCAAGGATGATCAGATCAATCTTTTTTAAAC  
245201 TTCATCACTACTAAAGTTAGTTAACTACTGGTAGGTTAATGATCTCAT  
245251 TGATAAACTTAACCCCAAGTTCAATCACCTCATCAATCGTTTGTGTTGC  
35 245301 TGGAGAATAACACTTCTTAAGCGGGTTTTTCAGATCGTTAGTGGTGTACT  
245351 AACATTTAACACTTTGACATAATACTGATAACCAATTTGGGAAGGAACAC  
245401 GGCCTGAAGAGATGTGGTTTTTCTTTAAGAACCCTTTTTTCTCTAAAGCT  
40 245451 GCCATCTCATTTTCGTAATGTTCCCCAGAGAGGTTTTTAAATATTTTTT  
245501 GGTAGTAATTTACTGCCAACAGGGATAGCATAAGCAATGTATTCATTGA  
245551 TAATTGCTTTGAGAATTTGGGCTTGCCGTGGCGTTAAATCTTCATTAGT  
45 245601 TATCTAATTTTATCTTTTAAACAATAACCAGCTTGACCACTAATCTAAAAC  
245651 AAAAGTTAAAACTGCACCTAAAAAACCGGGGTGTTATTTGTGAAAAGAT  
245701 AGTAACGGTAAAGTTTTATATGTTGGTAAAGCTAGTAATATTTTCAACAG  
245751 GGTCCACCAGTATTTTCAAAGAATAATCCTTATAAAACCCAGCTATTAT  
50 245801 CAAGCCAAATTAGTGATGTTGATTTTTTCATTCTCAAAGATGAAAATGAT  
245851 GCTTTAAATCTGGAAGCAAAGCTCATTAAATCAATATCAACCCCGCTTTAA

245901 CTTAGTTTTTAAAACAAAACAATGGTTATCTTTATTTTATATCACTAAAG  
245951 CCAAAAAACCTACCTTGGAATTAGCCAGAAAATACCAGATTAAAACCACT  
5 246001 AAGTGCTTTGGACCGTTTGCTTCAAGTAAGTTTAAAGTTACGTGAGATCCA  
246051 TGACCTACTTTTTAAACTCTTTCCTTTAAGAAAGTGTGCACCTCACCAA  
246101 AAAACCACCCGTGCTTTTATTTTCAGATGGGTTTATGTATGGGGCAATGT  
10 246151 ATGCAAACTGATACTAAGGAAAAATACCAACAGGTAATTAGTAACATTGA  
246201 ACAGTTTTTTAATGACCCTAGTGTGGTAATTAACATTTTAAAAGCTGCAG  
246251 AAAAAAAGGCAAGTGATAATCAGGAATTTGAAAAGGCCAGCAGTTTCTA  
246301 ACACTGCAAAAAGCAGTTTGTAGAGTTAACAAAAACCCACCATAACCTAT  
15 246351 CATTAAACAAAAATCAAGCCATGATTTTATTGGGTATGTCTTTCAAATA  
246401 ACGTTTTGGCCATTACCATTTTTTGTATGAAAAAGGGGAGTTAACTGAT  
246451 AAAGAACAAGCAGTGTTTACCTAGAGCAAACTGACATTGTGGAAGTTGA  
246501 AAGTGCTATTATCACCTTTATCTACCACCCTATAAACTACCCCACTTC  
20 246551 CAAGTAAGATTACTGTTTCACTTGATGAACTAACCTAAAATTATTAGT  
246601 GATAGCTTAAAAATTGGTGTTTTTAAGCCCAAGAATGGTAATGAAAACT  
246651 GATCTTACAACTGTTATTGATAATGCCAAACATGCACCTGCAACCAAGT  
25 246701 GGTTGAAGTTTACTAGTAATATGATAAAACCCAGCTCCACAAGGATTTA  
246751 GCACAACTTCTAAATACTGATTATATCCATAGTCTTGAGATTATTGATGT  
246801 GTCATTCTATGATCAAAACCATGTTGTTGGTTGCATGTTAAGGTTTGAAG  
246851 ATGGTAAAAAGATCAAACTTATCAAGAAGATACAACATTAACAGTTTA  
30 246901 AAAAAAGGTGATACTAACCACATGCTTTACTTGTTTACAGAAGGATCTT  
246951 AAGTGCGATGCAAACCAAAGCTAACCTCCCTTTTAGTGATCTTTTAATTA  
247001 TTGATGGTGGTAAAGCACAAATTAAGAGTGTAAAGCAAGTTTTAGTCTC  
35 247051 TTCAGTAATGTTAAACCAACCATTTATCATTGGACTAGTTAAAAACAAAA  
247101 CCACCAAACTGATCACATTATGTTATCTGATTTCCAAGTTAAAAAGATAG  
247151 CAATTAACCTCCCACTCTTTCACTATTTAGCAACAATCCAACTGAAGTT  
247201 GATGGTTTTGCTAAAAGAAGTGCTTTTAATAAGTTAAGTAACCACCACT  
40 247251 GCAAAACCCGTTGCTACAAATCCCAGGAGTTGGCAAGATAACTGCCCCAA  
247301 TTCTCTTTGATAACTTTCAAACGCTCAATAACATAAAATTAGCTTCAGTT  
247351 AATGAGTTAAGCCAGTTTATTAATAAACCATTAGCACAAAAGATTAAAAAC  
45 247401 TTACTTTGCAAAACAACTGATTAAGGTTTTGGTAATTGCTGATACCCAT  
247451 GGTCAAAACCAAGAGGTGGATTGAACTGAAAACTACCATAACCTGATGT  
247501 GATTATCCATGCAGGAGATCACATGACCACTAAACAATTCATGGATCAAA  
247551 ATGCTACTTTTTGAGTGGCAGGTAACAACGATTCAATTGGCAATGAAATT  
50 247601 GAAATTTTCCAGTTAGGGCAAATTAACCTTGTGTTAATGCATGGTCACCA  
247651 AGCACCAAGAGATAACCTGAAAAAGTGGTACCAATTATTAGTTTTAAAAG

247701 CACAACAATACCCTTGTGATGTTTTAATCTTTGGTCATAGTCACATTGAA  
247751 TATACCAACAAAATTAATATGATCCAGTTAATCAACCCTGGTTCTCTACA  
247801 ACTACCAAGAAACCAACCAACCCCCTTCATACTGTACCTTTATTGTCA  
247851 ATAAAGACGAGCTAACTGATCTAACTATCCACTATTACCAAGCTTCAAAA  
247901 GTTAGTTAACAGGATCTTTTAGATAGATAGGTTGTAAGGTTAGAGGATCT  
247951 TCGATTCTTTCAAAGTGATCGATGTTGCTTAATAACAGCTTGCTATAACT  
248001 CTCAATGTTTTCAAAGTTTTCATACATAGGAAGTTCATTGTTTGCCTTAC  
248051 ATAACCTTCACAAAATCAGCTTTACTAATTAGCTTTATTTCACTAGTAGTT  
248101 TGGCTGTATAGTCCACAATAGTTCTGATCATTACCACAACATAATCTTGCT  
248151 AATCCCATGTTTCATATGGGATTTGAAAGCGGAGTGAATTTAAAGCATAAA  
248201 GTTCACAAC TGGGATACAATAAACACCAGCTTTTAGCAATGATAGTTGCT  
248251 ATCCTCTGACCGGTGAAACTACCAGGGCCAATTGTGACATAAAACTGTTT  
248301 AATACTGCTTTTTTTCAAAGTTGTTTTTGTAAACATTGTCTCCAGATAAT  
248351 AAACAGCAAGTTCAGTTAAGTTCTGTTCAACACCAATGGACAACATCATCA  
248401 ACCACTGCATTGGTTTTTCATCTCTAAAATAATGATGTTAAGGGTTTTATA  
248451 AGCACAGTCTAAAAACAGCTTATACTTACTTAAAAAGAACATGGAGTGGA  
248501 TCGGTAAAGATAAGTTTAAACTCTTAAGTTTCGTTGAAAACTTAGGTTT  
248551 AAGTGGGGCGTGAAAGTCCATAGGTTTGTAAAGTGGGATGGATAAAAC  
248601 AGATCCTGTTTGCATGGAGAACTGACCATAGCTATCTTTCTTTTCACTT  
248651 TTAATTCATACAGTGGATCATTATAAACTGGATGTTGGATAAAATTCAG  
248701 ATGCACTCTAATTTGGTGGGTTCTACCTGTTAACAATCCAAGCTAATTA  
248751 GTGCTGCTTTTTTCATTCTGATTAATCACTTTAAACTTAGTTATTGCTTGC  
248801 TTTGCTTTAGCAGTTTGGGCTATTTTAAACATTACCTTGTGTTATTAAC  
248851 CCTTGCTAAAGGTGCATTAATTGAACCAGTTAAGGCATTAAGGGGAAGT  
248901 GGACTAGTGCTACATAATAACGTTTTAAGGTGCGATTTTGCAGTTGATTT  
248951 TGCAAAATTTAATAAGCTTGCTTGGTTTTTACAGACAACAATTGCCCCACT  
249001 AGTATCACGGTCCAATCTGTGCACTAAGTAAACAGGGTTTTTGTGTTGT  
249051 GAAAGATACAAGCAGCTAACAAGCTGGCTTTTTTCATTGAAAGTGGTGGGA  
249101 TGGGTAAACAAACCTGATGGTTTTGTTAATAACCATCAAATCCTTGTCTTC  
249151 AAAAAAGAACCTCAAGCTTTAAGTTATAAGGTTCAACACTAGTAATGAAAT  
249201 CACTAGTTGTCTCATCATGAATCTCAACTTTAATTACATCATCTTTTGCA  
249251 ACTATTAAACTGTTTTTAAAGTTAGTTTTTCATTAACTTTAATCTGTCC  
249301 ATTCATGATCAGCTTCACTACCTTTACTCTTGAAAGGTTGAGTAAGCTAG  
249351 CTAAAAGACTATCTAAGCGTTTGGTAGTTGTAACAACAAAACACTGTTTC  
249401 ATTACTGGTTTTTGGAAATGTTTAACTCTTTGAACATCTGGATTAAAAAA  
249451 CAAAAGAATAAACCTATAAAACCAAAGGTAATACAACAATCAGCAAAGTT

249501 AAATACTGAACTACCATTCTGAAAGATAAAGTAATCTAACACTGAATCAT  
249551 TAGCTGAAGTTAAACGATCAAAGAAGTTTCCAAGTGAACCAATGCTAAA  
5 249601 GTTGTAAATTCAAAAGATGTAAGTATATTTACCATAAAAaCAAGAAAAAC  
249651 TAACGCAATTACTGATAATAATCCCTGGAGAAAGTAACTAAGCCAGTTT  
249701 GGTTTTGTAATAAGCTAAACCCTACCCCTTTGTTTCTAATCACATAGATA  
10 249751 TTAATAAAACCACTATTGCTACCATGGTGTTATCCATCTCACCATTAA  
249801 CGCATTCTTAATATGAAAACCTGCAGTAAGATAATAAGCCAACAAACC  
249851 CAATCATTGTCAGTTTATAGAATAAAAAATGGTTTTTGGTTGTCAGTTAAA  
249901 ACCTGGTGTTAAGTTGTGAAAAAACTTGGTTTTTCTTAATTTTATCTA  
15 249951 CTTGTATATTCAGTTAAAATTCATAATTAACAAAAATTATTAAGG  
250001 AGTATTAACACTTTTTTACTAGTTTTTAACTAAGTTTTTTAAGTGAAT  
250051 CCTAGTTTAATTTCTGGTAGTTTTCTTTACTAATAGCTACTTGTAACAAA  
250101 TTAAAAGTTAGAATTAATGGCACTATTTAGTATATAGATATCAGGCTTTG  
20 250151 GGGAAAACAAAAACAAATCAGACTGACAGATCTTTCTAGAAGATTACCG  
250201 TTTTTATTTTGAAACAGATTTTGATTGGGTTACATACCTGAACAACTGTT  
250251 TAAACAGCTATCCTGATTTTGACATCATCAAGTTCATTAAGAAGTATGGC  
25 250301 CCTGAGTGTGAAAAGAGCTTTCTAAGCTGACAGAGCAAAGCTAAGAGTGA  
250351 TGTTTACAGTGAAGTGAACAAAGATTAAAAACAACAGTTCTCAGAAC  
250401 AGTTAATTTACCAGCTAGTCCAACCTTGATGCTTTACGAACCTAATTTTA  
250451 ATGGGTTTCGTTGTTTTTTCAGATAACAAAACCCAGCGCAAACCTCCTGAAGCG  
30 250501 TTCTTGAAAAATGCTAAGAAAGAAGGTTATACAAAACAAGATGGTTGA  
250551 TGATCTTAGTTGGTTTACCCTTTGAAAAAGGTGCTTATCATAAGCAGTTA  
250601 TATGACCATTACGTCAGGAGATCTTAGATCTTACTGAAGTTATTAACAAA  
35 250651 GCTTTATCTAAAAACAGAGACCAACAACGATAAGCTTGAGTTTGCTGCAA  
250701 CTACTAGTAAACAACAGCGCAGCTAACTAAACTATGCCCTTAAACAGT  
250751 AGTGATCTTGATAAGGATCTAATGGAGTTTAGTGGTGAGAAGTGAGGTGA  
250801 TAATTAGTGCCTAAGATTGAAGTTAAAAATGATGATTTAGAGCTAGCTTT  
40 250851 AAAAAAGTTTAAAAGGATATCACTGGAAGTACGCAGGTTAGCACACCGCC  
250901 ATGAATACCACTTTCGCAAGGGATGCGGTTAAGAGAAAAACAAAGATA  
250951 GCACAGAAAAAGCGCAGGAAGTTTCGCAGTTTAGCTAGCCATTAGATGG  
45 251001 ATAATAAAAACCCCCAGAACTTATTACTAGTGAATTGTTGGCAAACCA  
251051 CGCTTTAATTTTGCTAAAGATGATAAAGGTGGGTATGATGCTAATGAAGT  
251101 TGATGCATTCTTAGATCAACTAACCAAGACTTTAATCCACTATGAGGAGA  
251151 TGAAAAACAACGAACAAGAATTGAAAAATGCTTATGACAAGTTGTTTTCA  
50 251201 GATCGTGATCAGATTTTAAGTCGTTGTGCTAAATTAGAAGCTGATTTAA  
251251 CACCTTTTATGAAATGGTTATGCAACAAGGTGTTAATTAACCGGGTTC



251301 AGGAGTTGGAGGATAAACTTGAAAACTACCTGATCGTTACACTGAAAAA  
251351 CTAGAAAGGATTGAAAACTGTTAAAAAGGTCATTAAACACTGAACTGA  
251401 TGGGGAGGACATTAGTAACTTTGAAGATGAGTTTTTTTAAAGATGGTTGT  
251451 TGGGATAGGGATTGATGTTGTGCAATTAAAGCGCTTCTTAACTTTAGTTG  
251501 AAAGTAGTGATTGTTTTGCTAAACGATTGTTAACTAGCAATGAACTAAAC  
251551 AGTTATTGAAAGCTAAACAATAACCAAAGAGCTAATTTTCTAGCAGTGCA  
251601 TTGAACTTTAAAGAAGCGATTTATAAAGCTACCAGTCACATCAAACCAC  
251651 TTTTCACTAAACTTGAAATTTATAAACTTAACAACCAGTACCGGTGTGAA  
251701 TTTATCCAAAACATCAACCTGTTGTTATCAGTTAGTTACACTAATTGCCA  
251751 TGTTAGTGCTATCTGTTTAGCACAAACAAATGGATAAACTATTTAAACA  
251801 AGTTTTAGATTCCATAATAAGGTTTTTACAAATCCTGAGTTTACCAGTTGT  
251851 TTTTCCTTACTTTTTTATTAAGCTTTTTAGCTTGTTTAATTACTAGTAAAA  
251901 ACTATGAATCACTCCCTTATAACTATCCCCCTGAAATCCGATTCAAAAAG  
251951 GTGTATAGATTGGTATCAATGTGACTTTACATTAAGGGAATTAAAGTAGT  
252001 GACAGTAAATGACAAGATTATCCCTAAAAAACAGTTTTAGTGGTAGCTA  
252051 ACCACAAATCTAACCTTGATCCTTTAGTATTAATTAAGGCCTTTGGCAGG  
252101 TTGAAAAATAGTCCACCATTAACTTTGTGCTAAGATTGAACTGAAAGA  
252151 TACAGTCCTTTTTTAACTGATGAAATTAATTGATTGTGTTTTATTGATC  
252201 GAAAAACATCAGACAAATTGCCAATGCATTGGAAACCAACAACACTA  
252251 ATTCGCCAGGGCACTGCTATTGCTGTTTTTGCTGAAGGGACTAGGATTTT  
252301 AAGTAATGACATTGGGGAATTTAAACCAGGAGCACTAAAGGTTGCTTACA  
252351 ATGCTTTTGTACCTATCTTACCAGTTAGTATTGTGGGTAGCTTAGGAAAG  
252401 ATGGAATCAACAAAAGGCTAAAAGAACATGGTGTTAAGAAAAGTTCAAA  
252451 CTATGAGGTTAAAGTAATCTTTAACAAGCTAATTAACCCAATTAGTTTTA  
252501 ACCAGATTGATTCTAATAACCTTGCTAATAACATTAGAAGCATTATTAGT  
252551 GATGCATACACTAGTGAAAAACCAAGCAATGATTAGTTTAATTTTTGATA  
252601 AAAGCAACAGTTTTTAACCCCACTTTGTGTTGAACTTCTCAACCACTTT  
252651 AAAGTGGTTATGCTAACTAAAACCATCGTTGTTGACTATCCCAGCTTTCA  
252701 AGCATGAAAAGCACAACTCAAACCGTTTTAAATTAGCAGTTTTTAGTGATA  
252751 ATTTGCAAACCGAATTAACCCCAAATTCAAACTCACAGTTTTTAACAAC  
252801 TACCAGCAACTTTTAGTTGATAATAATGACCTAATTATCTTTGCAACCCC  
252851 CACTTTAGTTCAGCTTTTTGATAATGAGATTGACCAGTTAATAGTTATCA  
252901 ATCCCACTAGTAAATCTAAAGATCAGTTTAACTGTAATTGAAACGACTTT  
252951 GTTTTAATTAAACAACTAATTTCAAGAACCATCAAGTTGGTTATTTTGA  
253001 TAAAAAAGTAGTTATGAACCACCTTTCAGTGTGTACAGACCACTTCT  
253051 TTGGGAACCTAACTGATTTATTTAGTCTTTTAGTTGATAAAAAGGTAAGT

253101 GTAAATGATGTGGATATTGGCTTGATTTCTTACAATATCTCAATATCAT  
253151 TGCAAATTACACCAATAAAAAAGCCATTGAAAAGATCACTGATTATCTGG  
5 253201 TGATTACAAGCAAAATTCTCGCTAAAAAAGCAGATAATCTGCTCAATGAT  
253251 CATCAGGAAGAGAGTGTGTTGGAATATGATTTAGCTACTAATAACTTTTCG  
253301 TGATAAGATGATCGCTAACTTAGTGGAACACAAACGCTATTGTGATTAC  
253351 TGGGTGAATTTGAAAACTCAGGGTTAACCGCTTAGCTTACTTTTCCAAA  
10 253401 GCTAATGAGATGGAGCAATTTATCAAAACAGCTAATGATCAACTTGTTAC  
253451 AGTTGAAGATCAACTCCCTAACTATATTAGTGTCTTAAACTCTTTCATG  
253501 CTATGAACAAGTTACTGGAGATGAGACTCAGCTCTCTTCTAACAATAAAA  
15 253551 AACATCACCATTAAAGAGTTATCAGTTGAACAGGTTCAAAGGAGTTGGT  
253601 TTTAGCAATCAAACAGTTTAACTACCAAACAGTTTCTTTAAAGCGGGTGT  
253651 TATTAAACTTAACCATCCTATCTCTTTAATGTATTTtGTTACTGCTTTT  
253701 GTGGCACTTTTAGTGCTATTAAACAACCAGGTAATAGGTTTGGAAACAAA  
20 253751 AGATTATCACAGTGAACTTTACATCTTTTTACTAGATGAAAACCAACTGA  
253801 AAACCTTCCAAGAATCACCAGATGAAATGGTAAAAAGAATCCAAGCTCAA  
253851 CAACAGCAAAACGAACTGATAATTGCTAAAAACAAGCAACTAAGAGCTAT  
253901 CAAAAACAACAAAAGCGAGCTGATTATCTAAAAAGAAATATGGTGAAA  
25 253951 ATTACTTAGATAAACTAACTTAAAAGATGAAAAACAATTAATATTGC  
254001 CACCCCTACCCTAAAAAACCTAGCAAAGAAGCTAACTTGGTTGCTAGTA  
254051 TCTATGGGTTGTTATTTGTTTGTGGCGCGAAAGGGATCACTTTAAGAGAA  
30 254101 CTAATTAGGATCTTTAAAAAAGCAGGGATTGAAAAGGTGAAATTAGCACT  
254151 CTTAGCACTTGAAAGGAAGTTAGCAGATGATGAGCAATCAGGAGTGGAGT  
254201 TGAAAAAATTTGGTAATAGTTTTTCTTTGGTAACAAAACCAATTATCAAA  
254251 GACTATCTCCACTTATTATTGGCTCATAAAGTCAAAAATCCCCTTAATTC  
35 254301 CAAAGCAATGGAAGTGTGGCTATCATTGCTTACAACCAACCTTGCACCA  
254351 GACCCAGAATTAATGAAATTAGGGGAGTTGATTCTTTCAAATTGTTGAT  
254401 GATCTAATAGCAAAAGAGTTAATTGTGGAGTTAGGGAGAACTGATAAACC  
40 254451 AGGTCGACCTTTTATTTATGAAGTGTGAGCTAAGTTCTATGATTTATTTG  
254501 GCATTGATAGCTTAGATCAACTCCCTAAGATTGAGCATTTTGATCTTGAT  
254551 AAATTTAAGCAAGGTAGCTTTTTTGATTCCAACCGCTATGGTGATGAATA  
254601 ACCTTATATAATTTACAACATGGATAAAATAGCTATTTTAACTTCGGGTG  
45 254651 GTGATGCTAGTGGGATGAATGCCACCATCGCTTATCTAACCAATATGCA  
254701 ATTGCAAAGCAATTGGAAGTTTTTTATGTAAAAAACGGTTATTATGGCTT  
254751 GTATCACAACCATTTTATCACCAGTAAGGAACCTTGATTAACTGACTTTT  
50 254801 TCTTTATGGGGGAACAGTAATAGGATCAAGTCGTTTCAAACAGTTTCAA  
254851 GATCCTAGCTTACGAAAACAAGCAGTTTTTAAACCTCAAAAAACGTGGTAT

254901 TAACAACCTTGTTGTTATTGGTGGGGATGGGAGTTATATGGGTGCTAAAG  
254951 CACTCAGTGAATTAGGATTAAACTGCTTTTGTGTTACCTGGTACGATCGAC  
255001 AATGATGTCAATTCAGTGAATTTACCATTGGTTTTTGAAGTCTTTAGA  
255051 AGCAATTCGGGGTTAATGTTGAAGCAATTTATCACACCACCAAATCCCATA  
255101 ACCGCTTAGCAATCATAGAAGTGATGGGGCGTGATTGTAGTGATCTGACC  
255151 ATCTTTGGGGGGTTAGCTACTAATGCTAGTTTTGTTGTTACTAGCAAAAA  
255201 TAGCTTGGATCTCAATGGCTTTGAAAAAGCAGTGAGAAAGGTGTTGCAAT  
255251 TCCAGAACTATTGTGTTGTTTTGGTTAGTGAAAACATCTATGGTAAGAAC  
255301 GGTTTACCTAGTTTAGAAATGGTTAAAGAGCACTTTGAAAACAACGCAAT  
255351 TAAGTGTAACCTAGTTTCACTAGGACACACCCAAAGGGGCTTTAGTCCTA  
255401 ATAGTATCGAACTCTTTCAGATTAGTTTAATGGCTAAACACACGATTGAT  
255451 CTGGTTGTAAATAATGCCAACAGTCAAGTAATAGGGATGAAAAACAACCA  
255501 AGCAGTTAACTATGATTTTAACACTGCTTTTAATTTACCAAAAGCTGATA  
255551 GAACCAAGTTACTTAACCAAGTTAACACTGCAATTATTTAACGATGATTG  
255601 ACCATTTAAAAAGAACAAGATAATCGCTACCTGTGGCCCAGCTTTAACA  
255651 AAAAGCTTGGTTAGCTTAAAGATGCTTGATGATAATGAGTATGCAGCTAT  
255701 TAAAAAGGTTGCTTATGCCAACATTGAAGCAATTATTTAAAGTGGGGTTA  
255751 GTGTGATTAGGCTTAACCTCTCTCATGGTACCCATGAAGAACAACAAGTG  
255801 AGGATCAAGATAGTAAGGGATGTAGCGAAAGCAATGAACATCCCTGTTTC  
255851 TATTATGTTAGATACAAATGGTCCTGAGATCAGGATAGTAGAACTAAAA  
255901 AAGAGGGTTTGAAATCACCAAAGATAGTGAAGTGATTATCAACACCATG  
255951 AGTAAAATGATCGCTAGTGACAACCAGTTTGCTGTCAGTGATGCTAGTGG  
256001 CAAATACAACATGGTTAATGATGTGAATATAGGTCAGAAAATCCTTGTTG  
256051 ATGATGGTAAGTTAACCTGGTTGTCACAAGGGTTGACAAACAACATAAC  
256101 CAGGTTATCTGTGTTGCAAAAAACGACCACACAGTTTTCTACTAAAAAAG  
256151 ACTTAACCTACCCAACGCACAGTACTCTATCCCTTTTCTCAGTGAAAAGG  
256201 ATCTGAAGGATATTGACTTTGGTTTAAGCCAAGGTATTGACTATATTGCT  
256251 GCCTCTTTTGTTAATACTGTTGCAGATATTAAACAACCTGAGAGATTATCT  
256301 GAAATTAAAGAATGCTAGTGGGGTGAAGATCATCGCTAAGATTGAATCTA  
256351 ATCATGCTTTAAATAACATTGATAAGATCATTAAAGCTAGCGATGGGATT  
256401 ATGGTTGCTAGGGGTGATTTGGGCCTTGAAATCCCTTATTACCAAGTCCC  
256451 TTA CTGACAAAGGTACATGATTAAAGCTTGTCGCTTTTTTAACAAGCGTT  
256501 CTATTACTGCAACCCAAATGCTTGATTCACTAGAAAAAACATCCAACCA  
256551 ACCCGAGCTGAAGTGACTGATGTTTACTTTGCAGTTGATCGGGGTAATGA  
256601 TGCAACTATGTTAAGTGGGGAAACTGCTAGTGGGCTTTACCCTTTAAATG  
256651 CAGTAGCGGTGATGCAAAAGATTGATAAACAATCAGAAACCTTCTTTGAT

256701 TACCAGTATAACGTTAACTATTATTTGAAAACTCCACGGCAAATAAAAG  
256751 TAGGTTTTGACACAACGTTGTTTTACCTTTAACAAAAAGACTGTTCCCTA  
5 256801 AAAGAAAACCTTGTTAACAGTGCCTTTAAGTATGACTTTATTGTCTATCCT  
256851 ACTAATAACATTAACAGGATCTATGCATTATCAAACGCACGCTTAGCAGC  
256901 AGCAGTTATTATTTTAACCAACAACAACGGGTTTACACTGGCCATGGTG  
10 256951 TTGATTATGGGATCTTCTGTTATTTAATTGATAAAAACCCCAACCAGCTA  
257001 ACCAAAGCTGAAGTGAAGTCTGCTTGAAAAGCAATTAACCACTATCA  
257051 GGCTTATGGTGATTTAGAAAACTCAAACAGTGTTTAGCTGTCTATAATG  
257101 AAACAATTATCAATCTTTAGATAAAAATTGGTGAGAGTTTGTAAAAATATT  
15 257151 GTACACGGTGCCTTAGCCAAGTGGACTCAAGGCCTGGAGCTGCAACCTCC  
257201 ATATCGTCAGTTCGAATCTGACAGGCACCTCCATGTACATGAAAGTTAAC  
257251 TACTCTCCATGTGCAAACGGGAAGTAGCTTAGTTTGGTAGAGCACTTGGT  
20 257301 TTGGGACCAAGGGGTCGCAGGTTCAAATCCTGTCTTCCCGACCAAAAGGC  
257351 TGGATACCTCAGTTGGTTAGAGGGCCCGGTTTCATACCCGGGTTGTCGTGA  
257401 GTTCGAGTCTCACTCCAGCCACCAAAGTTACTTAAATATTAAAGGATCTA  
257451 TAGCTCAATTGGTTAGAGCCCCGACTCATAATCGGTCTGTTACAGGTTT  
25 257501 AAGTCCTGTTAGATCCACCACCTTGCTGTGTTAGAATCATATTTGCCGCA  
257551 ATTTTGTGGAGACTTACCCAAGCGGCTGAAGGGTTCGGTCTTGAAAACCG  
257601 AGAGGTGCTTTATAAGCACGCGAGGGTTTGAATCCCTCAGTCTCCGCCAA  
30 257651 ATAATATTTAATCGCGGGATAGAGCAGTTGGTCAGCTCGTCAGGCTCATA  
257701 ATCTGAAGGTCGAGGGTTCAAATCCCTCTCCCGCAACCATGGTTCCATGG  
257751 TGTAGTGATAACATATCTCCCTGTCACGGAGGGGTTGCGGGTTTGATTCC  
257801 CGTTGGAACCGCCATTGGTCTTGTAGCTCAGTCGGTAGAGCAACGGTCTG  
35 257851 AAGAACCGTGTGTGCGGCAGTTCGATTCTGCCCCGAGACCACCATTAAGT  
257901 TTTTAAAAAAGCCCTAAAAAGGGGCTTTTTTAGTGTTACCACCAATTAA  
257951 ATATTTTTATAGCAAGCAGTTGCATATTTTAATATAAGTTAGAATTATT  
40 258001 GGTATAGTGCTTCAGCTGTTTAATTCATATTAAAGCGCATGGAAAAAA  
258051 TAGATCAGCTTTTCAACAAAACCAACAAGCATCAAACCAACCTTTTAACC  
258101 AAGATCAAAACAGTATTACCAAGATCCTAACCAACAACAATTTAACCA  
258151 TCTGGTTTTGATCCAAATCAACAGCAATTTAATCAACCAGGATTTGATCC  
45 258201 TAACCAACAATATTATCAAGATCCCAATCAACAACAATTTAATCAAGCTG  
258251 GTTTTGATCAAAACCAACAGTATTACCAAGATCCCAATCAACAGCAATTT  
258301 AATCAACCAGGATTTGATCCTAACCAACAATATTATCAAGATCCCAATCA  
50 258351 ACAACAATTTAATCAAGCTGGTTTTGATCAAAACAGTATTACCAAGATC  
258401 CTAACCAACAACAATTTAACCAATCTGGTTTTGATCAAAACAGTACTAT  
258451 CAAGATCCTAATCAGCAACAATTTAACAGCCTAGTTTTGATCTAAATAA

258501 CCAACAATTTAACCAACCTGGATTCAACCAATCCCCAGCATTTGAAATCA  
258551 CACCTCAAGAGCAAAAAGCTGAACAGGAAATGTTTGGTGAAGAACCACCT  
5 258601 CAAGTAGTTAGAGAGATCCATGAACTACCATTTGAAAAGATCCGTTCTTT  
258651 TTTACAAAGTGATTTTGATAGCTATAACTTTGCGTTAAACTCACTTAAAA  
258701 GCAAACCTGGATAATGCCTTGTATTCACTTGATAAAACAATCCAAAACACC  
10 258751 AATGAAAACACTGCTAATCTAGAAGCAATTAGACATAACTTAGAACAAAA  
258801 GATTCAAAACCAAAGCAAGCAATTAAGAACTAACTTTGATACCCAAAAGC  
258851 TTGATGATAAGATCAATGAATTGGAGATCAGAATGCAAAAACCTAACCAGG  
258901 AATTTTGAATCTCTAAGTGAACCTTTCAAAGCACAACTCTTATCCTAATTA  
15 258951 CTATGAAAAATTGTTACCAAATGGTGGTGATAGTATGACCAATGTCTTTG  
259001 AAAAAGCACTAATGATGAATTTATTGAGAACTACATTACCCCTCAACCC  
259051 CAAGTTCAATACTACCCTCAACCCTATCCATACATAAGACCTTACTATGA  
259101 TGAACCTATTTACGCTGGGTTTAGAAGAAGGGGTACCGTGATGACTTCT  
20 259151 ATGAATAAAAAGCGTGTTTTAACTAATGAAACCATTTGATAAAAAACCTT  
259201 CGCTGCAACCAATTTATGACATTGGTTTTGATGATGGTTATCTCCAAAGT  
259251 GAGTATGAAAAAATCGTTCTAAAACCGATGTTGATAAGATCGAAAACCA  
25 259301 GCTTTTAAAAGAGATTAAAAGCCTGGAAGATGAACTTAAAAACCTTAAGG  
259351 GCTTGAAGAATCAAGCAGAAGATAATCCTGAACTTGATAAAAAGATTAAC  
259401 CACTTGGAAGTTGATCTAAACCGTTTGGTTAATGAATATAAAAACCTTCCA  
259451 GTTCCAAAAGAACCACATGGTTGATAAGGTTAGTGAACCTTGATAACTTAA  
30 259501 CCCGTTTTTATAAGAATGAACTAACCCGCTTACAACAAGAAAACGCTGAT  
259551 TTTCTCAACTCCAAGTATGCTAATTTAGCTAACTTCCAAGCTAACTACCA  
259601 CAATAAACTAAATGATTTTACCAGCTTAATAGAAAATCAAAACCAAACCA  
35 259651 TTAACCGCTTAAACCAAAGATTAATGGTAACCAAATCTGATTGATAAT  
259701 AACGTTGCTTTTACTGCAAAACCCCAACATCACAGTTGAAAAAAGAAGTA  
259751 CTTACTAAATGTTATTGATCAACTTTACAATGAGCTTGATCAACTTGAGA  
259801 ATCAAAAAAGATTATTAAGTATTGAGTATGAAAATACCTATAGAGAGTTA  
40 259851 GTTAGTGAGATAATGAACTGCAAAATGTTTATGAAAACATCGATCAAAA  
259901 TCAGATCCAGTTTAAACACCAATACCAAACCTTATAGAGATGAGTTAAGTC  
259951 AACTTGAGCGCAAGATCCAGCTCACCAACAAGAGTTAGTTGATAAAGAA  
45 260001 TCAGCACTAAGAGTAAAGATAGATGATGCTGATTTTACATTAATGCCCCG  
260051 TTTAGCTGAACTTGATGATGTAGCTAAACAACCTTAGCTTTCAAGATGGTA  
260101 TTACCAAGCAAAATGCTCAACATGTTGAGGATAAGTTAGTTGCTTTAAAC  
260151 AAAGAAAAAGACCGTTTAAATACCCAAAAAGAGGCCTTTTTTAACCTTAAG  
50 260201 ACAATCTGCTTTAATTGATATCAATAAACTCCAGCAGGAAAATGAACTGT  
260251 TTGCTAAGCACTTAGAACACCAGCAAAATGAGTTTGAACAAAAACAGTCT

260301 GATAGCCTCTTAAAGCTTGAACTGAATATAAGGCTTTACAACACAAGAT  
260351 TAATGAATTTAAAAATGAAAGTGCCACTAAGAGCGAGGAACTTTAAACC  
5 260401 AAGAACGGGAACCTATTTGAAAAACGCAGGGAAATTGACACGCTTTTAACC  
260451 CAAGCATCTTTGGAATATGAACACCAACGTGAGTCAAGTCAACTACTCAA  
260501 AGATAAGCAGAATGAAGTAAACAACACTTCCAAAACCTTAGAGTATGCTA  
10 260551 AAAAGGAGCTAGACAAAGAAAGAAACCTCTTAGATCAACAAAAAAGTT  
260601 GATAGTGAAGCAATCTTTCAACTCAAAGAAAAGGTTGCTCAAGAACGTAA  
260651 GGAGCTTGAAGAACTATACCTTGTTAAAAAACAAAAACAAGATCAGAAGG  
260701 AAAATGAAGTGTGTTTTTTGAAAAGCAGTTAAAAACAACCAAGCAGAT  
15 260751 TTTGAAAATGAATTGGAAGCTAAACAACAGGAGTTGTTTGAAGCTAAACA  
260801 TGCATTGGAACGTTCTTTTATCAAACCTGAAGATAAAGAAAAAGATCTTA  
260851 AACTAAAGCACACAGATTGCCAATGAGTTTTCCCAACTAAAACTGAT  
260901 AAGTCAAAGAGTGTGATTTTGAACATAATGTTGCAAAATGAGTATGAAAA  
20 260951 CTTGCAACAAGAAAAACAAAAGTTATTCCAAGAACGTACTTACTTTGAAA  
261001 GGAATGCTGCGGTTTTATCAAACCGGTTACAACAAAACGTGAGGAGTTA  
261051 TTACAACAAAAGAAACGCTTGATCAGCTTACAAAAAGCTTTGAGCAAGA  
25 261101 ACGGTTAATCAACCAAAGGGAACACAAGGAGTTGGTTGCATCAGTTGAAA  
261151 AACAAAAGGAGATATTGGGCAAAAACTCCAAGATTTTTCCCAACTTCA  
261201 CTGAACGCTTCTAAAAATTTAGCTGAACGGGAGATGGCAATCAAGTTTAA  
261251 AGAAAAGGAGATAGAAGCAACTGAAAAGCAACTGTTAAATGATGTTAATA  
30 261301 ATGCTGAAGTTATCCAAGCAGACTTAGCACAACTCAACCAATCACTTAAC  
261351 CAAGAACGCAGTGAATTGCAAAACGCCAAACAAAGGATTGCTGATTTTCA  
261401 CAATGATTCATAAAAAACTCAATGAGTATGAACTTAGCTTACAAAAAC  
35 261451 GGTTGCAAGAATTACAAACCTTGAGGCTAACCAAAAACAACATTCATAT  
261501 CAAAATCAAGCTTACTTTGAAGGTGAACCTTGATAAACTTAACAGAGAAAA  
261551 ACAAGCTTTTTTGAACCTACGTAAGAAACAACTATGGAGGTTGATGCTA  
261601 TTAAACAAAGGTTGAGTGATAAACATCAAGCTTTAAATATGCAACAAGCA  
40 261651 GAGCTAGATAGAAAAACCATGAGTTAAATAATGCTTTTTTAAACCATGA  
261701 TGCGGATCAAAAGAGTCTACAGGACCAACTAGCAACTGTTAAAGAGACCC  
261751 AAAAATAATTGATTTAGAACGTAGTGCACTGCTTGAAAAGCAACGTGAG  
45 261801 TTTGCTGAAAATGTTGCTGGTTTTAAGCGCCATTGGTCTAATAAACTAG  
261851 TCAACTCCAAAAGATTTATGAACTGACCAAAAAACAGGAAAGTGAGCAAA  
261901 CCCAAAAGGAAACAGAACTAAAGATTGCTTTTAGTGATCTACAAAAGAC  
261951 TATCAGGTTTTTGAACCTCCAAAAGGACCAAGAATTTAGACAAATTGAAGC  
50 262001 TAAGCAACGTGAACCTTGACAAGTTAGCTGAAAAAATAATCAGGTCAAAC  
262051 TAGAACTTGATAACAGGTTTCAAGCGCTGCAAAACCAAAGCAAGACACA

262101 GTACAAGCTCAGCTAGAACTGGAACGTGAACAACACCAGTTAAACCTTGA  
262151 GCAAACCTGCTTTCAACCAAGCTAATGAATCACTTTTAAAAACAACGTGAAC  
262201 AACTCACCAAAAAGATCCAAGCTTCCACTATGAGTTGAAAAAGCGTAAC  
262251 CAATTCTTAGCTTTAAAAGGGAAAAGGTTGTTTGCAAAAGAGCAAGATCA  
262301 ACAACGCAAAGATCAGGAGATCAACTGACGCTTTAAACAGTTTGAAAAGG  
262351 AATATACTGATTTTGATGAAGCTAAGAAAAGGGAACCTTGAAGAGCTTGAA  
262401 AAGATCAGAAGAAGTTTAAGTCAAAGCAACGTTGAATTAGAGAGAAAAAG  
262451 AGAAAACTGGCTACTGATTTCACTAATTTAAATAAGGTTCAACACAACA  
262501 CCCAAATTAACCGTGATCAACTTAACAGTCAGATCAGACAGTTCTTATTA  
262551 GAACGCAAAAACCTCCAACGCTTTAGTAATGAAGCTAATGCTAAAAAAGC  
262601 CTTTTTAATTAAGCGCTTAAGAAGCTTTCATCCAATCTAAAACCTCCAAA  
262651 AAGAAGCGTTAGCAATCCAAAACTAGAGTTTGATAAGCGTGATGAACAA  
262701 CAGAAAAAGAGTTACAGCAAGCTACTTTACAAC TAGAACAGTTCAAGTT  
262751 TGAAAAGCAAACTTTGACATTGAAAAACAACGCCAACTAGTTGCTATTA  
262801 AAACTCAGTGTGAAAACTTAGTGATGAAAAAAGGCACTAAACCAAAAG  
262851 CTAGTTGAACTAAAAAACTTATCCCAAACCTATCTTGCTAATAAGAATAA  
262901 GGCTGAATACTCCCAGCAACAACCTCCAACAGAAATACACCAATTTACTTG  
262951 ATCTGAAGGAAAACCTTAGAGAGAACCAAAGATCAATTAGATAAAAAACAT  
263001 CGTTCTATCTTCGCTAGATTAAC TAAGTTTGCAAATGACTTACGTTTTGA  
263051 AAAAAAGCAACTGTTAAAAGCACAGCGCATAGTTGATGATAAAAACCGTC  
263101 TTTTGAAAGAAAATGAACGTAACCTCCATTTCTTTCCAATGAAACAGAA  
263151 CGAAAACGAGCAGTTCTCGAAGATCAAATTTCTTACTTTGAAAAACAACG  
263201 TAAACAAGCTACTGATGCGATCCTAGCATCACATAAAGAAGTTAAAAAGA  
263251 AGGAAGGTGAACTGCAAAAGTTACTGGTTGAATTAGAAACAAGAAAAACC  
263301 AAACCTCAACAATGATTTTGCAAAATTCTCAAGACAACGTGAAGAGTTTGA  
263351 AAACCAACGCTTAAAGCTCTTGGAAGTGCAAAAAACCTGCAACCCAAA  
263401 CTAATTCACAACCTTTAAAACCAAAGCAATCCAAGAGATTGAAAACAGT  
263451 TATAAAAGGGGGATGGAAGAACTTAAC TTCCAAAAGAAGGAGTTTGATAA  
263501 GAATAAATCACGCTTATATGAATACTTTAGAAAGATGCGTGATGAGATTG  
263551 AAAGAAAGGAAAGTCAGGTTAAGTTAGTTTTAAAAGAGACCCAAAGGAAA  
263601 GCCAACCTCTTAGAAGCACAGCCAACAACTTAACATTGAAAAAACAC  
263651 TATTGACTTTAAAGAAAAAGAGTTAAAAGCCTTTAAAGATAAGGTTGATC  
263701 AAGACATTGATTC AACCAATAAACAACGCAAGGAGTTAAATGAGCTTTTA  
263751 AATGAAAACAAGTTATTACAACAATCACTAATCGAAAGAGAAAGGGCTAT  
263801 TAATTCCAAAGATTCAC TTCTAAATAAGAAGATAGAAACGATTAAACGCC  
263851 AACTCCATGATAAGGAGATGCGGGTGTTGCGCTTG GTTGATAGAATGAAA

263901 TTAGCAGAACAGAAATACCAAACAGAAATCAACCGCTTAAGAACCCAAAC  
263951 TTTTCGATTCTGAAAAACAAGACATTA AAAA ACTTCTTCCCACCGTTATTTA  
5 264001 AAATTAACGGTAATGATATGGCCTTTCTTACTTGTACCCCTGACTATAT  
264051 CCTCAACAAAAGCAAGATGATAATACTCTGCAAATTCGTCAGCTTTTTGA  
264101 ACAGCAGCTGCAGTTCATGCAACAACGCTATGAAAATGAGTTAAATGAAT  
10 264151 TGCCTAGACAACGTAATTTACTTGAGAAAAAACTTGATCAAATCCAACCTA  
264201 GAATCCCAACTTAATAATAAGCAAAGTGAGTTTAGTAAGGTGGAATCAAT  
264251 GATGGAAAACTACTTGAAAAAACTGAGAGTAGGTTAAATGATTTTGATC  
264301 AGAAAATTAATCTCTACCAAGAAAGTTAACCAACACAACACCTATCAA  
15 264351 CCAAGTTCCTATCAACCAACTCCTTCTTATCAAGACAGTGATAACAACA  
264401 GTTGTTATTTAGAAATCCAAGAACTGGAAAAACAAACTTATTCCAACAAC  
264451 AATTTCAACCTGCACCAGCTGTTGTCCAACAACCTACTAGTTTTGCAGCC  
264501 CCTAACATCACCACAAACAGCAAATTGCCCAACTTAATGCTGAAATTAA  
20 264551 CAACATTA AAAAGGTTGATTGCCCAAAAAGCAGCAAAGTAAATAAAGATGGT  
264601 TAATAATGAATATCAACAATAAACACTTTAGTTGAGAGTGATGATGAAG  
264651 CGGATCTTGTGATTGCTAACCTAGTTAAACAACCTCAATGAACTAAAGCAA  
25 264701 ATCCTTGTTTCACTAGATAATCAAGAAGCAAGTGCCACTGCAGTTACTGA  
264751 TAAAAAGGAAGAGGAATACAACCAAAACCAATCCAGTTTCCATAACTTCA  
264801 GCAAAGAAACACTGCAAAAGCAAGCAAAACGTGGTTTTCTTTTACTGGAA  
264851 CGCTGTTTCGTTGGTTGGGTTACAACAACCTAGAGTTGGAGTATGTTAATTT  
30 264901 GTTGGGCAGAAGTTTGTATTCTTATCAACAAAAAACAGAGCTTTTAAACA  
264951 ACTTAAAGGAGCTTGTTGATGAACATTTCACTGATACTGAAAAATTATC  
265001 AATACCCCTGAAAAGATCTTTGATGTTATTGGCGGTAGTGAATATACCCC  
35 265051 TGTCTTAAACTCGTTTTTTTAAACAAGCTTTTAAAGTGATCCTGATCCAATCC  
265101 AACGGGAAATTGGCTTAAGACAATTTATCATCACTCTCCGTCAGCGCTTT  
265151 AAAAAGTTATCACAAAAGATTGACAGTTCTCTCAAACAGATAGAAACAGA  
265201 GGCTAAAATAGCCACTGAACAGGTTCAAATAGTGAAGTGATGTTTCGGTC  
40 265251 CCCCTGATATTGCTAATGATCATGAGTTAAACCTGAACTGACCTGATAGT  
265301 GAAACAGATGCTATCTTAAGTTCAATGGAAAATGAATTGGAAGCTGCTTT  
265351 ATTAGCAAAACACCAAGAAGAACCCGTTAATTGTTACCCACCCAGCT  
45 265401 TAATAAAACCAACTGTTAGTCAACCTGAAGTTGAAGTTGTTACACCTACT  
265451 AACAACTAATTTCCAACCCCAAGTTGATCTCAAACCTACTGATTTGAA  
265501 AAAACAACAGAAGAAAAAACCACTTAACCTTTATTACCCGTCCTGTTTTCA  
265551 AAAGTAATTTGCCACCGAACTAAGTAAGGATGACATAGTTCAATTATGCG  
50 265601 CACCAGTTACTTGAAAAAAATACCCATAATGAATAGTGATAGTGATCTAA  
265651 AACTCCAAAAGGTGTGGATCGAGCGGCATGTTGATCAAGATGAACTTAGT



265701 TTAACAAC TACTGCAGTTGAACTTAAAAAGAGTGATGAACAAAAACCTGT  
265751 TGCCATTAAAAGTAGTGACTTTATTGGTCATGAAGAGTTAATCTCTGTTC  
265801 CAGTTTTACTAATCCCAACCCCTGTTGTTAAAGAGATTGATCAACCAGCA  
265851 GTTATTCCTCCAGTTAAAGCAAAACCAAAAGCAACTAAAAAGAAAACCTCC  
265901 TGTAAATCAAAACCAACTAGTAAATCAACTAAACAAACAAAACCTAAAC  
265951 AATCCAAGCCCAAATCAAAACAAGTTCAACAAACCAAGCTAAACCAACC  
266001 CAAATTCAAAACAAAAAAGCAATAAAAAAACAGATCTTAATCTGGTTT  
266051 TTTTAGTGTTAACAACAGTAGTTTTAACTAAAAACTGGAAAGGAATAGGA  
266101 AGAACTACCTGGGGTTAATCCTAGTTTAAACCGTGC GGTTAAAGTAAT  
266151 TGCTTTTAGAGCGATAACTATTATTTTATTCTCATTATCATCATCAGAA  
266201 CCATTGGCATTAGCTGTGGTACTTTGAAAAATGTCATTTACTGCATGTGC  
266251 AACCCAGTAAGTGCATTAAGTATCATAATAAGTCCTGCACTAAAAGTTC  
266301 AGAAAGATAATCCACCAACAACCTGCTTAGCTTGCTGCTTTTCTAATTTA  
266351 TACATATAACTCCTTTGTCTATTAATCACATCTAAATCTAAAAGTGCCA  
266401 AAGTTTATAATTGATCAACTGTCATCATAGCTCAATAGGACAGAGTATC  
266451 AGCTTGCGGAGCTGAGGGTTACAGGTTGATTCTGTTGGTGACGCCATT  
266501 AACTTTATTTGCCTATCAGTTAAATAACTGGTAGGCTTTTTATTGTTTT  
266551 GTAGTTTATCAAGGGTTAATTTAAGTTGTAGTCATTTCATTTTGGACAAA  
266601 AAGAAATTTTTATGCTAAGATAAAAGTGTTTAAAGTGTCGCAAAGTGTG  
266651 ACAAAGTGGA AAAAATGCTGCTAGGTACCTTTAATCTTACCCTTGATAAC  
266701 AAGAACAGAATTAGCTTGCCAGCTAAGCTCCGTAGTTTCTTTGATAGCAG  
266751 CATAGTTATTAACCGCGGCTTTGAAAAGTGTGGAATTAGAAAACCTG  
266801 CAGACTTTGAGAGTTATTTTCAAACCTTTAATAACTTCCCTAACACCCAA  
266851 AAAGACACAAGAACATTAAAACGCTTAATCTTTGCTAATGCTAATCTAGT  
266901 TGAAGTTGATAGTGCAAAACAGAATCCTAATCCCTAATAACCTAATTAGTG  
266951 ATGCTAAGTTAGATAAAGAGATCGTGTTAATTGGTCAATTTGACCATCTT  
267001 GAAGTTTGGGATAAAGTGCAATATGAACAATATCTAGCTAGTTTCAAGATC  
267051 ACTAGAGACAGTAGCTGAAAGGATGAAAGATGCTAAATAACCAACAGATC  
267101 CACCAGAGTGTA CTGATCAATGAAGTGATCCATAACCTCAATATTAACCC  
267151 TTGTGGTA ACTATTTAGATCTAACTGCAGGGTTTG CAGGACACAGTCAAA  
267201 AGATCTTAGAAAACTAACAACAGGAACCTTAAACAATTAATGATGTTGAT  
267251 AAAGAAAGTATTAATTTTGGCAAAAGCTTTTTTTTTAAAAACAACAACGT  
267301 TGTATTATTACGATAACTTTGCTAACTTCCAGTTCATCTTAAACAAC  
267351 TATCAATAACCAAGTTTGATGGGATCTTAATGGACCTTGGTGTATCAAGC  
267401 CATCAACTCAACCAACCTAATCGCGGTTTTAGTTTTAAGAATGATGGACC  
267451 GATTGACATGCGTATGGACCAATCCAATCAGAAAAATACCGCACTAACAG

267501 TTTTAAAAAAGTTAACTGAACAAAAGTTAAGTCTAATCCTTAAAAAGTAT  
267551 GGTGATATTAAACACCCTAAACCAATTGCTATTGGATTGAAAAAGCAGT  
5 267601 TCAAAGTAAAAAAATCTTACCACAACTCACTAGCAAAAGTGGTAAAAAG  
267651 AATGTGCTACTGGATTGAAAAATACCAATCAAGAACTATCTTGCCAAA  
267701 GTTTTTCAAGCAATTAGGATCTATCTTAATGATGAGATTACTAATCTGAA  
10 267751 AACTGCGTTAACTTTTATCCCTAATCTTTTAAAAACAACAGCAGGTTTC  
267801 TTGTGATTGTTTTTCACTCCATTGAAGAAAAATTGTAAGGAATTTTCATT  
267851 GCAAACTAACCAGCTTTATCCAACCTGAAGCTCTACCCATTAACTCAC  
267901 TCCTGCTTACCAGTTAATTACAAAAAACCAATCCTACCTTCCCAAAAAG  
15 267951 AACTTGAATTAAACCCGCGTTCGCGTAGTGCCAACTCTTTGTTATCCAA  
268001 AAAAAGTAGTATGTACAAACCAAAAAATATTAACAGCGTATTAACCTTTT  
268051 ATAAGGATCAGATCCAACTGGTTGTTAGTGATGATCAAAACCAGTTC AAC  
268101 ATCTTGTTTTACCAACAATTGATAACGATGGCTTTTATTCAAAACAACA  
20 268151 GTTGAAAAACAACTAAGACTCAAGTTAGCATTAAACCAACTAGTTGATC  
268201 AAGCTAACTATTTTCTTGTTTTTAACTGGAAAAGGTAGTTGTTGTTCTC  
268251 GCTGAACTGATTGATGATTGAAGATCCATAATTTCAAGAGTGAGATCTT  
25 268301 TTTTACTGGTTATGATTTTGATCATAAAGCGATGATTAAGAAAGAAAAAC  
268351 AACGCTTTTGAGCAAAATAACCAACTAACAGTTATGGATACAATGGTT  
268401 TTAACTACCATGATGTTATTAACAATAAGATCACCAAAAGCTTTGCATT  
268451 TAACAAGAGCTATGTAGCTAATTTAGTGGCATATTCCTCTAAAAGTAACC  
30 268501 TGATCGGGGAGTTGAAGTTCTTTTTTAAAAAGAAACGTTAATCTTAAGGTT  
268551 AAGAAAATTATTAGTCACCACTTAGCATTAGCCAACTCCTTAAGTAAGAA  
268601 ACAAACAACATGTTTGTATTATTAGGACAAAAAACTACTGAACTGATGC  
35 268651 TATTTATGGACAATGCTTTAGTTGATGTTATTACCAACCAGTTTGGTAA  
268701 AACCACCTTATTGATATTCCAGCTAACCAGGAAAAACAAACCACTGCTTGA  
268751 GTTTTTAGTTGATAACACCACTAAGATTGGTGATTGTTATTCGCTTGGTA  
268801 TGACCTATACAGATGGTGATAGTTACAAAGAGATTAAGGCTTTGACTATT  
40 268851 GGTGATTTAATGCAACAGTTAGTGACAAGATCAAAACCTTAATTGATTT  
268901 TATTAACAGTGGTTCTCTAACTTTTTTCAACAAGTTTAAACCTTACCTA  
268951 AGCTATTGTATTTTTATACAAGATCAAAACAAATTACCAACCTTTTTCAA  
45 269001 GCTAATGTTGCACTTATCAATCCCCAGTTTAAACTGTTGATATTTATAA  
269051 GAACAAGATCCAGTTTATTAGTGAAAACTACCTGTTAAGCTGTGAAGCGA  
269101 TTAGCTTGCAGATTACCAATAGAATCAAAAACCAAATTAGTTTTGATTTTC  
269151 ACAAATGCTGATAATATTCAAAAACCTAAACCAAAAAAACCTTCATGAT  
50 269201 CTTATCAAAACACCTAACAAAGTTTGTCCAACGCTTGGTTAAATAACTAT  
269251 GGATGAAATGAACTCAATTCAACAAGTTAAACCAAGTTAAAAACAAGC

269301 TGAAAATTGGTGT TTTTGGGATTGGAGGTGCTGGTAATAACATTGTTGAT  
269351 GCATCACTTTATCACTATCCTAATTTAGCAAGTGAAAACATCCACTTTTA  
5 269401 TGCTATAAATTAGATT TACAACACCTTGCAATTTAAAACGAATGTTAAAA  
269451 ATAAACTCTTAATTCAAGACCATACTAACAAGGGCTTTGGAGCGGGGGGT  
269501 GATCCAGCTAAAGGAGCTAGTTTAGCAATAAGCTTTCAAGAACAGTTTAA  
10 269551 TACACTTACAGATGGGTATGATTTTTGTATCTTAGTTGCTGGATTTGGTA  
269601 AGGGTACTGGTACAGGTGCTACCCAGTTTTTAGCAAGATCTTAAAAACT  
269651 AAGAAGATCTTAAATGTTGCTATTGTTACCTATCCATCTTTAAACGAGGG  
269701 ATTAACAGTGAGAAACAAAGCCACTAAGGGGCTTGAAATTCTCAACAAAG  
15 269751 CAACTGATAGTTACATGCTATTTTGTAAATGAAAAATGTACAAATGGTATC  
269801 TACCAACTAGCAAACACAGAGATAGTCAGTGCCATTAAAAACCTAATAGA  
269851 ACTAATTACTATTCTTTGCAGCAAAACATTGATTTTGAAGATGTACGTG  
20 269901 CCTTTTTTCAAACCAAAAAAATAACCAAGATCAACAGCTTTTTACTGTT  
269951 ACTCACCCCTTTAGTTTTAGCTTTGATAGTAAAGATAGTATAGAACAGTT  
270001 TGCTAAACAGTTTAAGAACTTTGAAAAAGTTAGTTATTTTGACCACTCTA  
270051 TAGTAGGAGCTAAAAAGTGTTATTGAAAGCTAACATTAAACCAAAGATA  
25 270101 GTCAAGCTTAACTTCAAGCAGATCCAAGATATTATCTGAACATAAATTGA  
270151 CAACTACCAACTTGAGATTAGGTTAGGGGTTGATTTTGTGACAACCATCC  
270201 CTAATATCCAAATTTTTATCCTCAGTGAACACAAAAATCCAGTTTCGCTT  
270251 CCCATTGATAATAAATCAACTGAAAACAACCAAAATAAGTTGAACTTTT  
30 270301 AGATGAGCTGAAAGAAGTTGGCATGAAATATGTTAAGCACCAAAACCAAA  
270351 TCTACTAATTAATTTAATTTATCGTTTAGAATTGCTATCTTAAGCAATAG  
270401 TTTATGGGTCAAATCAATCGGAAGTTTAGCGAAAAGCAGTTCTTACTTTT  
35 270451 TGTTGTTAACTATATTGCTGGATTTGGCTTTATGCTACTGCTATCTCAC  
270501 TGTTTCGCTTAGGACCTTTTCTTGTTAATCTTCTGCTTGTTAGCTTA  
270551 GTTAGTTAATTGTTACCTTATCATTGCGACGGCTTTTATCAATAGATAG  
270601 TCAAACTATGGTGGGCCTTATCTTTGGGCTAAGAAAGCGGTTGATAAAG  
40 270651 AGAAGATAGCAGGGAGAATGTTTAGCTTTTTTACGGGGTGAAATAACTTT  
270701 ATCATTGGTCCTCTTTCAGCAGCAACTGCACCACTTTTTATCCTCAATTC  
270751 CTTTAGTGGTATTGATGGGATTAGAGGTAACCTAGTTAACACTTGAATCC  
45 270801 TAATTGCAATAGGTTTTTCTTTTTATGTATTACTAGCATTTATCTCAACC  
270851 AAAGGAACCTCACTAAACAAGAACTAATAGCACTATTTGCTTCAGTAAA  
270901 GTGGATTGTGATCCTCTCAGCACTAATAGTAGCAATCTATGTTATTGCTA  
270951 GAGATGGTAATGGTTATAGTCAAAACAATAACTTAGAAAGTGGTTTTTTT  
50 271001 GGGAGAAGAGAGATTAGTTTTGCACAGATAGCAACGGTATTTATTACCTT  
271051 CTTTTATTCTTATGCAGGGGTTGAAGATATCTCAGTGATGACTCCTGATG

271101 TTAAAACTAATAACTTTAGAAAAGATATTAATTGTCTCTTTTATAGCAGTT  
271151 TTCCTCTTTTATTTTCATTGGGATTATTATTCTAAATGGTTTGCAAAACAT  
5 271201 TGCTCAAAGAGGTGGGGAAGCCAATTCAATTGGTAATGTAGCGGATATCT  
271251 TTAAAAAAGCTGCTGGGCTTGGGACTTTAATCTTTTATGGAGTTGGAGCA  
271301 TTGTTTAAACAATGTCTCAACCAGACTTTCAACTATTATTGCCAACTCCAG  
10 271351 AAAGATTCTTCCGCTTGCTTATGATAACTATTTACCTAGTTTCTTTTACA  
271401 AGCAAAACAAAAAAGGTGAGTTTCAGAATGCAATTTGGTTTACCTTTGGT  
271451 ACTACTTTAATTGCAATGACTTTGCTTGTCTTTATCCCTTTAGTTGCTTC  
271501 TAACTTTGATTTTGATAATGCTACTGAGTATGCAGCATCTGTTGGCTCAG  
15 271551 CTGCAACTTTGCTACAATATATTTTTGTCTTTTTTATAATCTTTAAGTTT  
271601 ATCTATAAAAAAGAACCCTCTACCAGAAAAAATGGGTTAAAACAACTGA  
271651 AGAATTATTGTTTTGTTTAGGAACAATTGTCATTGTTTTAATGTTGTTGG  
271701 TTTATCTGTTTCTGTTATAGATGGATTTTCAAATGGGAACTAAACAC  
20 271751 ACATTAACAATTGTGTTATATGGGGTTTTAAGCCTGATAGGATTGGTACT  
271801 TTTTTTGCTCCAAGAATACAAACATAAAAAAAGCAAAATGCAACAAAC  
271851 AAACAACCCAAACAACAGTTTAGTGAAAAGCAATTCATTGCTTTTGTCTT  
25 271901 TAACTATATTGCTGGATTTGGCTTTATATCAGTGGTGATGACCATGTTTG  
271951 ATGTTGGGCCATTTTCTATCTTGTTTTAGGGTTAACTTCGTTTGCTATT  
272001 TTAGGAGTTGTGCTTTCTTTTCTCGCCTTTCAGTTCTCTGTGGTAATAG  
272051 TGCTTATGGAGGGAGTTATTTAATTGCTAAAAAGCAGTTGGTACTAACA  
30 272101 GTAAAAACAAAAAGGTTTTTTTGTTTTTTTAAGTGGGTGGAATGTATCGTTA  
272151 ACAGGATCTTTTAACGGTGTTGTTATTCCAGCAGTATTAATCTTTTCCTT  
272201 TGCAGATATTCCAGTAGTTAAAGCGAATAATAACATCATTATTGGCCTTT  
35 272251 TAGTAGGTGGGTTTTTGTGTTTGGCTTACTTACTTTTATCTCGTTATTT  
272301 GGTTTAAAAATTAAACAAGAAAGCAATCTTTTATTTTGCTGTTATTAAGTG  
272351 GATAGTAGTAATAGGTGGGTTTATCTTAGGGATCTATTTAATTGGTACTA  
272401 CCAATGGTAAAGGTTTTGTTGAAAACAATTTAATTGGGACTAGGGAAAAC  
40 272451 ATTGATTTTTTCAAGATTATCTTTATTAGTCTGGCTTTAACCATTGCTTT  
272501 TGCAGGGACAGAGGATTTAGCTTCGATTACTCCTGATGTCAAGTCAAATA  
272551 ACTTAAGAAAGTGTTTTTTAATTGCCTTTGGGTGTGTTGTGTTACTTTAC  
45 272601 CTAGTTGGGTTTGTATTATCAGTGGACTTGATGGGATTAGAGGTTATGG  
272651 ATTAGCATTAGGTAATAAAGATCCCAAGGCAATTAATAACTATGGATCTA  
272701 TCTACCGTTTGGTAGGAGGAGTTCCTTTACTTGTATCTATGGACTGGG  
272751 TTACTTGTCAAATTCCTTAGCATCACGCCTATCAATGACAATTACAACAGC  
50 272801 TAGAAAATATGTAGCTTTAGCTCAAGATGGGTTTTTACCCTCTTTTTTAG  
272851 CAAAACTAATAAACATAATGAGTATCATCATGCAGTTTAAATTAGTAAT

272901 CTAATGACTTTATTAGTGATGCTAATTATGGTAATAATCCCCTTTTTACC  
272951 AGACCATAACAACAATAACAATAGTTTGTTTAATGCTATTGAACAGTTGG  
273001 TTACAGTTACCATTTGAAATGGCTGCAGCCATTTCTTTGATCCAATACTTT  
273051 ATTACCTTTATCTTCTTTTTTATGATCTTTGCTAAAAAGGAAAACCAGAA  
273101 GTTAATTCCCTTGTGAGAAAAGGTTAGTTATGTAATTAGCTTTGCTTTGG  
273151 TAAGTGTGTTGTTGTTGTACCCTTTTCCCTTTTAATCAGTGAACAGTG  
273201 TTTAACACCTTTAAGATAGTTGTTCTAATTTGTTTTTATCTACTTGGTGT  
273251 TGGTTTTTTTTGGTTATGCTGAATGGAAAAATAAAAACAAATACCAATTAA  
273301 TGAATAACAATAGCTAATCTACAGTTCATTAAGCGAAATTGCTTTTGAAT  
273351 CGGCAACAACAACCCCTTCTCCAACCTCCCCCTCCCCTTCAACTTCCGCTT  
273401 CCTCTTCTACCCCCCTCCCCACTTTTTCTAACATCAATGTTGGGGTTAAA  
273451 TCAATGATCACTCAACATTTTAAATAAAGAAAACACCCGGTGGGTGTTTTAT  
273501 ACCTAACTTTTACCTGACATCTGAACAGGAGCAGGGTATCGCAAACAAG  
273551 GTAACAATAATGGCATCTCCTTGACCAGGTGAAACCTAGTAGTAGTAGCA  
273601 ACACGTTTAAATCCCAATTCTTCTGATAATAAAGTCACTCAAGGTGGTGGC  
273651 TCCCCAGCCAAAAAACAACCACCTATCCTGCTTTACCAAACCTCCATCAG  
273701 TCCCACCAGTGACTGTTAAAATGTTTATTAAAAAACAAAATAAAAAGCG  
273751 GTTTTATACAATGTATAACCTGTCTAAAAGACAATTTTATGAAACAGTAT  
273801 TTAGATTTAGCTAGTTATGTTTTAGCAAATGGTAAAAAAGAAAAAACCG  
273851 TACAGATACAGATACTTTAAGTGTCTTTGGTTACCAGATGAAATTTGACC  
273901 TTACTAATAGTTTTCCTTTATTGACAACTAAAAGGTTAATTGGAAGGCA  
273951 ATTGTCCATGAATTGTTGTGATTTATTAAGGGTGATACCAACATTAAGTA  
274001 CTTAGTTGATAATGGGGTGAACATCTGAAATGAATGACCATATGAAAAC  
274051 TTAAAAAATCACCAAGTTTTTCAAACGAAACACTCCAAGAATTTATCTTA  
274101 AAGGTTAAAACCTGATAATGAGTTTGCTAAACAATTTGCTGATTTGGGTCC  
274151 TGTTTATGGCAAGCAATGACGTAATTTTAATGGTGTGATCAACTCAAAA  
274201 AAGTCATCCAAGAGATTAAAGAAAATCCCAACTCAAGAAGGCTAATTGTC  
274251 TCAAGCTGAAACCTAGTGAATTGGAAAAAATGGCATTGGCTCCTTGTC  
274301 TTCCTCTTTCAGTTCTATGTTGAAGAAGATAAACTAAGCTTACAGCTTT  
274351 ACCAGCGCAGCGGTGATATCTTCTTGGTGTCCCATTTAACATTGCATCT  
274401 TACGCCTTACTTGTGTATTTAGTTGCTCATGAACTAAGTTAAAACCTGG  
274451 TTATTTTATCCATACACTAGGAGATGCACATATCTATGAAAACCACATTG  
274501 AACAAATTAAATTACAACATAACAAGAACAACCCTAGACCCCCCTCAAGTG  
274551 GTTTTGAAAAGTGATAAATCAATCTTTGCTTATAGTTTTGATGATATTGA  
274601 GTTAGTTGGTTATAATTACCATCCATTTATCTATGGGAGGGTTGCAGTTT  
274651 AATGCTAATTGCTATCTGAGCGATGACACAAGAAGGACTAATAGGTAATA

274701 ACAACACTTTACCTTGGATGATTAAACAAGAGCTAGCTCACTTTAAAAAA  
274751 ACTACGTTATTTCAAGCTTTGTTAATGGGGAGAAAACTTACGAATCACT  
5 274801 CCCCAGGTATTTGAAAAAGAACAATTTCTCCTTTCAAAGATCAAA  
274851 ACTACCGTTTTGAAGAAAAGGGAAGTGAAGTGAAAGTTATTAATGATTTT  
274901 TGACCACTAATTAAGTTACCAAGCAAATAAAGAAAAGGATTTGTTTAT  
10 274951 TTGTGGTGGAAAAAGTGTGTATGAACAGACCATTAATGAATGTGATCAGT  
275001 TAATTGTTTCAATCATTAAAAAGAAGTATAAGGGTGATCAGTTTTTGAAG  
275051 GTTGATCTCAGTAAATTTGTACTTAATGAAGTTGTAGAGTTTGAGGAATT  
275101 TAATGTTAATTATTATAGAAAGAAACAACAATAAGAGATATGGCAGCTAA  
15 275151 CAATAAAAAGTACTTTTTAGAATCATTTTCCCCACTTGGGTATGTAAAGA  
275201 ATAATTTTCAGGGCACTTACGTTCTGTAAACTGGAATTTGGTTGATGAT  
275251 GAGAAGGATTTGGAAGTGTGAAACAGGATTGTTTCAGAACTTTTGGTTACC  
275301 TGAAAAGATCCCTGTATCCAATGACATCCCCTCATGAAAGAACTCTCAA  
20 275351 AGGATTGACAGGATCTGATCACTAAGACCTTACTGGTTTAACACTACTT  
275401 GATACTATCCAAGCTACCATTTGGTGACATCTGTCAAATTGATCATGCTCT  
275451 AACTGATCATGAGCAGGTTATTTATGCAAACCTTGCTTTTATGGTAGGGG  
25 275501 TACATGCCCGTTCCTATGGAACGATCTTCTCAACTTTATGTACATCAGAA  
275551 CAGATTAACGCTGCTCATGAGTGGGTTGTAAACACTGAAAGTCTCCAGAA  
275601 AAGAGCAAAGGCATTAATCCCTTACTATACGGGCAATGACCCGTTAAAT  
275651 CAAAGGTAGCAGCAGCTTTAATGCCTGGGTTTTTACTGTATGGTGGGTTT  
30 275701 TATTTGCCTTTTTACTTGTTCATCAAGAAAACAACTACCAAATACATCTGA  
275751 TATTATCCGCTTAATCCTTCGTGATAAAGTGATCCATAACTATTACAGTG  
275801 GTTATAAATACCAACGTAAACTAGAAAACTCCCTTTAGCAAAACAAAAG  
35 275851 GAGATGAAAGCATTTGTTTTTGAACATAATGTATCGGTAAATTGAACCTGA  
275901 AAAGGACTATTTAAAGAGCTTTATGAAGGGTTTGAATTGTTGATGATG  
275951 CCATTAAGTTCAGTGTTTACAATGCTGGTAAGTTTTTACAGAACTTAGGT  
276001 TATGACTCCCCGTTTACTGCAGCAGAAACCAGGATTAAACCAGAGATTTT  
40 276051 TGCCCAACTATCAGCACGTGCTGATGAAAACCATGACTTTTTCTCAGGAA  
276101 ACGGTTTCGTGATGTGATGGGAGTTAGTGAAGAGACAAATGATGATGAT  
276151 TGGAACTTTTAAGTTATGCATAAAGATATCAAACCTAGTTAAGGAACTGA  
45 276201 AATTAGAAAACCAATTGGTTCTCCTTTTATTGTCTATTTTTCATCTATCT  
276251 CCAACAACACCCACCGTTTTATTGAAAACTGGGTTTTCAACACAAAAGA  
276301 ATCCCAGTTGATATAACCCAAAGCATTACTGTAAGTAATGAGTATGTTTT  
276351 AATCTGTCCAACCTTATAGTGGTGGGGTAACCAGGTTGAAGGAGCGGTAC  
50 276401 CCAAGCAAGTTATCCAGTTTTTAAATAACAAGCATAACAGGGAGTTATGC  
276451 AGAGGAGTTATTGCATCTGGTAACACTAATTTTGGAGATACTTTTTGTCT

276501 TGCAGGAACTGTTATTTCCAAAAAACTAAACGTCCCTTTGTTGTATCAGT  
276551 TTGAACCTTTTGGGAACAAAAAATGATGTAGAACAACCCAAAAAATAATT  
276601 GCCAATTTCTTTCAAAACAGCAACTAGTATTTATAGTTATCCACTATGAC  
276651 ATCCAAAGAAAAAATCCCTACTTTTAACTGAAGAAGATGTTGAAAGTT  
276701 ACATTTCTTTTAATGCCCAAGCCAAAATCTATGATGATTTTGCAATCGAT  
276751 TTACAAGCAGTTGAAAGCTATATTCAAGAGCATGTAAAACCCAAAACTAA  
276801 GGTCTTTCATTCCACCAAGAACGCCTTGATTTTCTGATTAAGAACGATT  
276851 ATTATGATGAGAAGATCATCAACATGTACAGTTTTGAACAGTTTGAAGAG  
276901 ATCACCATAAAGCATATTCATACCGCTTTCGTTATGCTAACTTCATGGG  
276951 AGCATTTAAGTTCATAATGCCTATGCTTTAAAGACATTTGATGGTAAGT  
277001 ACTACTTGGAAACTATGAGGATAGGGTGGTGATGAATGTATTGATGTTA  
277051 GCTAATGGTAACCTCAATAAGGCATTAAACTCTTAAACAGATTATCCT  
277101 TAACCGTTTTCAACCAGCAACCCCTACCTTCTTAATGCTGGTAGAAAGA  
277151 AACGTGGTGAATTTGTTTCATGTTACCTGTTAAGGATTGAAGATAACATG  
277201 GAATCAATAGGTAGAGCGATAACAACACTACACTACAACATCAAAACGTGA  
277251 TGGGGGAGTAGCACTTTTGCTTTCCAACCTTACGTGAAGCGGGAGCGCCCA  
277301 TCAAAAAGATAGAAAACCAATCATCAGGGATTATCCCAATTATGAAATTG  
277351 TTAGAGGACTCTTTTTCTATTCCAACCACTTGGACAAAGACAAGGAGC  
277401 GGGAGCGGTGTATCTCCATTGTCAACCATCCTGATGTTATGCAGTTTTTAG  
277451 ATACTAAAAGGGAAAATGCTGATGAGAAGATCAGAATTAAATCACTCTCC  
277501 TTAGGACTTGTGATTCCAGATATCACCTTCCAATTAGCAAAAAATAACGA  
277551 GATGATGGCACTTTTCAGTCCATATGATATCTATCAGGAGTATGGTAAGG  
277601 CTTTATCTGATATCTCAGTAACTGAGATGTATTATGAATTGCTTGAAAAC  
277651 CAACGCATTAAAAAGACCTTTATTAGTGCTAGAAAGTTCTTTCAAACAAT  
277701 TGCTGAACTCCACTTTGAAAGTGGTTATCCCTACATCTTGTTTGATGATA  
277751 CAGTTAACAGGAGAAATGCCCAAAAAACAGGATAGTAATGTCTAACCTT  
277801 TGCAGTGAAATTGTCCAACCATCTTTACCTTCTGAATTCTATTCAGACCT  
277851 TACTTTTAAAAAGGTAGGTAGTGATATTAGCTGTAACCTGGGGAGTTTAA  
277901 ATATTGCTAGAGCAATGGAAAGTGGTAGTGAGTTAGCTGAATTGATTCAA  
277951 CTAGCAATTGAATCACTGGATTTAGTGTCAAGGATCAGTAGTTTAGAAAC  
278001 CGCTCCTTCCATTAAAAAAGGTAATTCAGAAAACCATGCGTTGGGATTAG  
278051 GAGCGATGAACTTACATGGATTTTGTAGCAACAAATGCTATCTATTATGAT  
278101 TCAAAGGAAGCGGTTGATTTTACTAACATCTTTTTTTATACAGTAGCATA  
278151 CCATGCGTTTAGTGCTTCCAATAAATTAGCATTGGAAC TAGGTAAATTTA  
278201 AAGACTTTGAAAATACTAAATTTGCTGATGGTAGTTACTTTGATAAGTAC  
278251 ACTAAGGTAGCTAGTGACTTTTGAACATGTAAAACAGAAAAAGTTCAAGC

278301 CCTTTTGTATAAATACCAAGTAAAAATTCCTCACTCAGGAAAATTGGAAGC  
278351 AATTGGTAGCAAGTATCCAAAAAGATGGACTTGCAAACCTCCCATTTAATG  
5 278401 GCTATTGCCCCAACTGGATCTATCTCATATCTCTCTTCATGTACCCCTTC  
278451 ACTTCAACCAGTAGTATCTCCTGTTGAAGTGAGAAAAGAAGGGAAGTTAG  
278501 GACGGATTTATGTCCCTGCTTATAAGCTTGATAATGATAACTATCAGTAC  
10 278551 TTTAAAGATGGTGCTTATGAACTGGGCTTTGAACCTATTATTAACATAGT  
278601 AGCAGCAGCCCAACAACATGTTGATCAAGCAATCTCTTTAACCTTGTTTA  
278651 TGACTGATAAAGCTACCACCAGAGATCTCAATAAAGCTTATATTTATGCT  
278701 TTTAAAAGGGTTGTAGTTCTATCTATTATGTCAGAGTAAGACAAGATGT  
15 278751 TTTAAAAGATAGTGAAGATCACACTATTAAATCAAGGATTGTGAGGTTT  
278801 GTTCTATCTAACTATTAAAGCAGTTAGAATTTGTTAGAATTACTTGTTTT  
278851 AAAACTATCTTAATCCCTAATATATAAATTAGAAAGGCAACGGTTTTGAG  
20 278901 AAGATGCATGCTATTGTGGTTTGTGGTGCTAAGCAGTATTTAGTCCATGA  
278951 AAACGAGTCTATTTTTGTGAAAAATTAGCTGGTAAAGTTGGTCAGGAGA  
279001 TCCAACCTTGATAAGGTATTGATGCTTGATGAAAAGATAGGCAAACCTTAC  
279051 CTTGAAAAAGCTAAGGTTGTTTGTGTGATTGAAAAACACGGTTTAAATC  
25 279101 GAAATTAATACTAATTAACACATCTCCCAAAAACACCACCTCAAGCGTT  
279151 ATGGCCACCGTCAACCCTACACCAAATAAAAGTGGTACGCTTTATCCAT  
279201 GATTAAGATTAATATCTCCCAAACTTTCTAGTTGCAAAAGGTCATGCTT  
279251 TGTTTGCTGAGAAGGGTAAGGACATAGTTTGTGCTGCAATTAGTGGAATT  
30 279301 ATCTTTGGGGGGGTGGCTTGGTTTGAACCTGATAAGATTGAATTTACTGA  
279351 AAATAAATTAGTACCTAGTATAGCACTGAACTCATTGACCCAACCCCTA  
279401 ATGTAGCAGTTGCTTTTAGTGTTATTACAGTACAATTAAAAGCAATAGCC  
35 279451 AATTCCTATCCTAATCACATAGTTATCAATGAAGAGAGTTATGAGTAAAA  
279501 ACAGTTACTGCTACCAAATTAACCTTACAGTTTTTCGCTTCCAAAAAGGG  
279551 GTTGGTTCCACTAAGAATGGACGTGATTACATTCTAAGCGCTTGGGCGC  
279601 TAAGAAGGCAGATGGTCAGATGATTAGAGTTGGTCAGATTATCTATAGAC  
40 279651 AAAGGGGAATAAGATCTTTCAGGACAAAATGTTGCAATGGGTAGTGAT  
279701 AACACCCTCTTTGCTTTGAGCGATGGCATTGTCCGCTTTCAAAGTTTGG  
279751 TAGTAAACAAAGCAAAACCCGGGTTAACATCATCAAACACCAACTAAATG  
45 279801 CCTAAGCTACTGGGTAGCTTTATTAGCTTTAAAGCCCCAATTACTTTGT  
279851 TCAAAGTGCTCAGGATGCAATTGCTATTGATGCAACTGCTCTAATGGTAT  
279901 TTTTAGGTCCACCCCATTTCTGCTTACCGTGTTCTTTTTACAAGATGCAG  
279951 TTTAGTTTGGGCTATGAGTTGTTAAAAACAAAGAATATTAATAGTAATGG  
50 280001 TTTGGTTGTTTCATGCTCCATATATCATTAACTGTGCATCAAAGACCCAC  
280051 TAAAACAGCAGAATGCTATCAGTGTTTTTAACCAATGAGATTACAGCTTTGT



280101 AACTTGGCTGGTGCTCACTATTTAGTTTTGCATCCAGGTTCTGCAGTAGC  
280151 CCAAACAACCAACGAAGCATTAGATAACCTGGTTAAAGTACTCAATCAAG  
5 280201 TTATCAATAAAACCAAAACAACAGTTATTTGCCTTGAAACAATGGCTGGT  
280251 AAGGGTAATGAGATAGGCAGAGACTTAACTGAGTTGAAATATGTTATTGA  
280301 CAGGATCGTTGATAAAGATAGGATCGGGGTTTGTCTTGATACCTGTCACCT  
10 280351 TCCATGATAGTGGGATTGACTTTAGTGATCTAACTGGTGTTTTTAACACC  
280401 ATTACAACATAAAGTTGGTTTTGAGTTTCTCAAAGTAATCCATTTAAATGA  
280451 ATCTAAAAATAATTGTGGTTCTAAAAAAGATAGGCATGCTAATATCAATG  
280501 CTGGGATGATTGGTTTTGAGAACTTAATGAAGTTCATTAGTCACCCCCAA  
15 280551 ATTAAGGATTTACCTATTATCTTAGAAAACCCCTTCACTAGTTTAAACTA  
280601 CCCAACTATTTACCGTGAAGAGATTAGTCAAATCCGCAGCTGATTTAAAA  
280651 CTTACCAACCAGATGCTAACTAGTTATGTGAAGGTATTAGAACAAAACAA  
20 280701 TCTGCGCTTAACAAAACCGCGGATTGCTTTATTAAAGTGTTTAATTGAAC  
280751 ACCAAGATTGGCATAATCTCTCCCAAATTAACCCACCTTGATTTAGCC  
280801 AATCAACCTCAACACTCGCTTCTATCTACAACAACTTAAGAATCCTAGC  
280851 TAAACTTAACTGATTAACATCTTTGTAGATCCAGAGCGGTTTGAACTT  
25 280901 ACTATTGCCTGCGCCATGCAGAGCATAACCATATCTATCTTTTGTAGAA  
280951 GTTAAACAGCAGTTTTTTACCTTACCTTTAACAGATGGCCAAATTA AAC  
281001 ATTGCTTGAAACCCAAAACCATAACCAGTAAGGTAAAGCTTAATGATTTTT  
281051 ATATTGTTGCTAGGGGTGAGATAAACAATGATTAACAAACCAACCAATT  
30 281101 TTTAAACCACCTTGATGGCTTAAAGCAACATTTTTCTGATTATGATTAC  
281151 TACAAAAATCCTTTAAGAAATATCTATCAGAAAATCAAACCTGAACTTAAC  
281201 AATTTCTTTTTTAACCAGTTTGAAAAGATCATTGTTCTGGTCAAAAAAA  
35 281251 GGAGTTTAAACTGCTCAAGAGAGGTGTGAAGAGGAGTTAGCTACCCCTT  
281301 ATTTTTCAAAGCCATTGGTTGGTTTTTTCCAATCACTATTACAACATAAT  
281351 AACCATGATCTCATCGAACAGAAAAACCAACAGTTAGCTAACATGAGTTG  
281401 TGAAAAAATTGTGGAGATGGTGTAAAGTGATTACCCCAATAAACTTAACT  
40 281451 TAATCCACTATTTGTTAGCAAAAGAAGCGAGTTTTGTAAACCCTAACCTT  
281501 TTACAGCGGATGACTTTTGTGTTAACTGATCTTGAACGTGTAGAGTTAAA  
281551 GCGTTTCTCTTTTTTTAAAGCCCTTAACCAGATACCTGCTTTTAAAAACC  
45 281601 ACAAAGTAACATACTTTAACAGCAAACTCAAACAGAAGTTTGTAATAACA  
281651 TTAGGTGAATTTGCTTTCCCCCAAACCTGATAAAACCAACAGTTTTTCCA  
281701 ACAACTAATTAAAAAAGTAAGTCAACTGTTTTTAAAAAGAACCTGTTAGTT  
281751 GTGAATTTGCTTATGAAATTATTGATGCATTACTCGTCAGTTTTTTTTCCA  
50 281801 CTCCATCCTAATTTAGAAGTAAACCACTTAGCTAAAAAGATCCACCAGTA  
281851 TGTTAGTAAGATTGTCATTAATGAAGTTGTTGATCTGAAAGATCCAACCA

281901 CTAAACTAATTGTTGATACACTTTATGAACAGTTAGATAGAGCAATTGGT  
281951 GAGGAAAATTAAAATTAAGTTAGCACTAGTAGATACAAAAGATGAAGTTA  
5 282001 TACAAAGTTCTTAACAGTAAAACAACTGATAAAAGTCTTTGTTTGGAAGT  
282051 TGAGATTGATCCAAATTACTGACAAGCTACCCAAAAAACTAGTAGGTG  
282101 AAATGGCTAAATCGATAAAAAATTAAGGGTTTTTCGTCCCGGTAAATCCCC  
10 282151 CCTAATTTAGCCAGTCAGTCGATTAATAAAGCTGAATTAATGCAAAAAG  
282201 TGCCCAAAACGTCATGAACAGTATTTATGAATCAGTTCAACAAGAAGAGA  
282251 TCGTTGCTAGTAATGATAATGTCATTGATGATTATCCTACCATTGATTTT  
282301 AAAACGATCACTGAACAAACTGTGTACTTTTGTTTTACTTTGATCTGAT  
15 282351 CCCTAATTTCAACTCCCTGATTACAAAAGATAAAAGATTTAACACCAC  
282401 TTACCAAGTTAACTGAAGCTGAATTTAACAACGAAATTGAAAAGCTGGCA  
282451 AAAACTAAAAGCACAATGGTAGATGTTAGTGATAAAAACTAGCTAATGG  
20 282501 TGATATTGCTATCATTGATTTCACTGGGATAGTTGATAACAAAACTAG  
282551 CATCAGCTTCAGCACAAAACATGAATTGACAATTGGTTCAAATAGCTTT  
282601 ATTAAGGGTTTTGAAACCGGGTTAATAGCAATGAAAGTTAACCAGAAAAA  
282651 AACTTTAGCACTAACTTTTCCTAGTGATTATCATGTTAAGGAGTTGCAAT  
25 282701 CAAAACCAGTTACATTTGAAGTAGTTTTAAAAGCAATTAAAAAACTGGAA  
282751 TTCACCCCAATGGATGAAACTAATTTCAAATCCTTTCTCCCTGAACAATT  
282801 CCAAAGCTTTACTTCTCTAAAGGCATTTAAGAGTTATTTTCATAAGCTAA  
282851 TGGAAAACAAAAACAAGAGACAATTCTCCAGGAGAATAACCAAAAAAATT  
30 282901 CGTCAGTTCTTACTTACTAATACCAAACCTCCTTTTCTCCAGAAGCGTT  
282951 AATTAAACTAGAAAGCTAACCGCTTGTTAAAGCTCCAGCAAAGCCAAGCTG  
283001 AACAAATATAAAATCCCTTTGAAAACTCTTAAGTGCTTCTAATATCACC  
35 283051 CTAACAGAGTTACAAGATCGCAACATAAAAGAAGCTAAGGAAAATGTTAC  
283101 CTTTGCTTTGGTAAATGAAAAAGATAGCTGACATTGAAAAGATTAAGGTTG  
283151 ATAATAACAAGATTAAAGCTGAAATTGAAATGTTATTGCTGTTGAATAT  
283201 CCCTTTGCTAGTGATGAAATGAAAAACAACCTCTTTTAAATATGGAACA  
40 283251 ACAAAGGAGTTTGTGGAATCAATTATCATCAACAGATTAACAACAACCTA  
283301 AAATCGTTAGCTATTCAACTCATTAGCACTCAAAGCTTGAGTGCTAAG  
283351 AAATGTGTTAAATTTATTGAAATTCCTAATTAACCTTTAAATATGCCC  
45 283401 GTTACGAAGAAAAGTCAGATCTTAGTAGTTAGAGGTCAAGTCATTTTCC  
283451 TTTTGTCCCTTTAGTTTGGATGTTGGCAGGCCCGTTTCGCGTAAGATCA  
283501 TCAAAGCGCTTAAACTCTGAAAACCAAACGTTTGGTTTTAGTAACCCAA  
283551 AAGTTTACTGGTGAACAAAACCTGAGTTTAATGACATCTATCATGTCCG  
50 283601 TACACTCTGTGAGATTGATGAGATAGTTGATGTTCCAGGGTTGATAGTA  
283651 AAACAGTAGACTACCGTATTAAAGGCAGAGGTTTACAACGGGTTTTAATT

283701 GAAAAATTCTCAGATGCAGATATTAATGAAGTTAGTTACCAATTACTTAA  
283751 CTCCACAGTTAAAGATGAAGCTAATGTTGACAGGTTCTTACAGCGAATCT  
283801 TTCCTGAAAAAGAAGAAATTGAACAGTTAATGGAAGGAGCTGAGAAGTTT  
283851 TTAGAACTTGAAAACATCAGCAAAACAGTTAATGTTCTAAGGGTTTAAA  
283901 GCAACTTGATATTATCACCTTTAAACTGGCTAATCTTGTCCCTAACACTG  
283951 AAAGTATTAAACAAGCTATCTTAGAGGAAAATGAGATAGCAAACCGATTG  
284001 GAAAAGATTATCCAAGCAGGGATTGAAGATTTACAGAAGATCCAAGATTA  
284051 TGGTAGATCTAAAAACAAGGAACTGAGTTTGATAAACTTGACAGTAAAA  
284101 TTACCCGCAAAATTAACGAACAACCTCTCAAGACAACAACGTGATTTCTAT  
284151 CTTCTGAAAAGCTAAGAATTATCCGTGAAGAGATAGGGATTAGTTCCAA  
284201 AAAAGAGGATGAAGTTGCTAGTATTAGAAAGAACTGGATGAAAACCTT  
284251 ACCCTGAAGCCATTAAAAAACGGATTTAAGTGAACCTGAACTATGAA  
284301 AACTCTTCCTCCTCTTCCCAAGAATCAACCTTAACCAAACTTACATTGA  
284351 TACGCTTTTAAACCTGCCTTGATGACAAAAGAGCAAAGATAACAGTGATG  
284401 TTAAAACTTAATTAAGACGTTAGATAAAAACCACACTGGTTTAGATAAG  
284451 GTTAAAGAAAGGATTGTTGAGTATTTAGCAGTACAATAAGAACCCAAAA  
284501 AAACAAAGGTCCTATTATGTGTTTAGTAGGTCTCTGGGGTTGGTAAAT  
284551 CAAGTCTAGCTAAGTCTATTGCAGAAGCATTAGATAAGAAGTTTGTCAAG  
284601 ATCTCATTAGGGGGAGTACATGATGAATCGGAAATCAGAGGTCACCGTAA  
284651 AACTTACTTAGGTTCTATGCCAGGAAGGATTTTGAAAGGGATGACCCGTG  
284701 CTAAGGTAATTAATCCCCCTCTTTTACTTGATGAAATGATAAGATGACC  
284751 TCCTCCAACCAAGGTTATCCTTCAGGTGCTTTACTTGAAGTATTAGATCC  
284801 AGAGTTAAATAATAAGTTTAGTGATAACTATGTTGAAGAAGATTATGATC  
284851 TTTCTAAAGTAATGTTTATCGCTACTGCAAACTACATAGAAGATATCCCT  
284901 GAAGCTTTACTTGATAGGATGGAGATAATTGAACTCACTTCTATACAGA  
284951 ACAAGAGAAGATTGAGATAGCAAAAAACCACTTAATTAAGCGTTGCCTTG  
285001 AGGATGCTGATCTTAACAGTGAAGAATTGAAGTTCACTGATGAAGCAATC  
285051 AGCTACATCATTAAAGTTTACACAAGAGAAGCGGGGGTTAGACAATTAGA  
285101 ACGATTAATCCAACAAGTTGTAAGAAAGTACATAGTAGCAATGCAAAAAG  
285151 ATGGCATCAAACAAGAAACGATTGATGTAAACGCTGTAAAAAATACCTT  
285201 AAGAAGGAGATCTTTGATCACACTATGCGTGATGAAGTGTCTCTACCTGG  
285251 AATTGTCAACGGGATGGCATAACCCCCAACTGGAGGGGACTTACTTCCCA  
285301 TAGAAGTTACCCATGTTGCTGGTAAAGGAGAGTTGATCTTAACTGGTAAT  
285351 TTAAAGCAAACAATGCGAGAAAGCGCTAATGTTGCTTTAGGCTATGTAAA  
285401 AGCTAATGCAGAGCGTTTTAACATTAATCCTAGTTTGTTTAAAAAGATTG  
285451 ATATTAACATCCATGTTCCAGGTGGGGGAATTCCTAAGGATGGACCTAGT

285501 GCTGGTGTCTGCTTTGGTAACTGCAATCATCTCATCATTAACTGGTAAGAA  
285551 AGTAGATCCTACAGTGGCTATGACAGGAGAGATCACTTTAAGAGGCAAAG  
5 285601 TGTTGGTTATTGGTGGGGTGAAAGAAAAAACTATCTCAGCTTACCGCGGT  
285651 GGGGTTACAACATCTTTATGCCTGAGAAAAACGAGCGCTATTTAGATGA  
285701 AGTACCCAAAGAGATAGTAGATAAACTTAACATTATCTTTGTTAAGGAAT  
10 285751 ACAGTGATATCTACAACAAGCTTTTCAGTTAGTCTTTAACTAGGTTTTGG  
285801 ACATATTTTAAGGTAATTAAATAGGCCTGTTTTAAGTTGCTTTTAGCTAG  
285851 TTTTACTAGTTGATCAATCTCAATCCCCCACTCCACTGTTCTGTTTAC  
285901 GGTTAGGTTCTAGTTTATCTGCTAAATAAACAATCATATCTAGCTTGCTA  
15 285951 ACTTGTTTTGGTGGGATGGTGTGGTTTTTGATGGCATTAAATAATCATTTT  
286001 ATCTTTAACACCAAATCAGTTTTTTAAGATATAAGCCCCACATAGCTAT  
286051 GTAATACTTTTCAACTTGGGTAGTTAGTTATCTTCAGTTCAGTAGTTGCA  
286101 ATGTTAACTAACTGATCAACTGGTAGTTGTTTGGCCAAGTCATGATAAGC  
20 286151 CCCAGCAACAAATGCTCTTTTAGCATCTAGTTTGTTGCAATTGCTAGTT  
286201 GTTTTGCTAGTTTACCAACCCCTAAACAGTGTTGAAACCTCTTATCATCA  
286251 ACCATTGCTTTTAAAGTGGGAATTAGATAGAGGTGATTGGTATTGATGTA  
25 286301 ATTTAAACTGCCAGTGGTATCAGTTTTTTCTAGTTGATTTAAAGTT  
286351 TACTTGAAGCGATTTCAAGTGGGCATTTAGCCAAGTATTTAACATTAAAT  
286401 TGGTTTGCTATTTTTTTTATTAAGGATAAGGTTTTCGTTCATAACAAAC  
286451 AAACGTGCACAAATCTTTTAACTGTTGGATGTGATCTCACTTCTCAAGTT  
30 286501 CATTTAATTTATCACTCCCTATTAAAAAATAGATTTCACTAGTTGGATAA  
286551 CAACTTTTAAAGTGGTTAACAGTATTAATTGAAAAAGCGTTTTTAGTTTT  
286601 AATATCAAAATTGGAACTAAAGCATTGTTGACTGATTTAATTGCTAGCT  
35 286651 TTAACATAGCAATCCTATCCTTATTACTAGCATGAAAATTATTTTTAAAA  
286701 ATACCATTGTAAGTTGGTACAAAAAAAGCTTTTGCGCTTTTATTTTTTT  
286751 AATTGCATGTTTAGCAATGTAGAGATGGGCATTGTGAATAGGGTCAAAAG  
286801 AACCACCAAGATAATAATTTTTTGCTTCAAAAAAGATCTTAAACATTT  
40 286851 AATTCTAACTAAAATAATTGTGACACAAGAGCAATGATCCAAAAGGAGAT  
286901 GGAGATCTATAACCTCTTTACTTTTTCAAATTGATCTTGATAAAAACTGT  
286951 TGTTTGAAAAATCAAATGATCAGAAGAATTATCCAAGATTAGAACCCAT  
45 287001 TATTTCAAGCATAAATTCAAAAAATAAAGTGCTGTTTTTCTCAATAAAAA  
287051 CCTGATTAAAAATAGCTTAAATAAGGTTCTTTTAACTTTTCTGATTTTG  
287101 TTAGTGGTGCTGGAATTGATACAGTTTTTAAACCAATCATTGATGAAGAT  
287151 CCTGAGGTTTTTAACTATTTAAAGCAAGTTAAAAAGATCTTCCAAAGA  
50 287201 AAACAACGCTACATCCCACTAACCTTTAATGTAATTTAACCTTAAAA  
287251 ACACCCTCGCCAATTTTTTTGAAGGATTTAATATTTATCTCCATTTTAAT

287301 GAAGAAAACAATACAGTGATAGGTAGTTTCTCACTACAATGACACATCAA  
287351 AAAAAGTCTGATCTGTTTTCTGAAACAAAAAACATTGCCATTAACAATTTAA  
287401 TTCACACTTTTTGTGAAGAACAACATGCATGAAATTAGTTTTATGCAGATC  
287451 ATTAATTGTTTTTCCAAAAACAAAAATTAATAAACATGGTGAAATTGTTTT  
287501 AAAAAGTTGTGCTTTTTAAACAAAAATGACAAAATGTTGTTGCTGAAAAAT  
287551 ACCCATTCTCAACTGCATCTAAAGATTTGGAGAAAAATTAATGATTTTTTTT  
287601 GATGCTCTTTTTGTAAATGCTATTATTGGTATGTCACCTCAATAAAAAACCT  
287651 GTTATGATTATGTGAAAAAACTGATTTTTTTTGAATGAAAACCAAGTCAGA  
287701 AAAGTGCCTTTTTAAAGCTAATGATAGTGGAGCATACTTAGCTAGAATG  
287751 CTGCTCTTTTTAAACGATTGGTACAACGAAAATCAAGCAATAACAACCTGC  
287801 TGACATTGAAAATGTTAATGAGGTTGAAGACATAGGAAAATTAGTTGAAA  
287851 AATACAGCACTAATCAACCCCAAAAGTTATCGTTAAATTCAACAGTTTAT  
287901 GTATTACAAACAAAACAAAACAGTTTTTTTTTAAAAAATGATTTCTTTTT  
287951 TAATAATAACGAAGCAAAGCTGTTTTTTCTAATAACTATGAAGCCCAATG  
288001 TTTTGGTCTTGATGATACAGCAATAGCAAATAACTTAAACCTTAAAAAA  
288051 ATTAGTGATTTTTTTAAAGAGATTGATTTTAAATGATGAGGATATTCTAAA  
288101 TGACTTTAAACAAGAACAGGAAAAGTTATTGGTTAGAAGAACATTTAACC  
288151 AACTGTTATTTATGAACAAAAATACTGAAATTCTCAGTGTTGTCAATGAC  
288201 AAGCAAAGTCAGTAATCCATAACATTGTTTGAACCATTACTTATAGTAA  
288251 AGCGATCATGTTAAAAGCCTTTGATTATTCCAAAGCCTTTGAAAAAACC  
288301 GAACGAGTGATCCTTCCTTATTGCGATCTAATTTAACTGTTATCAACCGC  
288351 TTAAGATACCTCAGTGAATACTTTCAAATGCCTCACTTAAGTATGATCT  
288401 ACTCTACACTAAGGCCAAACAATATATGCAAATTGATAAAATTTATCAACG  
288451 ACATGATTTCGAAGGTAAACCATGAGGATGAAATCTTTGGCAAATTTAAA  
288501 GAAAGAATTTATTTAAGTTTGGGAATTATTAGTGCGGTAGTGTGTTGGCAT  
288551 AGTTGAATTTTTTAACTGTGTATGGACTATCTTAACTGTTAGTCAAGAAG  
288601 TGGTTGATAAAAGTGTGTTTGGATCCAAGGAATATTATCTTTATTAGTATA  
288651 GGTACTATTTTGGTTTTATTTCTTTTGGTTACTATCTTGGTTTTTATGAC  
288701 AAGAAGACTTTATCTGTTTGAATTAATAAAAAGCATAAAAATTAGGAAT  
288751 CATGAAATTCATAAGTTAAACCTAAGTCATTGTATCTCTTTTACATCT  
288801 CAGAAGTTTCAGAAGTTTTCTTTGAAAGTATCAACCAACACCCTAGTCGT  
288851 GATTTTGTTAATAACATTCTTCAAAGATTAAACTACTTTAAGTGAAGA  
288901 AGAGCTTGAAAAGTTAAACAGTATTGAAGAAGTTACTAAGGATGAGAAGA  
288951 TTGTGATCATGCTCAACCATGTTTTGAAAAAGATTGTTTCTAAAACCTGGT  
289001 AGTTCTAAGTGTGACTTATTTAATGTAATCAAACAAGATAGGTTTAATTC  
289051 TCCAGTGATATCCAAAGTATTAATGCTTTTGAACAACCTTATTAACA

289101 ATGAATTTGCTGAAAGAAGGTATGACTATTTGATTGAAGTTAATAAAAAAC  
289151 TCATACCTTAAAAAATTTGTCAATTCGATCAGAATTCCTTCTTCTTAGA  
5 289201 TTTAAGAGCACAAATTTGTTCAGGTTCAATTTACCCTTAATTTAGTTAATA  
289251 AGTCAATTGAAAAACAAAAAAGACAGAAATTTTAAAGATATTTTGT  
289301 AATGCCCTTAGTTAAGCATTTTATCTGTAATCAACTTTATCCTATCTCTTT  
10 289351 AAATTCCTTTATTTTTGACAGTGAAAATCCTAGCAATAAACTCGCTCTAA  
289401 AAGAACGGATTAAGCTTTTAAAAACAACTGAAATTCCTCTTTTTTGAT  
289451 AAGTTTTACAACCTGTTTAAACAATAAAATAAGCAGCAACTTCAAGAAAC  
289501 TAGTGATGAGATGTTTTATGCAGTGATTAACTTATTTAATCATGTTAA  
15 289551 TCTCTGTTGAAGAGTTAAGGGTTTACTTTACAAGTAAAGAACCAGCACTG  
289601 ATTTTAAAGGTATTAGATAAAAAAACACACTAAGAGAAGATCCTGATCA  
289651 AAACCTGAACTGATTTGTATGAACTAATACAGTTTATAGAACAAAACT  
289701 ACTTAAAAAAGATAAAAAAACAGCTGAAATAAAAAAAGGTACAGGAT  
20 289751 CTTGAACAGTTACTTGAAGAGATTAACAAGATTAATTTAGAAACAAAAA  
289801 TGAATCTTTAGCTTACCCTGATGAGATAACAGAATTGGAAATTGATAATG  
289851 ATAATTTTGTCTCTACAAAACAAGTATTTAGAAACCAATTAGAATTACAA  
25 289901 CTTTTGCATGGGATTGTAATTAATCCTGAGAAGTATGGAATTGGCATGTG  
289951 AAGTAGTTATTTTGCTGATTGAAGTGAGTACAAAAATTTAATAGAACAGA  
290001 TGCTCAATCCCAAAGTGGTAATGATTTTTATCAGTTTGAAAAGGACATA  
290051 GATGAAAGCATATGTCAAATTAACAAAAATATCTAACTTTTATTAGCAG  
30 290101 TGATAGTAATACCTTTTTAATAGTTAAAAATGATGATGTAAAGTTATTT  
290151 CTAACATATGTATGAGCACAACTTTTCTTTGAAACAAGAAGGTGAATTATC  
290201 AATGACATTGAATTTGACTTGTATGAAAAAGGATTTGATAAAGCCACTT  
35 290251 TTCACGTAACATTGCTTTACTTGAAAGTCTCAGTTTTAGTTGATTAGATC  
290301 CTTTTTATGGTTTGACATCAATTAAAGAGATCATGCAGAAAATAGATAGT  
290351 AAAAGTAATCTTAAACCTCGATTGAAGAGATGGTAAATAGGTTTAAACA  
290401 TGAGCAGCGAATTAATAAAAAGGACAATGAAAGGGTGTGATGATTTTTG  
40 290451 CTTATATTGCTGCTTTTGTAGTAGGATTTATCAATTTTTCTCAATGGTC  
290501 TTTACTATTCTCACTGTAAGTGATCTAAATGCTGGGCTTACTGTACCTAA  
290551 CATCATTGTAATCAGTATCGCTAGTGTTTAGCTTTTATTTTGATTGTGA  
45 290601 TTGCTGTTTTATTTCTGTTTTAAATGAAAACACATTAAGCACTAATAATGC  
290651 AAATTAAAGTTATTAATGAAACAAATAAACTGTTCAAATTTTTCAATGT  
290701 GCTAAAGTAAACATAGGGCATTAGCTTGATTGTGCGATGTATTTTTATT  
290751 AGCTATTGTACTTGTGGTTATCTTTTTAATTACTCAAGCCTTTAGTGATA  
50 290801 ACCGTTTTCTTTTATTTTAGTTTTAAGTTGTTACAAACAATCCTGTGA  
290851 ACGGTTTATTTTCAATTTTTTACCATTTTTTGGGATGGTAAAACTTTGTT

290901 TCGCAACCTTTTGAAGATTAAGCTATTTGCTTTTGACAAAAGGTTTTTGA  
290951 GAATAATGATCCATGAGTTGTTTTTATGGATTTGCTTTCAGTTTTGTTTT  
291001 TAGTGATTGCTAGTTATTTTTTATTAACCAAAATAGCAGCGAAGCGCTT  
291051 AATTTTTCTACTAATTTAGATAAGCCTAATGCAATAGCGATAACAATTAG  
291101 AACCATACAATTTTGATTAGTTTTTTACAACCTGATTTTTATTGGTTATT  
291151 TTTGTTTTAGTTCTGAAAAACAAGCTTTACAAGAGATACTGTCAAACACC  
291201 TTTATGGTTCAAGAAAAACACACTTTAAAATCAAAACCACTAGCTTAAA  
291251 AACCAACAATCAACCTGATCCAGCTAATTTACCAGGCGTAATAGCTCTTG  
291301 ATGAAGTGGAAAACTCATTAATTAATAACAATGAATGAACAAACAAAAAC  
291351 AAGCAATTAGTTGTGGAAAAGGGGTTAATGTTGTTTATTCTGGAGCAGGT  
291401 ACTGGTAAAACAACAATTATTACTAATCGCTTTCATACTTGGTTAATAA  
291451 AGAAAAAGTTGATCCTAGCAGAATTTTAGCAATCACCTTTACTAAGAAAG  
291501 CTGCTAAGGAGATGCAGTTTAGAATCTTGAACTAATAGATAGTTCTTTA  
291551 GCTGAGAAAACAAATATCTATACATTTACAGCTTTTGCAATAAGTTTTT  
291601 AATTCAAACATTAAAAAAGCGCTTTATCATCGATGATGATATTAGCTATT  
291651 TCCTAAAGGAATTTTTAGCTGATTCAAAACCTCGATATCAACCTAGCGAAA  
291701 CAAATTATTGATAACTTTAAAAATACTTTTGCTGATTTTGAAATAAATAA  
291751 GTTGGATCAAGATGAAAGGTTAATTAGTTTATGTGAGCATTCACTTCTAA  
291801 ATAAAGATGAAGAATATTCCACTTTAAAAACCCAACTGATTAATGCATTC  
291851 ATTAGCTATGAAAAGAATAAGATATTAAACAATAAACTTGATTTTCATGA  
291901 TCTTTAATTAAAACCTTGTAATTTATTGAGTAATGATAATGATTTACTTA  
291951 ATCAGTGGAGTGAACAGTTTCAGCATATTTTAGTTGATGAATTTCAAGAT  
292001 ACCAACCAAATCCAATATGAACTGATCAAGATGTTAGTAACTAAAAATAA  
292051 AAACCTGTTTTTGGTAGGTGATAATAACCAGATGATTTACCGCTGAAGAG  
292101 GGGCGGTAAACGGGATCATAACTGCTTTAAAGCATGACTTTAATGTTCCG  
292151 AAAAGCAATGAATTCCTTATTAATCAAAATTACCGTTGCGATCAGAATAT  
292201 TTTAGCAGTTGCTAACCAAATTCCTTTAAAAATTATGGCCTATGAAAAAC  
292251 AAGTTAAAACCTGAAAAAATCTCTTGTTCCTTCACTTTAAATTCTGATAAA  
292301 AAACCTGTTTATTTTCAAGCTGAATCAGTTGAAAATCAAGCCAATTGGAT  
292351 CTTCAATAAAATCAAAGCACTAAACCAACAGAAAAGATTAATTTTAAGG  
292401 ATATGGCCATCTTGTTTAGAAAGAACAGAGATATTACTACTATGGTTGAA  
292451 TTGATTGAAGCGGATGGAACAATTCCTTACCTAAACAAAAGAGTTATTT  
292501 TAACCAACTAGTAAAACCTCCAGCGGGTTTAAATTGCGATTTCAACCAGAA  
292551 CAAATCTTGATATTAAAAGAGCTTTGCAAGCCCTAAAAATTTGATCAAAT  
292601 GATTTAAAGGAATTGTGAAAACAGAGTGATAAAACAAACCTATTTGATTt  
292651 TCTTAAATGATCAGAATTAAATCAAAAAACCATAGTTCAAACTTAAAG

292701 CTACTGGTTATTTTAATCTGCTGATTAAGTTAGCAGAGGATCAGCAAATT  
292751 AACCTTTTGTCTTACTGAACTGTTTAAAAAACTCAAAGTGGATCAAATAT  
5 292801 TGAAATCTGCTTTGAAAAAACTAACTGAATTTCAAAAAGATAAACTG  
292851 AATTTAGCTTATCAGAGTTTATTACTAGCTTAGCATTGGAATTTGACTCA  
292901 ATTATTGAAAACAGCAGTGATACAATCAATTTGCTAACCGTTTCATGCAGC  
10 292951 AAAAGGACTTGAGTTTGAAGCTGTATTTATTTATGGCATGAATCAAGGGG  
293001 ATTTTCCCTTATTTTAAAGTCAAAATCAAAATGACGAACAACATTTAATT  
293051 GATGAATTAAACTGTTTTATGTTGCTATCACAAGAGCAAAACGTTTTTT  
293101 GTTTATCACTGCGGTTTTACAAATAAATAACAATTCTATAAAACCATCTA  
15 293151 GTTTTTTAAATTACATCAATAAAAGTGAGTATTTAGACATTGCTACTATT  
293201 AACTATGTATTAGAGCAGGATGATGATTTTTTTGATTCAACTAAAAAAC  
293251 AGACTATACAAAGAACTAAGAAAAGAAAGTTTAGACATTATAGTGGGTG  
293301 ATTTAGTTACTAGTAGATACTTTGGAAAAGGAGTTGTAGTTGAAGTGAGA  
20 293351 GACAAAGAGGTTTTAGTAGCTTTTAAAGACACACGCTATGGGATGAAATG  
293401 GATCTTAAAAAACCATAAATCACTAACAAAAGCTTTATATTAACAATGGT  
293451 TGATAAAACAGTTTAAAGAAAATTAATGCTTCTAAAAAGAGCAGAACTAA  
25 293501 ATGATCTTGAAAAATCGCATTTAGATCAAAAGATTAACCAAAAATTAATG  
293551 GCTTTTTTAAATAACAAGACCAACAATTAATAATTTAGCACTTTACATTCC  
293601 CATTAAAAACGAAGTGGCTTTTTTAGATACTTTCTAGATTTTCTTAAGT  
293651 TAAATAAAATTACAAGCTGTTTTCCCTAGTATTGTTGATCAATTTAACATG  
30 293701 AAGTTTATTGATCAAAATAATAATGAAATTAACCCCTAATGATATTGATTG  
293751 TTTTTTTATCCCTTTATTAGCTTTTAAATAAGGCAAACACAGGATTGGTT  
293801 TTGGTAAGGGTTATTATGACCGTTATTTATCATTAACTAGCAAAAAACAA  
35 293851 CTAAAAATAGGGATAGCATATGACTTTCAATATGCAGAATTCATAATGA  
293901 TCCTTGGGATTATCAATTAGATTTAATTATTTGCAATGGATAACATAAAG  
293951 GTTCTTTTTTTAGGTGATGTTTTATGGCAAAGCTGGTAGAAAGATTATTAG  
294001 TGATCATCTTCCCATAAATTAAAAAAAGTATCAGTTAAATCTAATTATTG  
40 294051 CAAATGCTGAAAACACTACTAATGGTAAGGGTTTAAAGTTGAAACCACTAC  
294101 CAAATACTAAAACAAGCAGGAATTGATTACATCACTATGGGTAACCATAC  
294151 CTGGTTTCAAAGCAAGATTTAGAAGTTGTTTTAAACCAAGTTGATGTTA  
45 294201 TTCGCCCCTTAACCTAATGCAAGATTTTAACTATTTTCAGCTTGGCAAA  
294251 GGGAGTTATTTATTAGCTTAAATGGTTTGAAAATAAGGATTACTAACTT  
294301 GTTAGGAACAAGTATTAACCTACCATTGCAATAACAAACCCATTTGTGG  
294351 AATTAaaaaagTTAGTTTAACTAAAGATTGTGATCTTCATATCGTTGAT  
50 294401 TTTATGCTGAAACAACTAGCGAAAAAAATGCTTTTTGCATGGTTTTTGA  
294451 TGGTTATGTTACTGCTATCTTAGGAACCCACACCCATGTTCTAGTAATG



294501 ATTTAAGAATCACTCCTAAAGGAAGTGTTCATTACTGATGTAGGGATG  
294551 TGTGGTCCTGGATTTGGTAGTGTTATTGGTGCTAATCCCAAGCAATCAAT  
294601 TAAGTTATTTTGTACAGGTGAAAGACAGTTTTTTGAGGTTTCTAATTGTG  
294651 GTGCACAACCTCAATGGCGTCTTCTTTGAAGTTTGTTCAAAAACCAATCAA  
294701 GTTGTGAAAATAGAACAGATTAGAATAGTTTTAGATGATGAAAAGTATTT  
294751 AGCTAATGACTACTTTAATTTAGTTGAGTAATCTTGCTTTCCTTACCATG  
294801 TAAAATTCTGATTATGTTTGCACGGTGTAATCAGAAAACAACCACAGTTA  
294851 AAGGTCAATATCACAAGCAAAAAAATAAAATGATATACCATTCATTTTGA  
294901 TAAGTAATCGACTTTAGAGGATCACTGTTAAAGAAGTATAAATAATCAAG  
294951 TCAGGGTATTAAGATGATTACAGCTAACACAAAGAATGTAATAAGACTTG  
295001 CTAAAGAAACATACTTAGTTATTAAAGTAATCATTATCCAAATTAAGA  
295051 CAGATTA AAAATCATCATAAAGATATTGCAAGTAAAGATCCACCAGTAGT  
295101 AGCAATTGCCTTACCACCCTTAAACTTAAATACAGCGGAAAGATATGAC  
295151 CTATTGTAGCTGCAAAACaACTTAAATAACTTAAAAAATAGGTGCTTTGA  
295201 TACACTTTTTCTGTAAATAACCTTGTAACCAAAACGGAATAAAATTCA  
295251 GGTTAATAAAAAAGCAAAAAACCTTTAAATGCATCAAAAATAGCCACCA  
295301 AAAAACCAATTTTTAAGCCAAAAACACGCATTGAGTTAGTAGCTCCTGGG  
295351 TTTTTGAACCAAAATCCCTGACGTTTTTCTTGAGTATTTTGCTGAAAAT  
295401 ATCAGCAAAAATAATTGAACCTAACAGATAACCAGAAGCTAGGCTAAAAA  
295451 TGACCAAAATGGCAATTGCACTAGCTTGATTATAGCTTGTAATTATCTT  
295501 ATTTAATGTTTCAATTATCTTAAGATCCATCAAGCTAGGTTTTTGTTTGG  
295551 GTTGATAAACTCTCAATAGGCATTGGTAGTGTTTCATTAAACAGTGTTTA  
295601 TCTTTAAAGTTAATTAGCTTTGGTCCTAAAATAACCAATTCCTTTGTAA  
295651 TTAAACGGTTTTTTTTAGTTTTTCAATAACCAAAATAGGATATATAAACT  
295701 CTCGATCCTGAACTAGTGTTTCATTAAACAATATCCCAACTGTTTAACTT  
295751 AAAAACTACGTAATTCAATTAAATTAGATTGGGGTTGGATTACAAAACG  
295801 ATTAATAAAGTTTTCTTTTTGGCTAATTATGTTAATGATTTTCAATCCAC  
295851 CAAGTCCAGCAATTACCCCTATTTTGGGATTAATATTTAGTTCTGGAAGG  
295901 TTATTAAATCCATCATAACAAAGAAGTGGATATTATTGTTATTTTTAAA  
295951 TTTTTGGTAATTACTTAATAAAGCATTTTTACTAATATCACTGTAAACAA  
296001 TGGTTAGGTTTTGATTAGTTTTTATTAGATAGGATGTTAGATAGGAATGA  
296051 TCACAACCGATGTCATACTAGCTTAGGATTAAATGATTGAACTAAATT  
296101 AGCAATTGTGCTAATCCTTTTTTTTCATTAAATCTTAGAAATGACATACTA  
296151 ATAGGATTGTTTCTAACTGCATGTCTCAATTTTCTAATTGCTTTGTTTTT  
296201 AATTTGTCTGATCTTCTCTCTAGGGATCAAAATCTTTTGACCTACTTCAT  
296251 CAAGTGTTTTAGGTTCAATTGTAAGGGGGCATGCCAATCCGCATTCTAACA

296301 ATTAACCTCTTCTTGTT CAGAAAGATTATTGTTCAACAATTCATCAATTTT  
296351 TTCTGAATTTGAACGGCTTTTCGGTAAACTCGTCAGGAGTTTGAGCGTCTG  
5 296401 TGTCTTTAACAAAATCACCAAACCTGGGACTCTTCATCATGTCCAACGTGT  
296451 TTATCAAGCGAAACTGGATCTAAACTTAACCGTTTAATTT CAGCAATCTT  
296501 TTTAACATTAAATCCTTCAGCTTGTCCTCCCATCTTTTCAGCTAACTCCT  
10 296551 CATCAGTAGGTTCTCGCCCTAACTCTTGATACAAAGCCCGTTCTGCTTTA  
296601 GCTAAGCGGTTAATGGTTTCTACCATATGAACAGGGATCCTTACTGTTCT  
296651 TGCTTGATCAGCTATTGCTCTTGTAATTGCTTGTTTAATCCATCAAGTAG  
296701 CATAAGTTGAAAACCTATTCCCTAAAGATCAGTTAAATTTGGAAATAGCT  
15 296751 TTTAAAAGCCCCAAATTACCCTCTTGAAATTAAATCATTAAATCCAACCC  
296801 TCTTTCTAGGTGTTTTTTGGCAATAGAAACAACTAGTCTTAAGTTTGAAG  
296851 TAACCAACTGATTAATTGCATACTTACGTGACTCTTCATCAGTACTATTT  
20 296901 AAAACCTTGGAATCCGCTGTT CAGATTCAAATCTAACATTTTAGAAAA  
296951 GTCAAGTGATCCTAAAAAGAACCTAACATTATCATCAACCTTATCACGGT  
297001 TAGAGATGTTCTTACTTGTTAACTCTTCAATATCTTCATCAATAATTGAA  
297051 AGGTCTTGGTTAGCACGAAATTCATGGATGTGCTCTTCAACATCGTGTG  
25 297101 GAGTTGAATCCCCTTATCACGTAGTTCATCCAAAACATAGATAATTTTCAT  
297151 CTTCAGGTAGTTCAAACTTAGCGAGAACACTAATAATTTCTTATTTGAA  
297201 AGCGTGATGTTTTTTTGTTTCTTTTGCTTTTCTTTCTCAAGCTTCTGT  
30 297251 TAGAAGGTTGATGACTGTGTTGGTGT CATCATTTTCAATGTGGCTTTTAA  
297301 ACGATCCTTCTAAGATATCAAATAACTTCAGATTATTTTTTTCTTTTAAA  
297351 GGAGCGTGTTTAGGTTTTCTACCCCTTCTTTTTTTAGGAACATCACTCTC  
297401 CTTATTTTTCATGAAGGGTTTTTGAGAAAAGCGATGTTTTTCATGACGGTGT  
35 297451 TCGGTTGCACCTTATTGTCAACATAAATCATCTTTTGTAAGGACGATTC  
297501 TTTTCAAGAATACGCTGTTTTTTAAGTTCAGCAATTAATTCTTCAGATAG  
297551 TTCTGGTTTGGTTGAATTGGGTTTTTCGCCTAGCGTTTTTTTGTCAGTGG  
40 297601 ACATTTAGCTCAATGCGACTAGCATTATAATTTTAGCTTATATAACTTTT  
297651 ATAGCGTTAACTTTAAATTTTTTAAGCGCTGCTTTTGTTGTTTTAATAAC  
297701 GTTTGAAAGGTCTTTAGATAGTTTTGAAAATCATTAGCTTGATAACAAGT  
297751 TAATTCATCTAAAAAATATCTTTAATTTCCAATAACCTTGCTTTATTGT  
45 297801 TTAAAAGGTAATTTTGATCTAAAACACTTTCAAACCAACTCAGTTAGCA  
297851 GTTTGATTTTCACTCCAATAGATCCTTGCTTTTTCAATAAAAAGTTCAAC  
297901 ATCAAACAAATTAAAGTTACATTCCTTAAAAACTTCATCTAGATGGGATT  
50 297951 GTTTTAATTCAACCAAAAAGCGTTTATCAATTAAAGCAAACGCAAAGATT  
298001 TCAGGTTTTCACAACTCATTAACTGCTTCTTCAAAGCTGTTTGCACTAG  
298051 TGCTGCAGTGGTTTTTTGCAATTCTTGTTGGTGGTTGAGCATGGCCTGAAG

298101 TATTTATGTAAAAACGGTTGTTATCAAACCTAGATACAAGTTTTTCTTTG  
298151 TGTTTTAAAACTGTTTCATACAGAGTTTTTTCATCACTATATTCAAGTAG  
298201 TTTAACCAAATTTTTAATGAGAAAAATTAAAAAACTATGGTCGTTTAAAA  
298251 TTGTTTGGTTTTTTTGTTAAAAAAGCAATGATTTTATTAGTAATAACCCTT  
298301 TGATCAAGTTGTTGCTTTTTTAAAAAACTAACAAGATATTCAATTAGATT  
298351 TTGCTCTTTTGTTTGCTTGTAATATAACTTGCTCACTACCCTTGTTTAAAT  
298401 ACAGTTCATCCCAATCTTTATAGTTGTGTCTCACTGAACAATTTCCACA  
298451 ATAAAATTGTTGTTATTAAAGTTTTTCAATTAAGCTAAACACAGCATTTTG  
298501 ACCACTAGCATCATTATCAAGTGCTAAAACTAAGGTTTGTAACCTCCTTAA  
298551 AGTGAGCTTTAATGGCTTTAATTTGCACATCATTTAATGCTAATCCCATT  
298601 AATGCAACAGCTTCAAACCTGGAGTTTGTTAGTGTA AAAACATCAAAATA  
298651 ACCTTCCACAATAAAGAGTTGATTGAGGTTTTTATTTAACCTGTGAAAGT  
298701 TAAATAACAGCTCCCCTTTTTTAAAAAATTTCGTGATCAGCACTATTTTTTA  
298751 TATTTTCAGTTTGTTGATGTTATCAACACTTCTTGCTGAAAAACCAACCGG  
298801 GTTACCATTAAAGTCATGGATAGGGATCATAATCTGGTTTTGAAAGGTAG  
298851 CTTTTTTGGGTATTAAAGTCAAAAAAGCCAAGACCTTGCTGGTTAGTTTTT  
298901 GAAAAAAGATACAATTCACTCGGTTTTATCTTTGGATTAATGAAGGGGTA  
298951 TCTTTCATACTTTTACATAGATACTTATCTTCATTGTGAAAAGCAAGTC  
299001 CTAGCTGAAACTGTTCAATTAATGTTTTATTAAAGCTTCTTTTTTCAACT  
299051 AAATAATTCATCCCATTTGGGTTTGTTTCTCTTTTTAATCTGGTTTGATA  
299101 ATAAGTAATTAAAGCATTGTTTATCTCCCAATATCGTTTTTGTGTTGGAT  
299151 CAACTTTTGTTAGTAAATTACTGTTCCAATTTTCTAACTTAATTCACAA  
299201 ATTTCAATTGCTTTTTTAAAGTGCAGTTTTTCAATCTAACTGGTCATGCTT  
299251 TTGGATAAACGCTATTCCGTTGCCAGCTGCATTACAAGCCCAACACTTAA  
299301 AGATGTTTTTAGAACTGGAAATGGACATAGAAGGATTTTTATCATCATGA  
299351 AAAGGACATAAAGCAAGTAGACTATTACCCTTAGTTTGGATTTTAACCCC  
299401 GTAGTGTTGAATAATTTCAAGTAATTTAATCTGCTTTAAAAGTTCATCTA  
299451 AACTGTTGCTTTTTATTGACCATTTTTTCATGAATCATTGTGGTAATTCTTT  
299501 GATAGCAATTCGCTGTTGAACTAAAGTATCTCTATCTCTGATGGTAACTG  
299551 CATTATCTTCTAAACTTTCAAAGTCAAAGTGAAGTGCATACTTTATTCCA  
299601 ATTGCATCTGCTTTTCGATACCTTTTACCAATACTACCAGTTGTCTCAAA  
299651 GCACACTCTTCACCTTGTTTTTGCTAGCGTTTCAAATACAGAAAATGCTT  
299701 CTTTTTTAAGTTTATTTACAAGTGGTAAAACAATAATTTGTTGAGGACAT  
299751 AAGTCAAATGGTAACTCAATACTTCCCGTTCTTCCTCATTAATAATTTTC  
299801 TCTCCTATAACTACTGACAAATTAGTGCATAAAAATAACCGTTCAATGCCAA  
299851 CCGCAGgTTCGATTATGAAAGGTAAGAAATGTTGGTTTAAATTCGCTATCA

299901 AAAAACTCATGCTCTTTTTTGAAAACTCTTGGTGTTGTTTAGATCAAA  
299951 ATCACCCCTGTTAGCCAAGCCTCATAACTCCTTAATCCGTGGGGAAAAT  
5 300001 TAAACAAAAAGTCAGTAGTTTTTTTGGCATAATGAGCCAATTCTGATTGA  
300051 TCATATTCATGTTTTTTTAACAATTCTGGGTAAATTTTAACTGTTTG  
300101 TAGAACTGTTCTACCATTATTAATTGTTTTTCAAACAGCGAATTTGCAT  
300151 CATCAGGTTTACAAAACCACTCAATTTCAAACGTTCAAACCTCTAGTT  
10 300201 CTAAACAAGAAGTTACCTGGGGTGATTTCAATTACGAAAGCTTTACCAA  
300251 CTGGGCAATAGCAAAAGGTAAATTACGCTTCTTAGCTTGCAAGATATTTT  
300301 TAAAGTTAATAAAGCTACCTTGAGCAGTCTCAGGACGGAGAAAAACAAGG  
15 300351 CGTTTATCGTTGTTTACAACCCGATTTCAAGTTGAAAAAGTAAGTTAA  
300401 ATCCCTCACTTCTGATCAATTTTGTTATGACAATTAGGACAGTTAACTT  
300451 TAAAACTATTCCAATCCTTTTTAGCTTTTATTTCAAGCATTAAATTGATCA  
300501 ACACGAAAGCGGTATTTACAACCTCTACAATCAACTAAAGTATCAACAAA  
20 300551 GTTAGCTAAATGTCCTGATGCTTTTCAAACCAATTCGCTGAGAATAATAG  
300601 GGGTTTCAACTAAAAGAACATCAGCTTTATTTTTAATAAAAAAGTTATAT  
300651 AAAGCTTGTTTGATTGTTGTTTTAAACTGCACCTAATGGACCAAAATC  
25 300701 CCAACTATTGTTTAAACCGTTGTAAATTTCACTACTCTGAAATACAAAAC  
300751 CATGTTGTTTGAGAACTGAACATAAACTTCTTGGTTGTAACTTTAGCC  
300801 ATTGTTAATTAATCTTAAAAATTAGTTTTTTCAAGCAAAACAAGATAATCC  
300851 CTAAAGCAACACTTACATTTAAAGAATTGATCTTATTGTTTATAGGAATT  
30 300901 TTGATTCTACAATCTGCATTCTTTGTTATTAGTTGATTACACCCCTATC  
300951 CTCATTGCCAACAAATTAAGATTTTTTTAGCAAAATCAACTTTGCGATAAT  
301001 CAATTGGTTTTTCAAATAGGATCCAGAGTTGAAACAACAGTTCAAAATCCT  
35 301051 ATTTCTTTTAGCTTAGTGATCGTATAACTTAAGTTAGCTACTTGCACTAA  
301101 GTTTTGATAAAAAACACTACCCATACTAGTTTTTCATGACTGTATTGTGA  
301151 TAGGGACTTGGTTATTCTTTTTAAAGATAATTCCATCAACCTCACTAGCC  
301201 AAACAAGTTCTTAGTATAGCACCAAAATTATAAGGGTCTTGATCTCATC  
40 301251 TAACATCACAAGTGTACTGCACCTCTTATTTTCAACTACTTTAACCAGTT  
301301 GATCAAGTGAATTAAGAGTTGGTTAGTATCTAAACTGCTACCAATTCC  
301351 TGGTGGTTAATATCTCTATACTGATTGTTAAATCAGTTAGTTGAATGGAT  
45 301401 TTGAAAATTAATTTTTTTAGCTTCAATTAAAGGTATTAGTTTTTTGTGAC  
301451 GAATGGAAATGTTTACCAATTTAATGTGAACCTGGTTATTAATCGCTTCC  
301501 TCAAAGGCTTTAACACCAAATAAGCAACTTTGTTGGCGTGGTTTTTTCAT  
301551 TATTACAGCAACATTTTTTTAATTAGTTTTTTCTAATTGATCAGCTTT  
50 301601 ATCCATTGCTTTTTGTTTGTGTAATATTGATCACTCTTTAATTAAACGCA  
301651 CATTAGTTTAGTATGGATAGATTTAAAGCTAATTCCTAATAAATCAATT

301701 GATCATTCCAAGAACTAAGTTGTTCTCTCAGCACACTAAAGTCCTTAGT  
301751 TTTAATACTTGTATTAATTTTTTTTATTAGTTTTTCAGATAGCAGCAACTG  
301801 CATTGGCAAAGTTGAGATTATCAAGTAAAGCTGAAAAAAGTGGATCATAT  
301851 TGCTTGGGACTAATCAACTCAGATTGTTCTGAATAAACTAATCAGGTTCT  
301901 AGCAACATTAAGTGTTTTTGCAATCCTTTGAATATCATTATTAGCTTTTT  
301951 CAATCAATGATTGGTTTAGATCAATAGGATGCAAATAGTGTTTTTGGTAA  
302001 AAGATCCAACGCAAAACACGAAAATCATGAAAGTTAAGAAAATCAACTGC  
302051 TAACAAGAAGTTCTGCAATGACTTTGACATCTTTTGGTTTTCAATCATCA  
302101 AATGACCAATATGCATCCAATGTTGGTAATGGGCTGGTTATATAAAGCC  
302151 ATGTGTAAGGCATTTTCATTTTCATGGTGGGGGAACTTTAAATCAACTCC  
302201 TCCTCCGTGGATCGTGAGTTCATTTTGAAACAATAATCAATTAAGAAGG  
302251 CACATTCAACATGTCAACCTGGTCTGCCAAGTCCCCACTTACTATTTTCAT  
302301 TTAATCCCTGCAGTAGTAATCTTTCAAAGTACAAAATCCAATTTGTTCTT  
302351 TTTATCAGTATCAGTTTCTTCTAAATGCACCATTGCGTTAGCTAGATAAC  
302401 CATATTGCTTTTAGTGAATTAAGTCAAAAATAAACGTTGTTTTGAGTTGAA  
302451 ACATAAGCATGGTTTTGATTTACTAATTGATCAATATAGTCAGGGATTTT  
302501 ATCGATTTTTTCAGTGATTTGAATATGTTTAATAGGCAGAATATTTAGTT  
302551 TTTTTAAAAGTGATTTGTAAGCAGTGATTTGTTGTTTTGTAACAAGTAT  
302601 TCGCTTACTTCTTGTGTTGAGCAATCTTGATGATCTTATCGTCAATATC  
302651 AGTGATGTTTTGAACAAAATTAACGGTATATTTAGCCTTTTTTAAAAGTC  
302701 TATTTAAAACATCAAAAACAATTAATGGTCTGGTGTGCTTAAGTGCAAA  
302751 TCGTTATAAACTGTGGGTCCACAGAGATAAATGTTAATGGTTTTTTGAAC  
302801 TAGTGTTGTTGGTTTTTGACTAACACTGTCAACAATCATAAACCTATGTT  
302851 CAAATTGCTTCATTAATGATAGGAATGTTGAGTTCTTTGGCGTGATTGAT  
302901 TTTTCTTAAAGTTGGTTTGTTCCTGCAATAACAAAGTCAACTGTTGGTT  
302951 TGACTTCACTTGCAAACTGGCAATCAAACTTAGCTGATAATAAAATCCTTA  
303001 ATTTGGTCACGACTAATGTTAAAGCTACCGGTAATAAGAAAGCGTTTTTG  
303051 aAAATAAATACTGTTAGTTTCAAAGTTAATTTTCAGTGGAATTGATCTG  
303101 TTTTACTTGTCCTTAATTCAAGTTGTTCAATTAAGTCAAAATGGTTAGGG  
303151 TCATGAAACCAGTTATACAATGATTCAGCTACTGTTATTCTACATCATT  
303201 TAAACTAATTAAGTTCTCTAAGCTAGCATGCTGTAATGCTTTGATATTTT  
303251 TAAAATGATTAGCTAAAATCTTAGCTAATACATTACCAACATGCTTAATA  
303301 CCAAGTCCTGTTAGTAATCTAGCCATTCCTTTTTGTTTGAATTTTCAAT  
303351 GTTATCAACTAACTTGTTGAAAAGTTTATCACCATCTTCAGATCTAATT  
303401 TTAAGAACTTGGTTTTTCTTGTCTTTTAAATCATAAAGATCAACTATAGAT  
303451 CTAACCAAATTGTGTTTCAAAAGTTTGGTAATAGTATTAATATTCAACCC

303501 GTTAATGTCCATAGCAGTTTTAGAAACAAAATAGTTAATTAAGTGGATGT  
303551 TTCGCTCCTTACAAGTTTCATTGGGTACAATACTGATCAACTTCATCAACT  
5 303601 ATTTTGACTAGTTTTGAATTACATGAAGGACAATATTTTGCTCTTGAAT  
303651 TATGATAGTGTCAATTTTTCTTTTTCAAGATTACCTTTAGTACTTTAG  
303701 GGATAATTTCCCGAGCTTTATAGATAACAACAGTGTCAATTGATCCTAATG  
303751 TCTTTAGTTTTAATGTAATCAAAGTTATGTAAAGTAGCAGCTGTTACTTT  
10 303801 TGTTCCATCTAAATTAACACTTTCTAATTTAGCAGTATAGTTCACTCTAC  
303851 CAGTTCTACCAATCGTTATAAGAAGTGTGTTAATTTAGTTTGAACAAAT  
303901 TTAGGACTAAATTTAAATGCTATTGCCCAACGTGGTGATTTACTTGTAGC  
15 303951 ACCTAATTGTTGATAAAAAAGCAAGCTGTTTAGTTTAATAACTAAACCAT  
304001 CAAGATTAAGTTAACTGTTCTCGTTTTTGTCAAACGCTTCCAAGTAA  
304051 TTAATTAATTGAAATTTGTTTTGAAAAACCCTGATGGTATCACTAACTGG  
304101 GAATTTTCACTGCTTAAGCTGTTCTAAAACCATAGTTTGAGTAGTGATTG  
20 304151 ACTCTTCAAACCATTAGGGATGTAATAAAATAATGCCCTTAATTTGCGC  
304201 TGTGCAGTGATTTCACTGTTTAAATTACGTATTGTACCTGCTGCTAGATT  
304251 CCTTGCATTAGCAAATGGTTTTTCAAGTTGATTGTTAATTGCTAAAAAG  
25 304301 TTTTTTTATCAACAAAAATCTCACCCCTAATCTCAATTGTTTTTGTGAAA  
304351 GGGATTGTTAAAGGATAGATTTAATGGTTTTAACATTATTTAAACATC  
304401 TTCCCAACACTTCCATCTCCTCTGGTTAAAGCATGAACATAAACACCAT  
304451 TTTTATAAGTTAGAGAGATACTAACTCCATCAATTTAGGTTCAACTACA  
30 304501 AATTCATTTTTTGAGTTTGTGTTGAAAGTTAATATTATCAATAAAATTAGC  
304551 AATTTCTTTAGTTGAAAAAGCATTTTCCAAGAGAGCATTGGACTGTTAT  
304601 GGTTTAACTTTTTAAACCCCTTCACAGCTTCTCCTCCCACCCTTTGGGTA  
35 304651 GGGGAATCAATTTGGATTAAATCAGGATGATCTTTTTCTAATTGTTGGAG  
304701 TGAATTATACAACATATCATACTCAAAATCATCAATTAAAGGTTGCTTA  
304751 AAACATAGTAGTGATAGTCATAGTTTTTTATTAAGTTAACCAGCTGTTGA  
304801 ATCTTCAATTTACATCCATCACTACTATAAATAAGAAAAATCCTGACTT  
40 304851 AGTTGATACCAATCAGGATTTTACAAAGAAGTTTTAATTTGGAGCAGATA  
304901 ACGGGAATCGAACCCGCATCTTAACCTTGGAAGGTTATGTTCTACCATT  
304951 GAaCTATATCTGCGTTGTTACTTTAATATTTAGTATATTTAACTTGCAT  
45 305001 GGAATCTGAAAACCAAATTGCAATCCTGGATTATATTTTAACCAAGTCA  
305051 ACCAGCCCAATCAACCAAAAATAGTTTGGTTCTCTGGGGAAGGGGAGGAT  
305101 GAGAAAATTAATTTTTTAATCCGCTTAAATGATTTTTTTAAACCAAAATT  
305151 TGTTGAAAATACTAATGATAGTAGCTTTTTATTAAGTTTTAGAAACCATG  
50 305201 TTGAACTAAAAATTCAACGCCTTTAACCCAAGCTAAGTTTGCTAATATT  
305251 GCCAACAAATTACTAGCGGTTTTATTTGGTTCAATGCAATGAAAAACAGTT

305301 AAATAAACCAACTGGAACTGATTTCTTGTAATTTTGTCTTTAGCTTTAT  
305351 TATGGTTAAGACAATGCTGACTAAACTTCAGTTAACTAAGATAAGTAAA  
5 305401 TTTGTAAACCAAAAGGGCATTGAGTTTATTAAACAACAATGGCCTAT  
305451 TCTAACACATTGGTAACAGTAGGGACCACATTAGGTACTCCAGTATTTT  
305501 CATTAACAATAGCCCAACAAGATGGTATTAAGCAAAATGCGGGAATGAT  
10 305551 GTCTTTATCTTTTGTATTATCTTCTCTGTTTTTCTATTAGTTTAGGGCT  
305601 TGTTTCATCACTTATCTTTTAGTCTCCAGCTTATTTTCAATTCGTCAGA  
305651 AAAAAACGTTGGATGCTTTGGATAAAGTGTATCAAAATTTATTGATAAA  
305701 TACTTTTTTTTAGATGAAAAAGAGATCAAAAAACAACCTAAATATCAGTT  
15 305751 TAAAAACAACGGTGTGCTTTTTTTTATGGTTTTGATTTTGATCAGGCAG  
305801 AGTTTCTTGAACAATCAATGAACCTAATGTTGTTGTTAAAGCAAACCAAT  
305851 TGTTTTATTTTAGTTGGTTGTAAAGAAAGTGAAATGACGCTCATTAAAAA  
20 305901 CAAGATAGAACCTAACATTAACCTAAAACAAAACAGTTTTTATCTGGATT  
305951 TAAGCAATGAAATTTACAAGTAGAACAGATCAGCAAATTTAACTTGTTG  
306001 TTTAGGCAATTGAGGCTCAGTTCTGAACTATTTTACTTAGAAGATTTTTT  
306051 TGATTATCTAACTACTGCAAAACAGATAGTTAACTTTCTTTTTTAAACA  
25 306101 AAACCTAACCTTGATCAATTTCAAGAAAATCAAAGAAATTTATTGATTT  
306151 TTTAGCGTTATGAGCATTAGTAATTGGTACTGATTTTGAGTTAATAACG  
306201 TGTGTGATCATTTAATAACCACTTTGTAATTGATAACAGTTTTAAACAG  
306251 GAATATGACAAACCAACATTACTGCTTCTTTAATCGTTCTTTGCAATT  
30 306301 TTTTCAAGAAAATAGCTTGGTTTTAAACCTGAATTGTTTAGTTTGCAA  
306351 AATACACAAAGGATGTTTATGGTTTAAATGTTATCAACCAACTAAACTTA  
306401 AATAAGCACCCATGCTAATTCCATTAACATGGGATAAAAAGCAAAAGTT  
35 306451 TATTAGCTTTATTGAAAGCTGTGTTCAAAAATACAGTCAAGTTAAAAAG  
306501 ATAACCAGGTATTTAGTTTAAACAGTTGGTAAGCGCGTCTTTTTTCTATTA  
306551 TTAATAAATAAGCAGTTTAAACAAATTAACTTGAAACAGCACTAAAGTA  
306601 CCTTGGCTTTTAAACTTCCCTTGGTGCAATGGACAGCACAACTGAGTCCT  
40 306651 AATCAGTAAATAGAGGTTCAACTCCTCTAGGGAAGGCCAATTTATGATAA  
306701 AAACCTAGTTAAATTGCTAGGTTTTTATCTAGTTTTAGGGGGTGTAGTTT  
306751 AGTGGTAGAACAACAGTCTCCAAACTGTCTGTGTGGGTTGATTTCCTTC  
45 306801 CACCCCCGCCATTTACAGATGCACTTCAATTCAAACCTTTAAAGAATGCTT  
306851 TAATAAGATTGCAAAAAAAGTTAATCACTGGACAGTGAATACTATGAGT  
306901 TTTCTTCTTTTATTGAAAGGATTAGAACTACCTTTGGACTTTTAATTGCT  
306951 TTAACGTTTTTAAGTAACCTAATCATTATTAGCTTTGTTTTAATTTGATT  
50 307001 TTTTACTGATGGCTTTGGTCAGTTAAGGCTGTTATTCTTTACGCTTTTTA  
307051 TCCCCTTTTTTATCTCTTTATTAGTAGCAATCTTTCTAATCTTTCTTAAC

307101 AATTCATTCCGTAATTTTTTTCAGATTAATGAAAAGAACTGGCTGTTCTT  
307151 ATGGACCTGTGTTTTTTCCTCATTACCAATCTTTAACTTGTGGTTAATTG  
5 307201 TGAGATTAAATAAACTATTAAGAATTCGCTAGTGATTATGGTTTTAAG  
307251 ATTGTTAATAAATATAACAGTTTAACAAGCGGAATTTTTGTGTTTGA  
307301 TGCTGATTATGTTAGTTTTGAAGCCAACCTGACTAATTGAAAAACACAA  
307351 ACGATAAAAATCGTAATTTTGTTAACTTCTTTGAAACAATAAGCAAAGAA  
10 307401 AAAACTGGTGTTGTTCAAAAACAGTTCTTAACTTTCAAAGATTATATGT  
307451 TAATCGTTTTGTACTATCAAAGTAAGCTAAGTGTGGTAGCAACCAACAGA  
307501 CTCCCCAACTGCTTTTGATAACCTAAGAACTATGTTGAAAAACAAACAG  
15 307551 CGTGAAACAGTAAGGGTTAAGCAGTATATCCTCACTTAATTAAGTGAATA  
307601 TATTAATATTTATTGGTCTTTGTCAAAAAATAAGATGAAAAAGGCAATCC  
307651 ACTTTTCAGAGTCAACCAGTTGTTTTTAACTGTGCTTCATGCAATAGCAAC  
307701 TTTACCATTGACTCCACTGCCAAACAAAAGGATCTTGCCATTGACATTTG  
20 307751 TGGAAAATGTCATCCTTTTTACATAGGGCAATTAACCAACAAACCGTGC  
307801 ATGGACGGGCTGAAAACTTTCTCAAAAGTTCAACGCTGGAAAGGCTTTT  
307851 TTAGAAAATAAACTAAAAAGAGTAACCAAGCTAAAGTTGAAAAACAAAC  
25 307901 TAGGCACCGTTCTATTAACGAGCTTTAGTGGATTTTGACAAACAACTCTT  
307951 TTTCAATGTTGAAAAGATTGTTGAACCTTACTGAACAACTTGAAAAAGATC  
308001 TCAATAAACCTAACCTTAGCTTTGAGCAGATTAAAGTTATTAACAAAGAG  
308051 TTAAACATAAACCAACCTTTAATAGTTAAATTCAAGGAGTTGCAAAAGCT  
30 308101 GGTGAAAATGCTAATGAAGCTGAACAAATCTTAACAATTCCAGCTTAA  
308151 AAGAATTGCATGAAGAAGCTAAAAAAGAACTTGAAAAAATCAAAGCTAGT  
308201 TTACCTAGTTTAGAAGAGGAAATTAAGTTCCTTTTACTACCGGTAGATGA  
35 308251 AAATAACCAAAAGAATGTTATTGTAGAGATCCGTCCAGCTGCTGGTGGGG  
308301 ATGAATCTTGCATCTTCTTAAGTGATCTTTTTAATATGTACAAAACTAT  
308351 TGTACTAGTAAAAATTGAACGGTTGAACCTTAATGAAATTATCCCTGCAAG  
308401 TGTGGGGATTAACTTTGTTTCTTTTGCGGTAAATGGTACTGATGTTTTTG  
40 308451 CTAAACTCAAGTTTGAATCAGGAGTACATAGGGTGCAACGTGTTCCCTTA  
308501 ACAGAAGCTAAAGGTAGAGTGCATACCTCAACAGTTACTGTTGCTGTTTT  
308551 ACCTCAATTAGAAGAGGTAGAGATCACCATTAACTCCTAGTGATTTGAGAA  
45 308601 TCGTACTTACCGTGCTTCAGGAGCGGGTGGACAACATGTTAACAGAACT  
308651 GAAAGTGCAGTTAGAATTACCCATCTACCTACGGGAATTGTTGTGGCTTG  
308701 CCAAGAGGGTAAATCCCAGTTTTCTAACCGTGATAAAGCAATGAAAATGC  
308751 TACGTGCTAAGTTATGGGAAAATGCTCAAAATAACAACCTCTCAACCCAA  
50 308801 GCGGATTTAAGAAAAAGTCAAGTTGGTAGTGAGAGAGAGCTGAAAAAAT  
308851 TCGTACCTACAACCTATCCTCAAAACAGAATTACAGACCACAGGATTAAAT



308901 TAACTATTAATAAGCTTAATACTGTTATTTTGGGAGATCTTGATGAGATC  
308951 ATTGAAGCTTTACAAGCTGATGAAAAGAAACAACAGTTGGAAAAGTTTAT  
5 309001 TAGTTAGATGACTCTGTATGAGTTTTTTTTAAATCAAAAGTTAGTTTACC  
309051 AATCCAGTCCCCATTTTAACGGGGTATTTTAAACAATATTGGAACACTAT  
309101 GGTTTTCAATTTAAACAATTGATAAACTCTGAAAAAGTAAGCTTCTAAT  
10 309151 TACTAGTGAGTTAACTGATAAAATCAAACAACAATTAAAGTGTTATTTTA  
309201 TTGAAAAGATCCCTTTGCCCTATTTGTTGGGAACAATTCAACTAAGGAAG  
309251 CTTACTTTTAAAACTAAGAAAGGAGTTTTTATTCCTCGAATTGATAGCTT  
309301 AGCACTAATTGCAAGTGTTAACTTAAAAAAAATAAAAACTGCACTTGACC  
15 309351 TTTGTTGTGGTTCAGGTACTTTAGCCATTGCTTTAAAAAAGAAGTGTGAT  
309401 ACACCTTGATGTTTATGGTAGTGATATTGATATCCAAGCATTAAAACTAGC  
309451 GCAACAAAATGCATTAATTAATAACGTTAGTATTAATTGAATTGAAGCAG  
309501 ATTGATTTGATTGTTTTAACAAGATAAAAACTCCGATTGATTTAATTGTT  
20 309551 ACAAACCCACCTTATCTGAAAAAAACACAATAAAACATTAAATTA  
309601 TGAGCCTAAGCACAGCTTGGTTTTTCAAATAAAAAATAGTTATTTTGCAT  
309651 ACAAGCAGTTGTTTAATCTATTACTAACAACGATCAATTAAACAGTTA  
25 309701 ATTTTTGAATGTTCTTTATTTCAAAAAGAAAGGCTATTAAATTTGTTTTT  
309751 AATCTTTAAATCAAGGCCGATTTTTAACTTTCAAAAACAGTTTATTGGTA  
309801 TGAAAGTTGATAATCAAAAACCCCAGTAGTTGATATTA AAAATACCAA  
309851 ACTATTAAGCACTTTTAAAAATGGGGCTAGCAGGAATTGTAAATACTGA  
30 309901 TACACAAATGGGATTAATTAGTTATTCAGAGTCTACTCTTGACAAAATTA  
309951 AACAACGTGCACTTAACAAACATTATGTATCAATGTTTGGGTTAGAAGAA  
310001 TTAAAGAAGTTACCAAAAAAACTACAACAAATTGCTAGTTACTTTTGACC  
35 310051 AGGTAGTTATACCTTTTATTA AAAATAACAAGAGCTACAGGGTTCCTAAAA  
310101 ACTTGGGCTTATTAAACCTTTTTAATGCAATTGGTAGGGTTTTTTGTACT  
310151 AGTGCTAATATCAGTAATCAAAAACCATACACCAAATTAAGTGATTATCA  
310201 AAACGATAGTTACTGAATAAAGCAACCTTGTTTTATTATTAGAAGCACTT  
40 310251 CTAAAGTGCAATCAAATAACACACCTTCACCTGTCTATAATTTAGATACA  
310301 AAACAGTTGGTTCGCACCACAGCTAAACAAACAAAACAGTTTCATAAATT  
310351 AATAACTAAACACCAGTTAGCTATCTAATACACAAACCAAATGAAACCA  
45 310401 AAGATAATAACAAGCTTTTCAATATAAAAAATGCTTAATTCAGTTTTATTT  
310451 TTGAAATAAACTATTTTTTTTTAATTAGTATATAGCATCAACTACTAAAA  
310501 CATAAGGGATGAAGCTCAAAGGTTTTTTAGCTGTTGGTGTTAGTGTTTTT  
50 310551 GGTTTTTCTGGTTTACTGATGGCTTGTAAGTGTGTAAGTCAGTTTGATCA  
310601 AGTGGATGATGGCAAATTAAGCTAGCATCTTCATTAACCTTCGAAACGCG  
310651 CAGCGGAAGCTTTAGAGACAGTAGTTAAAAAATATAACGATACTAAAGAT  
55

310701 CCTGGTGATTATCCAATTGAAATAGTACAAATTGCTGGGGGTTATGATGG  
310751 GGGTAAAAAGGATGTTCAAACCAAGGTTAGTACCAAAGATAAAAAATACT  
5 310801 TTTATAACCTGATTTTAACTATCCAGAAATAGTAAGTACCTTATCAAGG  
310851 TCTAAAAATGGCTTTGAATTTTGATGGGGTTAATGTTGATAAACTCCATCC  
310901 TAACTTTTTAAGCTTTAACAGCAGAATAGGTGGAATTAGAGATGATGGAA  
10 310951 TCTATGCTATTCCAATATCTATGTCCACTGATCTGATGGTCATTAATGGC  
311001 CCTGTTTTTACTATATTCTAAACAGTGCTAGAAAAGAAGGTACACCAAC  
311051 TAGCACTACTGTTCAAGCAACTGTCAGTTCAAGAAGTGCAGAAAAAAAAG  
311101 GTACATTAGAAAATTGCAAATGATAGTGAACTACTAACTTTGACAGAAC  
15 311151 ATCCAAACCACTGCTCAAAACAACAGTAATGAAACAATAAGGAGCAAAA  
311201 ACAAGTAAAAAGATCTAGTAGTTCTTCATCTACAACATCTACTACTGGTG  
311251 AAATAAAGATACTACAAAATCAGATAACAAGATTAAAGAGTTTTGGGGT  
20 311301 GAATATCAAGAAGTGGATGGAGGGTTAAAGAATTTTACCTTTAAAGCAAG  
311351 CATCTTTGAAAACTGAAATGAAACGTTAGATTTTGCTACTAGAATAGCAA  
311401 ACTCTTTTCCTGAAAAGGTTAAAAATATAACAAATAAACTGGGCTTGAT  
311451 TTACAAGGTGTTTTAGGAGTTGATAGTAGTTCTAATGCACCTTATGCAGC  
25 311501 AGTTTTTGCAGCTGGTCAAGCTAACTATGATAACTTCTTTTTTAACATCG  
311551 ATAAAAGAACTGGTTATGCAGATTACTCTAACTTTTTAAATAAAGATAGT  
311601 TCATACCAAAATTTAGAGAGTGTTTACAATGACTTTTATAAATTAATCCA  
311651 AGCTAATGGTTTTGTTGTTAACCGTGGTGGTTCCTATTCATCCAACCTTG  
30 311701 AAAAAATTCACCAATTGGCATTCTCAGTATCTTCTTCTGGAGGATACAGT  
311751 TATTACTTTGCTAAAGATAATGCTAAGCGCTTAAAGTTTAGTAATTATGC  
311801 TATTGAATATCCTAGTTTTACCCAAACAATTCAAGCTCCTAATCTTCAG  
35 311851 AAACAGAAAGTAATTTACTTGGTACTTTTAAATTAAGTAAAAAGATATC  
311901 AATCTATATAAAGGTTCAATTCCTAGTGAAAACAACAAGGAGTTGATGC  
311951 TATCTTAATTAGTAACCCAACTTAATTAATATTCTTGAACAAGCAAAAC  
40 312001 AAAAAAACTGCACAAGGAAGTGAATCAACCACTAACAAGATAATAGGT  
312051 TATACCACCACTGCAAATGTTAATGTTGATAATCAAAACATCTTTTCTGT  
312101 TAGCAAACCTTAACAACGAACAGTTTCAAAGAAAAATCATTGTTAATGCCA  
312151 CTGAAGAAACACTTGATCAATCCCAAACCTTACAGAGCAATGAATCAATT  
45 312201 GTTTTACCAATGCCTGGTAAATACAAATCAACTGATAAAAAATAAGTAAT  
312251 GATCACCCAAGGTCTTAACCTAATAGGCATCCATGCAAATGAAAAAGAAA  
312301 ATATTGAACTAAAAATTTGTTAATTGGTTTTTAAATCAAAGTATTACA  
312351 GATTGGAATAGTAATAATCAGCAAAAAAATAGTGATCAAACAACAAAAAC  
50 312401 TGCTGCTGAATATTTCACTGATCAAGCTTCTTACATCCTTCCTTTAAAGG  
312451 AAAAATTTAACAAAAGTTCAGATTTAGAATTGAAAGGCAGTAGTAGTTCT

312501 TCTAATTTAACAACCAGTAGTGCTAGCGCCTCTTTGTTAATAAGTAATAA  
312551 TAGTTCAACTGCAAGTTCTCCTGCTCCTAAAAAACAAACAATAATTCTA  
312601 ATACCTTTACAGCTAAAGCACTAGAATTATTCCAACAAGCTGCTAACAAT  
312651 GAAATTATTCCCTTTAGTGATCCAAGTGACTTTAGGAACGGCACATTCCG  
312701 TAATAATATAAGCAGTAGTTTTAATGCTGCGGTGAATTCTAAGGTTAGTT  
312751 TTAATCAATTTGTCCAAAACCTTTATTAATAGTTTAGGATCTGGATTTAGA  
312801 AGATAATTAGTTAACCTCCCCAACCTCTATTTTCTGTTACTAGTGCCTA  
312851 AGGTGGCATTAGAGTATCACAACCTGAATAACCAAGTAGTCAAAGAGAGT  
312901 TTGGAAGTGGAAGCAACTGATTCTTTTGATCCCACCCAAGGGTTGCAAAA  
312951 AGATAGTCCAGTGAAGGATTCAAGTAAACAAGGGGAGAACTCCAAGAGA  
313001 CCATGTCATCAATGAGTGGTATGGCTACCTCTACAAGAGATAAAGCCCTC  
313051 AAGATTGAGGTGGAAGGGGAGTCAAAGTGATTCACTTTTAAAAAACGA  
313101 CTTTGCTAAAAAGCCACTGAAACATAAGAACAGTAGTGGGACAGAGGTGA  
313151 AGTTGGATTACAGAAGGATTTTCCCCAAGGAAAGGTTGAAAACCGGTG  
313201 TTGAAAACAGATGAGATAGAAAAAATAGGGGGATGGGGGCGACTTAGAC  
313251 TTTCTCCCCTGAATCGGCAATGGTAAACCTTCTCCAACCTCCCCCTCCCC  
313301 TTCAACTTCCGCTTCTCTCAACCCCACTCCCCACTTTTTCTAACATTGGCG  
313351 TAGGGGTAAATCAATGATCACTCAACACTTAAATCAGCAAAACACCCGG  
313401 TGGGTGTTTACACCTGGTAGTACACCAGACATTTGAACAGGAGCAGGTTA  
313451 TAGAAAAGCTAATAACAACAATAACGGCATCCCTTTTGAACAGGTGAAAC  
313501 CTAGTAGTAGTAGCAACACGTTTAAATCCCAATTCAGATGATAATAAAGTC  
313551 ACACCATCAGGTGGCTCCTCAAACCAACCACCTACACCCATTTACCCAA  
313601 CAGTATCAGTCCCACCAGTGACTGGATCAACGCATTAACCTTCACCAATA  
313651 AGAATAACCCCCAGCGCAATCAGTTGTTGTTAAGAGCGTTATTAGGAACT  
313701 ATTCCGGTCTTGATCAATAAGAGTGGAACGGGAGATCAATTTAACAAGGA  
313751 TAGTGAGCAAAAATGAAACGAAACAGATAAAATTAGGAGGCAACCTCCCGG  
313801 GGTTTGGGGAGGTGAATGGTGCTTCTTATAAGATTTTTACTTATTTAATA  
313851 ATTAAAAAAGTGTTAGGTTTTTTTAGTTTTTTATCTATTTAATATTTAA  
313901 GAAATTCTCAAATTTTCTTAGTTTTTTATTTGTTTAAATAGTTAAAAAA  
313951 GCGTTATGTTTTATCTATTTTATTAGTTAAAAAAGTTTTGAATTTTTATC  
314001 TATTTTTAGTTAATAAAAAGTCTTATGTTTTTATCAAATTTTATCTGTTT  
314051 TTTGGTTAAAAAGTTTTAGATTTTCTTCTTAAATTTATTTATTAAATA  
314101 GTTAATAAAAGTGTTAAGTTTTATCTATTTTTAATTAATAAAACCTCGAC  
314151 CCTCTTCTATCAAATCGCTGACCAAACCATCCATAACACCAACCTGTT  
314201 TGTGTGTTCAAGTCTAGGGATGTGAAGCTTACATATAGTTCAAGTGGCT  
314251 CAAATAACCAGATTAGTTTTGATTCAACTAGTCAAGGTGAAAAACCTCC

314301 TATGTGGTCGAGTTTACTAATTCACCAACATTGGCATCAAGTGAAGGGT  
314351 AGTGAAAAAGTATCAGTTAGATGTACCGAATGTTACCAATGAGATGAACG  
5 314401 ATGTACTGAAAGAATTGATCCTAGAACAAACCCCTTACCAAGTATACCTTA  
314451 AACAGTAGTTTGGCCAAAGAAAAGGGCAAACCCAAAGGGAGGTGCATCT  
314501 GGGTAGTGGGCAAGCAACTAATTGACGATCGATGCGTAACTCCATTGGTC  
10 314551 TGAATGACAATCCCAGCCCCAATGCTTCAACTGGGTTTAAATTAGACAAA  
314601 GGCAATGCATATAGAAAACTAAGTGAATCCTGACCAATTTATCAACCAAT  
314651 TGATGGGACCAAGCAGGGCAAAGGGAAGGATAGTAATGGGTGGAGTTCAA  
314701 CTGAAGCAACAATGGCAGCAGGGGATGCGCCCTAAGTACAGGAGGGAGA  
15 314751 TCATCAGATCAAAGTAATAAATTCACCAAGTACCTCAACACCAAGCAAGC  
314801 ATTGGAAAGGATCGGCATCTTGTTTGATGGGGATGGAATGAGGAATGTGG  
314851 TTACCCAACTCTACCAACCCAACAAGGTGAAAAGTGGTCAATATCAACAA  
20 314901 AATAACACCTACAACAGGTTAATTGAGCCTGACAATGCAACAAGTGCAGC  
314951 GAGCAGCATGACCAGCTTGTTAAAGCTGTTGTCTAGTAAAAACATCAAAC  
315001 AGAAGTTGGGGAAGGGGGAAACAGCAATGCAGGGAAATAATGGTGGAGGG  
315051 GGTGTTAGTCAAACGATTAACACCATTACCACTACGGGAAATATTAGTGG  
25 315101 CAATGGAACCATTCAAACGGCTTATCCGGTGAAAAAAGATGAAGCTTCAA  
315151 ATGTAGCGATCAATTCCTTGATTAACGCTACGCCCTGAATAGTTATGGG  
315201 GATTTAAATAATGCTAGTTTTTCTAAATAATTAAATTGTTAATAACAAAA  
315251 AAATCTCTATTAAAAAACCACTTTAAAGTTGGTTTGAAATTCTAAATG  
30 315301 GCGCGCCCAATAGGACTTGAACCCATAACCTTCTGGTCCGAAGCCAGACA  
315351 CTCTATCCGATTGAGCTATGGGCGCATATATTAATAAATTTTATTAATAT  
315401 AAGCAAGAACAATCTAATTCCTTATTAGAATTTAAACGATTTTCATCTAAT  
35 315451 AGTTCAAATCACATATGGCAAAAGATAAAAAAATAAGGTTGATGGAACA  
315501 GaGCAATCAGTTGATCTATTTGAACGTACAAAACCTGAAGATACACAAGT  
315551 TTTAAATGAAGTTGAACCTTGATGATATTAAAAAGATAACAGAGCTTAGAA  
315601 AAGAACTTGAACATACTTTTGAACCACAAACAAGAATGCAAATTAAGCGT  
40 315651 GAAATTAAGAAATAGAACGCAAAATGAAACGTTCTAGTCGCTAATTGAT  
315701 GTTTGTTAATTTACATACAAATTCATACTATAACTTTCTCAATTCTGCCC  
315751 TTTCTCTAAAAAGCTAGTTAATCTAGCAATTAATGATCAGCAAAAAGCT  
45 315801 GTTGTATTACAGATCCTAATCTTTTGGCGCTGTTGAATTTTTTATAAC  
315851 TTGTAAGCAAAATAATATTAAACCAATTATTGGTTTAACTTAACTGTTG  
315901 AATACCAAAAAAATGATGTTAAGTTATTACTAATTGCTAAATCAAATAAA  
315951 GGCTTTCAAACGTTGAACAAAATAGCATTAAATCAACAAAACTTGAAAT  
50 316001 TAATTCCTTAGTTGATCAACTAACAGATATTGCAGTAATTATCTGTTCTT  
316051 TAACAACATGAAAATCTACTTATAAGGATGTTTATCAAGCAAAAGGAATT

316101 GAAATAAATCAAACCCCGATTGCCATTCTTGCAAATGCTGTAACTGTGA  
316151 AAAAATAATAGCGATCAAGTAGTTTTAACAGTTTTGAAACAAATGAAAC  
316201 AAAACCAAACGGGAAAAATAACTACATTTGATTGGGATCTTAAACAAAAA  
316251 TTAAATCAAATTTCAATTAATGAAAATTTAAAAGTAAAGAGTGAAATTCA  
316301 ACCTTTTTTAGATCAAAAACTGCACAACAATTATTCAGTGAAACAGAAC  
316351 TTAATAATCTGAATGATCTAGTTAATAGATGTGAATTAGATTTGGAGCAC  
316401 CTAAAGCTGCTTCACTTTCTTTAACTGATAATGATGCAGCAGTTTTAGA  
316451 AAGTTTGTGCCAAACCAATTTAAAACAGTTTTTAGATAAAAAATCAAGATC  
316501 TAAATAAAAAAGCCTATCAGCTACGTTTAGAGAAGGAATTAAATGTTATC  
316551 AATAAATTAATTTTGCTAGCTATTTTTTAGTTGTCAATGATCTTGTTAA  
316601 TTATGCTTTTAAAAAGGACATCTTAATTGGTTCTGGTAGAGGTTCTGCAG  
316651 TAGGATCATTAGTGGCTTTTTTATTAAACATTACCAAGATAGACCCAGTC  
316701 CAACACCAGCTTATTTTCGAACGTTTTATCTCAACCCACCGTCAAGATCT  
316751 ACCTGATATTGATATTGATATCATGGAGAATAAAAGAGCAGAAATGATAA  
316801 ATTATCTGTTTGAAAAATATGGCAAAGAAAAGTGTGCACAAATTGTTACT  
316851 TTTCAACGTTTTTAAAACCCGTTCTGCTGTAAAGAAGTTGCTAAATTATT  
316901 TAATGATTATGGCATTAGTGACATGATCCTAGGAGTGTTACCTAAAGATC  
316951 AAATAATAACATTCACTGATCTTAAAGCTACTGAAGATAGTGCTTTACAA  
317001 CTTTGTTTACAACAGTTTGGTTTAATTGTTGAATTAGCACTAGCAATAGT  
317051 TGATTTTCCAAGACAATCAAGTATCCATGCTTCAGGCATAGTTATCGCTT  
317101 CAAATTCCTTTGATTAAAACCATTCCTTGTTACAGCTTGACAATAATCAC  
317151 TTTTTAACTCAAGTTTCAATGGAATGGTTAAGTTTTTTTAACTCTCAATAA  
317201 GTTTGATCTGCTTGGTTTAATTAACCTTACTATGATTAGCGATGTAATTA  
317251 CCCAAATTAACCATCTAACAGACCGTTAACAGTTTTTTAAATACCATT  
317301 TCTTGAAGTATCAAAACACCTTTATAAACTTAGTAAATGAAGATACACT  
317351 AGGAATCTTTCAACTGAATCGTTTGGCATGAAAAAATTACTGGTTTCAGA  
317401 TTAAACCTAAAACCATTAATCAACTAGCAATTGTTCTAGCGCTTTACAGA  
317451 CCAGGTGCACAGGATAACATTAACCTTTTTTATTAACCGCTTGACAATGG  
317501 TTATGATCAATCTGACATTGATCCTAGGATTTTACCCATTGTGAAAAATA  
317551 CCTATGGAGTTTTAATTTTTCAAGAGCAGATCATTAAATCGTTAAAGTT  
317601 GTGGCTAACTACTCTTTAGAAGAAGCAGATAGCTTCCGTAGAGCCATTTTC  
317651 TAAAAAGGATGTTAAATTGATCCAAAAAATAAGCGTAACCTCTTTGAAA  
317701 GAGCAGTTCAAATAACTTTGATTTAAAGACTACTACCAAAATTTTAGC  
317751 TACATAGAACGCTTTGCTAACTATGGGTTTAACTTTCTCATGCGTTGGG  
317801 TTATGCACTGCTTTCATACTGAACAGCTTGACTTAAACTAACTATCCTG  
317851 TTTATTTTATTTATGGTTATTAAACCATTTTCAATCTAGTAAAGACAAA

317901 CAAAACTAATTATTAGAACTTTAGAAAAAGTGGTATTGAAATTTATCC  
317951 ACCTCTTTTAAATAAAGCTCAACCAAATAGTGTTATAGAAAAATAAAAAA  
5 318001 TTTATTAGGTCTAAACCTAATTAAGGGAATTAATGACAGGTACATCCAA  
318051 AACTTACAAAAAGTGCAACATTTAATTCAAACTCAAATAACTTACAAC  
318101 AACTGATGTAGTAAGTTGGTGTGGGATAAAACCATTGGTGATATCCCTT  
10 318151 TAAAAGATTTACTTTTATTAAAACTATGGGCTGTTTTGATTTTTTTGAA  
318201 TACACTTATGACTTTAATGATGCAAAGGATTTTTGAATTAAAAGCGATCA  
318251 CCTATTGTTTACCAGAATGCCTTTAGAAAAAAGGATAGTAATTTTTGAA  
318301 TTAAACAATTTTTTACCAATTAGTTGAACATGAAAAAGCAATCCTGATT  
15 318351 GATGGCAATTCCTTAGCATACCGTGCTTATTTGCAACGTGAAAACAAGT  
318401 TGAATATGCTAAGCAAAATAATTTACCTTCAATAATGCAATAAGAACAA  
318451 TGTTACTAATGTGTTGGAATTTAATTAAAGCCAATGTTTATCAATATGGA  
318501 ATTGTAAGTTTTGACACTAAAGCGCCAACCTTCCGTGATCAAATCTATGA  
20 318551 AGGATATAAACAAAAAAGGGTTAAACTCCAGTTGAACTTTAGTACAAA  
318601 TTCCTCTAATTAAACAAGCGCTTGTTTATTAGGGTTTTTAGTTTGTGAA  
318651 AAAGATGGCTTTGAAGCAGATGATTTGATTGGTAGTTATGCCAATTTATT  
25 318701 TACAAAGCAAGAAATAACAGTTGATATTTACAGTTCAGATCGAGATATGT  
318751 TGCAATTAGTAAACGCCTTTACTAATGTGTTTCTCTGTATTAAAGGTACA  
318801 AAGGAGATGGTTATGTACAACAATGAAAATTCAAATCACTTTTTTATGG  
318851 TTTGGCGCCCTATCAAGTTGTTGAATATAAGGGGTTAGTTGGTGATAACA  
30 318901 GCGATAATTTAGCAGGGATTAAAGGGATAGGTCCCATCAAAGGGATAGAA  
318951 TTACTIONCAACATATGGAACCATGATAACATCTACACTAACTTCAATAA  
319001 TCTCCCCAACCAACTTCAAAAACTTTTAAATAACCAAAAGGAAATAGCTA  
35 319051 AAACCTTTAGTTTTCTAGCTAAAATTAAGCTGATATTGAACCTGATCAA  
319101 AACATAGATCTTACTGGTTTTAAACCAATCCAAAAACAAGCGTTAATTCA  
319151 ACTTCTAAGTAAAAACAAATTAATACTTTAGTTGAAAAATTTTCAAAAA  
319201 TATAATGCCTGAACTTCCTGAAGTAACTACTGTTATTAATGAACCTTAAAG  
40 319251 AAAGTGTAAAAATAAACCTTTAGATCAAGTTCAAGTTAACCTAAGAAAG  
319301 GTTTTGAAAAATATTGATCCTCAATTGCTGAATAAACAATTAAAAATCA  
319351 GTTTTTTACTGATATTAAGCGTAAGGGTAAATATATCATTTTTCTTTTAA  
45 319401 GTAATGGTTTGTATTTAGTTTCGCATTTACGTATGGAAGGTAAATACTTT  
319451 TTTGAAGAAAGAGGTAGTAAATTTAATCAAAGCATGTTTGTAGTAGAATT  
319501 TCATTTTGATGATGGTAGTCAACTCAATTATCATGACACCAGACAATTTG  
319551 GAACGTTCCATTTGTATGAAAAGTTAGAACAAGCAGCACAAATTAATAAA  
50 319601 CTTGCATTTGATCCTCTAGAAGCTGGTTTTGACTATAGGAAAATCTTCCA  
319651 AAAAGCACAAATTCAAAACGTAAAGTTAAACTTTTATTTTAGACCAAA

5

10

15

20

25

30

35

40

45

50

55

319701 CAGTGATTAGTGGAAATTGGCAATATTTATGCAGATGAAATCTTATTTGCA  
319751 AGCAAAATTAATCCTGAAACAATGGTTGATCAACTAACAATTAAAGAGAT  
319801 AGAGATTTTATGTAAAAATGCTACCAAAATTTTAGCTAAAGCAATAGTTA  
319851 TGAAAGGTACTACCATCAGCAGCTTTAGTTTTAAAAAGATCATACTGGA  
319901 GGCTATCAAAACTTTTTAAAAAGTTCACACTAAAAAGATCAACCTTGCTC  
319951 AGTTTGTAACCAATTAATTGTTAAAAAGAAGATTAATGGAAGGGGAGCT  
320001 ATTTTGTGTTAACTGTCAAAAAATCACAACCAAGTTTCTACAAACTC  
320051 AATCCATAAATTTTTTAAACTTTAAATATCTTAAATTAACCTTTTAACA  
320101 AACTAATTGAAACTTTTATTTAACAAAGTAATGCTGTAATTAATCAATTA  
320151 GTTAATGAACATTAAATAACATTTATGAAAAACGAAATTAAATATCTTTA  
320201 TTCTGACTTGGATGGTACTATTGTTAGCTGAAATCCTAAACAGAATTTG  
320251 TTTATCAAAATAAAAGTTATAAAAAATTTCCATGAAGTTAGTGATGCTACT  
320301 ATTAGTGCTTTTTTACCGATTGCAACAAAAGGGAATTAAGGTTGGTATTGT  
320351 TACTGGTAGGGATTATTGTCGGGTGTTATGACTTGAAAAACAACCTTAGAA  
320401 CAGGATTGCCTACCATTACTTTAGATGGGGCTATTATCTTTTATCAAAAC  
320451 GAAATCTTAAGTCAAACCTTATTTAGATGATAGATTTATTGAAGGGATTAA  
320501 TAACATAGTAAAGCGCTTTCCTGAAGCTGCTTATAAAGTTAACAGTGGTT  
320551 GAATTAGTTACTTTACTAAAAACCTTCTGTTATCTTTGAAATTGATTAT  
320601 GCTTTTCTTGGCTATTTCACCCTAACACCAAACCTACAAAAAAGTTTAT  
320651 AGACAGTACTGAAATTGAGATCTTAATAAACTAAAAGTTAATCAGGTTT  
320701 ACTTTGATATTGATACTTGCCCCCTTAGCAATGCAAAAGGAAATAATTGAA  
320751 CTAATTAGTGTTAGTGATGTAAATGCCAAAATCTATGAGCACTCTATGTA  
320801 CATTATTAATAATGGTGTTTCTAAAGCTAGTGCATTGCAAAGCCTTAACC  
320851 AGTTTGCAATTCCAATAACAAAAGATAACACTATTGTTTGTGGGGATGGA  
320901 GATAATGACATTGAAATGATGCAGTGAGCTAAACACAGTGTCTCACTAAT  
320951 CGGTAGTAATCCCAAATGCTTTGCTCTAGCAAAATACCACACTGATAGTG  
321001 TTGACAATGATGGTATTGCTAACTGGATTGAAAAAACTTGTTATGTTAA  
321051 TTGCAATCGTAGGTAAACCAGGTGTTGGTAAAACCAGTCTATTGCAATAT  
321101 CTCAAAGATAACTATCACTTTTCAGTTTTTTATGCAGATAGTTTTATCCA  
321151 TGAACAGTACCAAAAAACAATCCAGGTTATCAATTAATCATGGATCATT  
321201 TTGGCAAAGAGTTTGTCAATCAAAGTTGATCGTAAAAAAGTAGCA  
321251 AACTATGTTTTTATGATGATAAGTTAATCGAAAACTTTCACTAGTAAC  
321301 AAAACCGCTGTTAATAGCGTGAATCAAATCCTTAAAAACCCAGTTTCAAA  
321351 AAAAGCTAGCACTAATAGAGATTGCTGTGATGCTTAACTATTGAAATGAA  
321401 TATAGATCGTTGTTTGATTATGTGATTAAATTAGAAAGGGATGATCAGCT  
321451 AGTTAACTTAGCTTTACAACAACGTATAGTCATAAAAAAGTTAAGGATT

321501 TGATTAAAGAGCCTAATTGCAAAATAGATACAATTTTCAACAACGATTCTG  
321551 ATTGCAACAGCTGCTTTAAAGCTAATTAAGTTGCTAGAACTTTTTTTAGA  
5 321601 AAGAAATAAATGCCGTTGTGATTGTTGTTCATATTCAGTAATAAACTTAGC  
321651 ATTTTTTTTAGCTAAATCAGTGCCATTAACCAAAGCaACTGGCCATTTAA  
321701 CACTTTGAAATATTTCAACATCATTATCAGCATCACCAAAGACCATAGTC  
10 321751 TTTTCAGGATCAAGATTATAATTATCAACTAATACTTTCAATCCATAAGC  
321801 CTTATTAACATCTTTTTGCATGATATCAAGAGCAAATGTCATTGAACTCA  
321851 CATAGTTAATATCTTGAATTGATCTAGTTGTTTTGCTAGAAAAGGAACT  
321901 TTTTCTCTGTTTTTAGTTACCAGTAAGATCTTTGTAATAGTATGTTGCTT  
15 321951 AAAATCAAAATCCAAAGCTTTTTCAAACCTGTAACTATGTAGTTATTTT  
322001 CAATGAGATCAATTCCTACTATTTGACTTCTAGTTGAAAGAATTTTAGCT  
322051 GAATCAAGCTCATGTGTAAAAGCAAAAACCTTTTTATCTGTATAGAAATA  
322101 AAATGTTTCTTGAAATTCCAACAACATTTGCATAATTGCAGGTATTACTT  
20 322151 TATTATCAATAGGTTTGATATGAACTGGTTTTTCACTAGCAAAATCATAA  
322201 ACAAGTGCACCATTGGAAGAAATTACAGGTAGATTTGGTGTAAATAAAGGT  
322251 AGCTGTGTTTCTAATTAATAATATGGCTTCTACCACTAGCAAAAGTGATTCT  
25 322301 TAATCCCTTTTTTCTGTAAATCCTTTAAAACTCAACTGTTTGTCTAAT  
322351 GGAATTTGGTTGCTTGAAAGCAAGGTACCATCAAGGTCAAAAATAATGTT  
322401 TTTCAGTTCATTTAGCTATATACTTTTATCTATTTTTTTAAAAGAACAT  
322451 TAATAATTCGATCCTGAACATAAACTACCCTCTCAATCGGTTGGTTGAGA  
30 322501 ATGTCATTTATCTCTTTATCCTGTTTAAATGATTCTAAACATCTATCTC  
322551 TAAACTACCTTTAGTAAATTCTTTAGCTGCTTTAAATTTGCCATTAATTG  
322601 AAAGAATAACCTTAGTTTTAGCAGTCTCAAAAAGTTGATAATCAACTAAA  
35 322651 GAAATCGCTTGTTTAAACAACAAATGGTTCAAGTCCACATTTTTTCATTCAA  
322701 TTCTTCAGCAAGAAAGGGCGCAAAAACGACAGTACTGTTAAAAATCCCT  
322751 TTGCATAATTTAAGCTAATTTTTTTGGTTTTATAGAGAAAGTTTAAAAAG  
322801 ATCATCATTTCTACTAATCACCAGATTTAGTTCATGTTTGTCAAGATGACA  
40 322851 ATAAGTGTTTTTTAAAAACAAATTGTAAGCAAAGATTGTCTCTTGACTAA  
322901 CTTGATCAGTAACAACAGCATGATTAAAAAGAAGTTATAAACTCGATCC  
322951 AATCACCTTCTCATCCCGTTTAACCCTTCATCATTTCAAGTTAACTAGC  
45 323001 ACTAATTGGGCCCATAAACATTAAGTACAACCTTAAAGCATCTGCTCCAT  
323051 GTGAATCAACAAGTGGTGTGGGGTTAATGGTATTACCTTTGGATTTGGAC  
323101 ATCTTTTTACCATCAGGACCTAACACCATAACCCTGATTAATTAATTTTTG  
323151 AAATGGTTCTTTTGTGTGATACTAGCTTCTGTCAAACAAAAATTTGTGTC  
50 323201 AAAACGGGCATACAAAAGGTGTAAACTGCATGTTCCGCACCCCCAACA  
323251 TAAAGATCAACTGGAAGGTATTGATCAAATAATTTCTTCGCTTCTTTTGA



323301 ATCAATTGGTCAAAAATTAGGGTTTTTAATCAACATTAAATAACCCAGAT  
323351 AATACCAACAAGAACCAGCTCATTGGGGCATGGTATTAGTTTCCCTTTGG  
5 323401 TAATGGATGTTATCTTTGACTATGTTTACCCAAGCTTGATTTCTCATTAG  
323451 TGGAGAATTACCACTTCCATCTGGTTTGTAATTCTCAAGTAAGGGTAATT  
323501 CAACAGGGAGTTGTTCTACCAAATGAGGAGTGTTATTTTCATCAAAAATA  
10 323551 ATTGGAAGAGTTTCGCCCCAATAACGCTGTCTACTGAAGATCCAATCACG  
323601 CAGTTTATATACAGTTGTTAATTTTCGCTTTATTTTGTGAAATTAACTCAT  
323651 TAGTAATAGCTACTTGTGCTTCTTTAGTTGTTAATCCGTTATATGCAAAT  
323701 GAATTTTGCAGCCGTTCTTTTTTATCAATGACGTTGATAATTTTCAACTT  
15 323751 TTGTTTACGTGCGAAGAAGTTATCATTTTCATTGTGTGCTCCAACACCCA  
323801 TAATAGCATCTGTTCCATATCCTTCAATTACATAGTTAGCAACATAGACA  
323851 GGGATCAATTCAATTTGTAAGAGGGTGAATAGCATTGTGTAATAAATCTAT  
20 323901 CCCATCATATAAAGTTGCTTTTTTGCTTTAAAGTTGTGGTTTTCTGGAGTT  
323951 GTTTTTTTAAAAAACTAGCTACTTTTTTATTTGTTTCTGCTATCTTTTTT  
324001 GCTAACCAATGGTTGGTTGAAACTGCAAGAAACTAACCCCAAAAATTGT  
324051 TTGTGGTTTAGTTGTAAAAATTGCAATAGCTTCCTTATGATCTTTTAGTT  
25 324101 GAAAGTTAATAGTAACACCTTTACTTTTACCAATTCAGTTCCGTTGCATC  
324151 TCTTTAATTGGTTCAGGTCAATCAAGTGTATCTAAGCCTTCAAGAAGTGC  
324201 ATCAGCAAAAGTAGTGATTTTCAAACTCACTGTTTCATCTTGCGTTTTT  
324251 CAACTGAAAATGAACCCCTTTCACTAACTGCGTTGCCATTACTATCAATT  
30 324301 AAAACTTCTTCATTAGCCAATACAGTACCTAGCTGTTTACACCAATTAAC  
324351 ATCAATATCAACTAATTCCGCTAGGTTTGCTTTAAACAGCTCACTGAAGA  
324401 TCCATTGTGTGATTTGTAATAACGTGGATCAGTTGTTTGTGAGACTTAAA  
35 324451 TGATAGTCATAATCAAAACCAAACTAGTTAATTGATTAATAAAGTTATT  
324501 AATGTTTTGATCTGTTCAACTGCCAGGGTTTTGATTAGAGTTAATAGCAT  
324551 ACTGTTTCAGCAGGTAAACCAAAAGCATCAAAACCAATCGGATGGATCACA  
324601 TTAAATCCTTTAGCTTTGTAATACCTACTTATTACATCAGTGATAGTATA  
40 324651 AGCTCTAACATGTCCTAAATGTAATCCTGCTGCTGAGGGATAAGGGAACA  
324701 TGTCAAGGACATAATATTTCTTTTGTACTATCGCTTTCAAAGCGGTTA  
324751 ACATCTTTGTTTTTTTCATTTTTTTAACCCTTTCTTCAATTAAATTGTG  
45 324801 ATTGTACATCTAATTGCTTTGATAAGAACGCTTGATTGCATATTTAGTTA  
324851 AGCGATAGAGTATGTCAACAATAATCGCAATAATCAAACCAATAACAAC  
324901 CCAAAGCCAACAGGGATAAAAAAGTGAACCATTTGTTTTAAATAAGACTGG  
324951 TTGGTTTGCAACTGTGGCATTAAACCAACTGTTAATGTTGGGAAAAATCG  
50 325001 TTAATAATCCCACTAGCATCACTGGAAGCGAGTAAATCAGCCCACTGA  
325051 GCTGTTTGGTATGTATTAAGTCAAAAACTACCAATAAAAAATAAAAAACCC

325101 AATTACCATCAAAAAAACTAGGATTGCAATTTTCACTAGTTTAAACAAAA  
325151 GTGTCATTGTAGTTTTTAGTAAGTTATTTCAATTATAAAGTTAGATAAAT  
5 325201 TTTCAATCTAACTTTTGTAACTTTAATTTTCAAGGATCATTTTAATAAT  
325251 AGTTACTATTGGTAGTTTTGCATCTATAATACAGTAATTAATCCCAAAAT  
325301 CATTACAAACCGCTTCCATAAATCCAGTGTAACCCGTGTGTAAATTTTGA  
10 325351 AAGTAAAGTTGATTTTTAGTAAAGTTATCAATCTCTACTTTGCGGTTACG  
325401 CATAAATAGTCTTTTTTCAAATAATTTTCAATCCCCATCCAAAATGACAT  
325451 ATAAATTAGGAACCCCATGCTTATTAAGTAGTTCTTTTGCTAATCTATTT  
325501 CACAGTTGGTTATAGTATGAAAAGACTGCAGGACGAATGATGTTGTGCTT  
15 325551 AGCAAACAACAGCTCTTCAAAGATAGAACGATCAAAAATGGTTGGATTGA  
325601 TAGTGTTGCAATTGTTCTGGTATTTACCAAAGCGATTAAGCGTAAATAA  
325651 AGCTGAAACAAAGGTGAATAGAGCAATTCATCACTACGTTCATACATCTT  
20 325701 TGCTAGTAAAGTTCAACCAACTGGTCATTAGTTTCCAATTCACAAACAA  
325751 CTTTTCAGCTTGAATGTGGTTAGCTAATGTATTAGCAATGGTGGTTTTT  
325801 CCTAAAGCAATCATTCCCCGATCACAATACAATTAGCAATTTTATTTGG  
325851 TTGAAAATGGGGCTTTTTTAGTTGCATATAAACACTTTTTAATATGTTGG  
25 325901 GTTAAGGTTTATTTTTAATAAAAAACCATCACACTCACTGACAAGTCTTA  
325951 ATGCTGCTCCATTTCTGGCCTGACATGATTGACTCTAATGATGTGATGG  
326001 TTCTAAATTCTAACAATTATTTAAATCTTAATCAATTAATTTACTAACCC  
326051 TGTTAATAGAAATTGGATTTGGGTTGTGTAGTGCCCTCTAGGCAATGAACTT  
30 326101 GAATTTGATTTTTTAGATGGTTTGATCGGTTCAATCTCTTGATCTAATTG  
326151 CTGTTGTGACGCTGGAGTTTCTTGTGATAATTTGTTGGCGTTGAATGAT  
326201 CAAGTTTAGTAATTCAGCTATCTTTTTTGTTAGTTTTGCTTTGGTTTTT  
35 326251 TCAAAGCTGCTTAATGAAGTTAGTAAAGCCAGTCTTGGATTCTTAGTTTC  
326301 ATCAAAAATGGTTGCAATAATCTCATCAAGCTTGGTGAAATCAATTTCTA  
326351 TTTCGGTGGTGAGCTTTTGGTGTTTTTGAAGCGAATTTACAACCTAATTA  
326401 TATGCTTTTTTTAATGCTTGCTTTTCTTTTTTCAGCGGTTTTTAAAAGTGA  
40 326451 TTGGGTTTCACTAATTTCCCATCTTTAAGTGCTAACTTGTCTTCAAATA  
326501 CGGTTTGGATGTGTTGATCACGTTTATAAATTGCTTCATTACACTGCACT  
326551 TCATATTCCTTTAACAATTCCTCTACATTAATACTTTCATGTTCTTCAAT  
45 326601 TAGTTTCTTATTGGCTTCTTTTATTGCATGTAAGTGTATTTAATGCTT  
326651 CAATTTGGTGTTCTTTTGCTTCTACCAGCTGCTGCATTTGGATAATTTCA  
326701 CTTTCACTTTGTTTGAGTTGTGAGAAAAGTTCGCTGTTCTGTTGAACCTG  
326751 ACGGTTAATCTCTCCTTCCAAGCGTACCTTAAGTTGTTCTTGCAACTTA  
50 326801 AGATCCTTTTTAAACGTTCTTTTTCACTTCTCGCTTCAGGACCAACTTT  
326851 TTTAATAACAAAACAAGCATCTGGTTCCAATCAACATTTTTTGGGTTGCT

326901 TGTTCTAGTTTGTACATAAGCAGTTTTTGCTTGTCTAAAAAACATCAA  
326951 GCTGGGCTTTGGAAGCAAAGGGAACTTGGCTAAAAAGAAGTTAATAGTT  
5 327001 TCTCTTCTTTGAAAGTCATCAAAGTCTCTATAGTAATCAAATTATTTCAT  
327051 GGAAAGCTAATTCTCTAAAGAAGCTAATGATAGCATCAGGATCATTAAAG  
327101 TCTAAATCATAATGGTGTCTAACATAAACTAACAACAACTAAAGATTGC  
10 327151 TAAACAAAACCTAGTAAAGAGGAAAAACGGGAGTTTATTGCCATGGTTT  
327201 TTAACAAAACAAATCTAACTTTTCATTAGCAATTTTTTTAAACCTAACTAC  
327251 ATCACTAACTGGTTAGGATCTAGTAAATAGTTGTTAAGATCACTAACTT  
327301 TACTTTCAACCCATTCCAAGTTAGCTTGGTTATATTGAAATTCACTTTTA  
15 327351 ATAGTTGCAAAATCAGTTTTTTCAACCTTGTTCAAAATTGATTTGAAGCC  
327401 ATTTGTGTATTTTTGAACAAAACATCCATTTTACTTGTATCAAATATT  
327451 ACTCCTAAGAGTTGCTCAGGTTTTAACTGCCAAAGTAATCACTAAAATG  
20 327501 ATCAAGTTCATTGAAGAGTTTTTCAAAGGTTTTATAATCGTACTTCTGAC  
327551 CAATTAGTTTTTTTTGTTACTGGGGTGATATCAACAACACTTAAAAAGTCC  
327601 CCATAAACTTAATATCAACAACGTTCCTTTCTCTACTTGAACATTGCA  
327651 CTCAAATAAACCAGCATTATTAAAAATAACGCTTGTTTTTAAAGTTGTATT  
25 327701 CATAAGTTTTACCAAAGTTTCACTCCCATGATTGAAAGTGTCTTTTGCT  
327751 CTTTTTTCAACCTTTGCTAGTGCATCTTTAGTTAAACAATTGTTTCTGC  
327801 TTTTTCAGTAACAGTGAAAAAATTAATCATCTCTTCTAAAAATTTTGCTG  
30 327851 TTGTTCAATTTGGTAAATACTCCTTTACATTAACAACGCGCTTAGCAACA  
327901 CTGTCAACACCCTTACTTGCTATCTTGGTCTTATCAACATTTAAATACTT  
327951 TGCTAACTTAGAAAAGTCAGTGTCAAACAATAATGTTCCATGGACTAATA  
328001 ACCTGTCTTTAGCGATATATTACAGCTAACCAGAAAACTTCTTGTTATTA  
35 328051 ATCTCAAGGTCATTACGACCATGAAATACAGCAGGTACATTTAAGCTATT  
328101 TAAGAACTTCACCACATTTCTTGTTAGTTTGTTCATAAGCATTTTCCATCA  
328151 CTTTACCTGTTCTTGGCAAAATAATAGAAAAACAGATGTTACCAAGGTCA  
328201 TGAAACACCGCTCCCCCGCTGAAAAACGTCTAAACAAGTTAACCTTATC  
40 328251 ACTTTCAACTCCTTTAAGTTAACCTCAGCATAAGTATTTTGGTTTCTTC  
328301 CCACCACAATAGTGTTAGCGTTCTGCCAAAAGTAGATGACCTTAACTAAC  
328351 TCATTTTTTCTAAATTCAGTTAGCAATCACTCCTCTAAAGCTGCATTAAA  
45 328401 ATACGGATTGAAAACAGGGGAAGTAATAATGAAAGTTTGCATCAACTACC  
328451 AATTAACATAAGTAATCAAAGATCGCTTTTTTACAAACATCAGTTACCAT  
328501 TTCATTATGGTAGGATGGGGTGAGATAGAATTGGCAATATCAAACACAG  
50 328551 TGAGGTTGTTTTCCATCACCAAAGCAAGCTCAGCGATAATATCACTAGCA  
328601 GTGCTAGCAATAATACATCCACCTAAGATAGCACCAGTTTTAGGATTAAA  
328651 CATCATCTTGACAAACCCATTGGTTTCATGATCTGCAATTGCTTTACCAC

328701 TATAAATAAATGGCAAGGAAGATTTGACATAATCAATCTTTTCTTTTGC  
328751 AATTCCATCTCACTATAACCTACAAAAGCAACTTCAGGATTTGTGTAAAT  
5 328801 ACAAGCAGGACACTTGTTTTTTTTCAGCAGGCTTTACCTGGTTTTGGTTCA  
328851 AAATTTGATCAACAGCATATCTGCCCTGTTGGTAAGCGTAGTGTGCCAAC  
328901 ATCATTGCGTGTTAACATCACCTATTAGATAGATGTTTGTAGTTGATGT  
10 328951 TTGTAGTTTTTCATTTAAAACAATTTTGTGTTATGGTCACGTTTTAAAT  
329001 CAAGTTGATCTAAACACTCTGTGTTAGCAATTCTTCCTATAGAACTAAG  
329051 ATTTTATCACCATTACAGACTGTTCAACTCCATTAAGTGTGTAAACAG  
329101 TTGGTTGTTTTTCAGCTCTAACAACATGAGCATTGGTAATAATCTGAACTC  
15 329151 CTTTGTTTTTTAAGGTTTTACTTATCAGTTCAGAAACATCACTATCACAA  
329201 ACCTCCAAAATCCTATCAACACCTTGGATAATGGTCACTTCACTCCCTAA  
329251 TGAAGCAAATAAAAAAGCAAACCTCAACCCCAATCACACCTCCCCCACTA  
329301 CAACAACTTCTTAGGTACTCCCTCTAAAGCCAAAGCTTGGGTTGAGTCA  
20 329351 ATGATAAACCAGCTTGTTGTGCTTTTTCAAACCCTGGTAAAGTTAAGTA  
329401 TCTTGGTCTTGATCCGGTTGCAACAATAATGTTGTTAGTGGTGTAAGTTG  
329451 TGTTGTTTACTTGCACCTTGTTTTTATCTATAACAGTAGCTTCACCTTCA  
25 329501 ATACTTTCTACCTTAGCACCCCTTAATAATTGTTTTTACCCCTGCAACTAA  
329551 TTTATCAACTACTTCTGTTTTTGTTTTAACAGTTGTTTTCAATCAAGTT  
329601 TAGCTTGACCATTAATAGTGATACCATAATCTTGGCATGAACTAAATAA  
329651 TCAATAATCTTGCTCTTTTTTAACAACGTTTTAGTTGGGATACACCCAAC  
30 329701 ATTTAAACACACCCACCAAAGTATTGCTTTTCAATCACTAGGGTTTTAA  
329751 GTTTATGTTTGCCAGCATACTCCGCAGCAATATAACCAGCAGGGCCAGCA  
329801 CCCCCAATAATTAGATCATAATCCATAAATTAAGCTACTGTAAGATCAAT  
329851 TAATTCCTCAATTTGTTTTGCAATCTCCTTACCAAACCTACCAACATCCG  
35 329901 CCCCATCAACCCAGCGGTGGTCTGCAGCTATTGTTAAAGGTAAGATGGTA  
329951 TGAAGTGAATTCATTTTCCACTTTAACAATGCGTTCTTCTAAATTACC  
330001 AGTAGCAACAATACACATCTCAGGGTACTTAATAATAGGTGTACCTACAG  
40 330051 CTGCTCCTAATGAACCGAAGTTAGTAACTGAAATAGTACCTTTATTCAA  
330101 TCAGTCAACTTAATCTTTTTTGTCTAGCTTTGTTAGCTAAATCAACAAT  
330151 TGCTTGGGCAATTTCAACCACAGATTGTTTGGGCTTGCTTAATGTTAG  
45 330201 GGACAATTAAACCTTCTTCAGTATCAACAGCAATTCCTACATTAATGTCA  
330251 TCATTTAAAACAATTTTCGTTTTGATCAGGATCATAACTAGCGTTAAAAAC  
330301 AGGGAACCTCTTAAGCGCATTAAACAATTGCTTTAACAAGAAAGCAAAGT  
330351 AAGAAATTTTCATGGAATACTTACTTAAAGCATAACCATTAACTTTTCA  
50 330401 CGATATTGTTTTAACTTGGTTGCATTAACATAAAAAGTTAATACAGTGGT  
330451 TGGGATAATTGCGTGCGACTTTGTCTGCTTCTGCAATCGCTTTACGCA

330501 TTGTTGAGATAGCAATGGTTTTCTGTTCAAGTTTACTTTCTGGTTTTTGG  
330551 GTTGTCTTACAGTAATGTTAGTACTACTTGCAACTTTAGTGTCTTTAAC  
5 330601 AGCTGGAGTTGCATGAGGTTTTACTCCAAAGATAGGAAAGAGGTTATCAG  
330651 AAACCTTAATTTCCCCTACTACTGAAGCCCCCGCTTCTTTTACCTTAGCT  
330701 ACTTCTTCAGTTGGTTGAGGTTTTGGTTCAACAAGTGGTGTACTAGTCTT  
10 330751 TTCACCAATAACTGCCATCACCTGACCAATGCTAACAACATCACCAACTT  
330801 TAACATTAATAGCACTAATTGTACCTGCAAAAGGAGAAGGTAGTTCAGTT  
330851 GTAACCTTATCAGTTTCAACAACAAATAAAGCTTCATCTATCTTGATCTG  
330901 ATCACCACCTTGTTTTAAGATTTTCAGTTACTTTTCCTTCATGTAAACCCT  
15 330951 CACCAACATCAGTGAATTTAAACTCATTTGCCATATCGTATTGATAGTAC  
331001 TTAAAGTTTAAATTTAATAGTAGTGATCTATAACAAATAAAAAAGCCAG  
331051 TTTAGTTACTGGCTTTTTAGTTGTTAGACAAAAATTTTGTCTTACTTTTTT  
20 331101 ACAGCAGCTGTTGCACTTAGCGCATTCGCACTTGCACTGGCAGCATTTCT  
331151 TGTTGTCTTCCATCACTTTAATTTATGAAATGAGGTACCTAGCTCTAAAA  
331201 AATAAAGCTAGGTAACATATTTTAAAAAGTGTTATTTTAAAGTTGAT  
331251 TAACTGCATCAATAACCCGTGCATTAATTTCAAAGTGGTATTTTTCACCT  
25 331301 CTAGCTAAAGGCACAACAATATCAAACCCAGTTACCCGTTGTGGGGCTTT  
331351 TTTGAGATAAGTGAATAGTTCTTCAGTTACTGAAGTGATAATCTCTGCAC  
331401 TTGTAGTGAACTTTTCACCGCTTCAGTCACTACAAGTAGTCTTCTGT  
30 331451 TTCTTCACTGAGTTAAATACTGTTTGTATCTCAAGGGGAGATAGTACG  
331501 CAAGTCAATTAACCAATTCCCTTATCTTTCAATTCCCGCTGTAAACTA  
331551 AGTTAATTAATCAAACATTGTAGGACCATAGCTAACTATTGTAAGTTCA  
331601 CTACCTTCACTAATCAAGTTGGCTTCACCAATAGGGACAGTGTAATAATC  
35 331651 ACTAGGAATCTCCTGACGAAAAGCACGATAAAGCTTCTTTGGTTCAAAA  
331701 AGATAACAGGATCAGGTGATTCAATAGCAGCTAGAAAAAGTCCTTTGGTA  
331751 TCATAAGGATTTGATGGCATCACTGTTTTAAGCCCAGCAATCTGTGCATA  
331801 AATTGCTTCCAATGTTTCACTGTGGTGTTCCAATGCTTTAATCCCCCAC  
40 331851 CCATTGGCATCCTCACTACTAGTGGAGCGGTATATACACCACGAGAACGG  
331901 TTTCTAATCCTAGCAGCATGGACAAAGATTTGAAACATAGCTGGGAATGA  
331951 AAAGCCTGAAAAGTGGATCTCTACAATAGGTTTAAAGACCACCTATAGCAG  
45 332001 CCCCACCCCAATACCAGCCATAGAGTTTTCTGCTATAGGACAATCCCAT  
332051 ACCCTTTCACTCCCATACTTTTGTGTAAGCCTTTAGTTGCACGGAACAC  
332101 ACCCCCTTCAAAACCAGCGTCCTGGCCATAGAGTACAACGTTTTGATCTC  
332151 TTTCCAGTGCAAGATCCATTGCGTTGTTTAAACGCTTCAATGTTATTTACT  
50 332201 TGGATTTTTGACATAGTTATCTTTTTTAAATTAGTCTTTAAAGTATTTT  
332251 TTTGCAATCTGTTTCTGTTCAACTAGTTCAGGGGTTAATTCTTGATAGTT

5

10

15

20

25

30

35

40

45

50

55

332301 GTAATCAAACACCTCATCTACTGATACAGGAGTATCTAGTACCATCTTTT  
332351 CATAAGCAGCTTGGATTTCTGTTCATTTTGCTGAACATCTCTTCTCT  
332401 TGAGCTTGGTTAAGAATTGATCTATCAAACAAGAAGTTTCGCAACCGCTT  
332451 CACTGGATCACTCTTCATTCCCTCCTCCTCTTCTTGGTTGGTTCTGTAGA  
332501 TAGAAGGGTCATCTGAAGTGGTGTGAGGACCTTGCCGGTAGCTGAAGAAC  
332551 TCAATTAAGACTGGTCCATTACCACCTCTAGCGTAATTAGCAGCATCTTG  
332601 CATCGCTTCATAACTAGCAATTAGATCATTACCATCAACCCTTACCCTTG  
332651 GGATCCCACATGCTATTGCTTTAACGCTTAGATCACTAACAGCAGATTCA  
332701 AGTTTAGTTCTTGTGAGATAGCAAACTGATTGTTGTTAATACAAAAAC  
332751 AGTGTTCACCTGTGGATGCTTGCAATGTTTCATCGCTTCATAAAATCCC  
332801 CTTAGCTGTACCTCCATCACCAATCATAGTAACAGCAACATTAGGTTGC  
332851 TTTTATAGTGCAACATGTAACCTAATCCAGCAGCATGGAATACTGAGC  
332901 ACCAATGGTGATGTTAATAGGTAAAGTTTTGTATTTAGCATCTATCTGAC  
332951 TACCTTTTTTCATTACCATTTTCAGTAGAGTAAAGTTGTTCTGGTTTTACC  
333001 CCACGATACAACATTAAAGCCCCACTACGAAACGTAGGACAAACCCAATC  
333051 ATTTTCATTTAAACCTAATCCCATTTCCAACCTGTAAAGCTTCCTCTCCCA  
333101 AATTAGGAGCGAAGTTTAACATCTTACCAGCACGCTGTCAAATAACATC  
333151 TTTTGTCCATCATTCTACTCAAGTTCATTAAGTAATAAGCGTGTTTTAA  
333201 CTGTTTCATCAGTTAGGGTAATTTTGTGGTTAGGATCAATTAATTTACCTT  
333251 CATTATCATAAACCTGATAAAGGGTAGTTGGAACCTTATTTTTAATCAAG  
333301 ATTGCCATATATCTCTATGCTAATTTAAACTAAGCTATTTTTTAGGAAT  
333351 GTAATAGCTAAACCAAGTGCTTGTAACAGTTGCTAACACAAAGTTAA  
333401 ACGGTTTGTGTGTAATGTGGAAGAAAATAAACATCCACTAAACCCAGTTCA  
333451 GTTAGTAACATCTGCTTTTGGATTGCAAGTGCAATATAGAAAATAATCTC  
333501 ACTGTGATTGGTATTCCAAGAAAGGAGTTGTGCTCCTAAAAATCTTAGGG  
333551 TTTTCTGTGCATATACAAGTTTAAACGACCTTGTGCATAACTGCCCATA  
333601 AACTCAGGACGATCATTGTCATCAACAACGATATGCCAACATCAAAACC  
333651 TAACTTCTTAGCACGCTGTTCAAGTTAATCCACATGCTGCTAAATTTAAAC  
333701 CAAAGATATGGAGTGCAATTGGTGCCAACGATAGATTGGAGTTTAACTTGG  
333751 TTACTIONCAATGATATGCATCGCAGCTACTAATCCACTCTTTACTGCATT  
333801 GGTAGCAAGATCGATGTTTTCTACTGTTCACTAGCAGCATTGTAATAG  
333851 CAGCACAAACCCCAATGACATAAACATCCTTATGATTTAGTGCTTGGAGA  
333901 AATTCATTAACTTAATTGAACCGTTGTGAATAAACTCAAAGTTTTGATC  
333951 TTTAGGAACAACTTAGTGCTAGGTCTAAACCCAATTGATTGGTTCACAA  
334001 GGTCTGCATTTACTATTCCTTATCAGTTTCAACTCCTTTGACAACGTTG  
334051 TTTGTACTATCAACAACAAAGCCCTTAACACTGCAACCCATCATTAGTTT

334101 TAACCCATCTTTTTGCATCACTTTTTCAAGTTCATCAGTAAACTCATGAT  
334151 CAAAGTTATTACCAGCAGGCTTATCAAGTAAGTCAATTACTGTTACTTGC  
5 334201 TTTTTGCATAACCAAGCTGCTTCAGCAAGTTCCAAGCCAATGTAACCAGA  
334251 ACCAACAATAGCAACTGATTTAATGGTTTTATCTTTACGAAAAGTATCGA  
334301 TTAAGGTAAGTGCATGTTGGTATAACTTACAGCTAATTAAGTTCTTAACA  
10 334351 TTACCACAATATTTGTCAGTGTAGTTAAACTCCAAAGGCTTGTGTGTCAC  
334401 CTTGTTTTCAACATTCATACATATAGGTCATGCTCCTGAAGCGATTACTA  
334451 GTTGATCAAAGTATCAGTGAAGTCTTTATTTGATGTTAAATCTCTAACT  
334501 GTTACCTGTTTTTTGATTAGATCAATGTTAGTAACATCATGACTCATAAA  
15 334551 GATGTTAGCGCCCATCTGTTTCAACTCCTCAGGGTTGGAATAGAAAAGAT  
334601 CATCAGTGTTTTTAACAACACCACTAACAGCAAGTGCAATTCACACCCC  
334651 AGAAACGAGATGTTTGTGTTTCTATCATAAGCGTTAACCTTAAAGTCCTT  
334701 ACTTTTTGAAAGTAAAGTTCTAATAAAAGTAGTACCAGCGTGATTTATTC  
20 334751 CAATCACAATCACTTTTTTTCATATATCTTAGCTGCAGTAATTTTTTAAGC  
334801 TATTTAAGGATAATTTGTGCAGTAGTGATTGATCTTTTAAAATTAAGCT  
334851 TTTGCTAGTAATGTAATAAAATCTTGCTAACCACATTTGGTTGTAACCTA  
25 334901 GCTTTACCATTGAGTTTTTTTCAGCTCAATTAAAAAGCAATATCCACAGT  
334951 TTCACCATTTAACTGTTTAAAGTAATTGGTCAATAGCAGCAACTGTTCCAG  
335001 CAGTGGCAAGTACATCATCAACAATAACACACCTTTTAGCATTATTAGCT  
335051 TGGATTAATGAAGTGGTTGACATCTCCAATACAGCATGTTTTCTGTACTC  
30 335101 CAAATCATAGCTAGCACTAATTAATTGCCCTGGGAGTTTATTGGCTTTTC  
335151 TAACCAATACTAACGGGAGTTGGGTTTTAGAAGCTAATGCTCCCCCAAAG  
335201 ATAAAACCCCTCGCTTCAGGACATACTATCGCTTCTGCATTAATAGCTTT  
335251 AATAAACTGTGCCATTTGGGTTAGCACAAAATTAAATAGTTGGGGATTGG  
335301 AAAATACTGGGGTAATGTCATAAAACAATGTACCTTGGTTGGGAAAATTT  
335351 TCAAAGCGCTTGATTGCTTGATCAAGCAACTTAAAGTTTGTATCCATAAA  
335401 TATCTTTTTTTTTAAAAAGTGTAAATTCCTGCAATTAACTGCTCTTCAATC  
335451 TGATCAATCTCTTTAAAAGGATGTTTTTTGTGTTTTAAGCTCAAACGGGA  
335501 ATGAACATAGTTGAAAGGACTGAGTCAACCATTGATTAAACCAAAGCAAA  
335551 ACATTGGTAAAAAGCAGTTGCAACATCAAATAAACCAACAATAGCAATT  
335601 AGATAAAAGATCACAAGGTTAAAGTTGCCATCAATCCCACCAAAGTTAAA  
335651 ACCACTGTAGATAATAAAAAATGAAAAGTAAAGCTAGAACTTTCAATCAGAT  
335701 CTATCTTCCACTGCGAGTTGAAGTTATCGTTAAATAAGTTTTTGATAAAT  
335751 ACCTTGTCCTTTAAGCTCCTTTTAAACCAGTAAAGTAAGTCCAAGTTGT  
335801 TGTTTGTGATACCTTAGCTGCAAAAAAGAGCCAAAACAGATAAACAAAGG  
335851 TAATTAAGTGGATTGTTGATTGGTCTATACTAAACAGATAGTTAGTTAGA

335901 TACATCACTGCAAACAAACCACTACATAACAAGATAAAGCTAACCAAATA  
335951 ACTTAAACAATAAGCAACACCATATCTAATCAAACAATAAGCTAAGTACA  
5 336001 GTAAACTAACTATTCCTATCCCAGCAATAATCCCGTTACTTGATTCAACA  
336051 TCTGCTGCTAAAAATTCTCCTAACAGGTTAGGTTGAACAAGATATAAAAC  
336101 TAGCATTACAACCTCTATAGCTAACAAGATTAGCCATACAAACAAAACT  
10 336151 TCCAGTTGTTTTTCAAAAAGAAATCATGTTGGTTTTTGGTTATAAAAAAG  
336201 TCTGTGTTCAAGTCACTAGTTGAACCTTAAAAGTGAATAGTTACTAGAAGT  
336251 TTTAGTTAGTGCTTTTGCATCCTTCTGATAGAGAAAAAGCTTTCAGTTTG  
336301 CACCTGATTCTGAACTGACAAACAGTGAGATTAAACGATGCTGATTCCA  
15 336351 TAACTAAAAAGTAAGAAGTAATGGCTGATATTGCCATCAAATTAGCTAG  
336401 TTGTTGGACCTGATAATTAGAAAGATAGATAACAACCTAAAGCACTAATTA  
336451 ACCAGGTAATGTGAACTCAAGATTAGCAAAAAGCTTCTTTTAAACAC  
336501 AGTTTTACGATTTCGATAATAGAAGCATTATTTCTAATATTTCTTAAGAA  
20 336551 TAACTCTCCTAAATTCAAGAGATTAATTAGGTTGATGGCAATAACAAAGA  
336601 AGATGCCACAAAAGAAAAGACATCAACAACCTCCACCACTGCACTAAAG  
336651 ATAACCAGTGATGACACCACACTTAACCCTAAAGCTAATGCTTTGTATAA  
25 336701 CCCTAAGAGCTTGTATCGTAGTGTTAATAGAACAGCAGCAATAAGAACGA  
336751 TGATACCAAACGCAATAAACTAGAAAGCAAAATTAGAAACATCTGTGATG  
336801 GTATTTGCAAGTGGAGCGTTAACCAGACTTGTTTTTGCAGTTGCAATGGT  
336851 AGCTGCTGTGGGAAATGGATTTGTTAAAAGCTCTTTAACAGTAGCTGCTG  
30 336901 TTACAAAGTTTGGTGGGGTGTATGTACCATCACTACTCAAGAAATTACCA  
336951 ACTTGAACTTAATATTACCACCATATTCTATCCGTTGGTTGTTAGTGTC  
337001 TAAAAAGCTTTGTAGAGTAGGATTAATCTTAACAGGATCACCGGTTTTGC  
35 337051 TAACCGGATCTTCAGTTCTAATTTCACTGATAATATAGTTATGGAATAAC  
337101 CCTGAAAACCACTGCTATCTGCACTCCTTAACCTTCTTGTATCAGCACT  
337151 ATTTGAACTGTAATTACATCTGAACTATTGTTGTTATTGTTATTATTCT  
337201 GGTATTATTGTCTACTGTTGCTAGCAACCGCTGAAAAGTGGTTAGGA  
40 337251 GCAGCGTAGATATAATAAAGGTTTTTGAGAGTAATGTCACTTGCTTTTTT  
337301 AATAGGAGATGCCCCATTAGCATCAGTGTTTAAAAACAGATTATCACCAC  
337351 TAGCAAAGCTACCCTTTGCATGTAAAAATTCCCAGAGACTCTTCTCTCTT  
45 337401 TCATTAAAGGTGAGATAATCACTACTACCCTCACTACATTAAAGATATT  
337451 ACGGACATAGTTTAAATGCGCCTTGTTTATCTTTTCACAATACTAAAGTTT  
337501 TATTACCACTACTTGAAGTTCCATTTCGCATTTTGCTTAAAAAATTTACCA  
337551 TTGCCCTCAACACTAGCTTGCCATTACCAGTATTATAATCAGAACTTGA  
50 337601 TAAGTTTTTAGAGTTGATAAAATCAAGAAAATCGGTGTGTAACTTTCTT  
337651 TGGTAACTACATTTTTATTAACTTGATTCAAAGGTTAAAGCACTGTTT



337701 ACAGAAGTGTTTTGGGGAACAACCTGCCCTAATGGAAGCATTAAATAAAATT  
337751 ATTATCCAGTGAATCAAATAAAACCACTCCATCAGTTGTTTCAAGTGAAA  
5 337801 GTTGGTAGTTGTGTTCAACTGAACTAATTGCATTTCTTCTAACCTGAGCA  
337851 TCAACTTGTCTTTTTCTTTGGCGGGTTTTGGCTTGCTCACGGTTTTGTTT  
337901 AAAGGTGAGAGTAACAGAAGGTAATCCCCATTAACCAATCAGGACTTGT  
10 337951 CAATGTTGTCAAGTTCAGTAGCAGTTTATCATTAGTGTTTTAGTAATG  
338001 TTTACAGAAGAAAAGCCCTGAATGAATAAACTGTTAGCATAACTTTTTTTC  
338051 AACACCATCTAAAAAGCTATCAATGTTAGTGATGTTTTCAATCCCGTTGG  
338101 TTGGTTTTGTTTGCTGAGGATCTAATGAGGTATTGTTAGTTGACTTATGG  
15 338151 TTTAAAAAGTAAACAGTTGTAGTGGTAGAACCGTTGAAAACAGCACCTAA  
338201 CCTGCTGTCATTTAACAGTTTGTAACTCCCAAAAATAACACCAAACAAAC  
338251 CCAGACAAACAAGTCCAAGAATAGTTCCTATTTTTTAGGATTCAGTCCAAA  
338301 GAAAAGCGCTTTTTGAACCTCACTAACTATTTTTAATAACTTAAATTTTA  
20 338351 TATAAATATTAAGTAATGGCAACCATTGAGGAAATCGAGTGTGATTTTTT  
338401 AGCTAAAATAGCACAAAAATTTACTAATGCAGAGATTGAATTAATTAACA  
338451 AAGCATTCTATCACGCTAAAACCTTGGCATGAAAACCAGAAACGGCTTAGC  
25 338501 GGTGAACCTTTTTTTTATCCATCCTTTAAGAACGGCATTATCACTAGTTGA  
338551 ATGGAACATGGATCCTATCACTATTTGTGCTGGTTTGTTACATGACATCA  
338601 TTGAAGATACAGACCAAACCGAAGCTAATATAGCAATGATTTTTAGCAAA  
338651 GAAATTGCTGAGCTTGCTCACTAAGGTTACAAAGATTACCAATGAATCTAA  
30 338701 AAAGCAACGTCATCTCAAAAATAAAAAGGAGAATCTTAACTTAAAAAGCT  
338751 TTGTTAACATTGCAATCAATTCTCAACAAGAGATAAATGTAATGGTACTA  
338801 AAAGTAGCAGATCGACTTGATAACATCGCTTCCATTGAGTTTCTCCCAT  
35 338851 TGAAAAGCAAAAGGTAATTGCAAAAGAACTTTAGAACTTTATGCAAAGA  
338901 TTGCTGGGAGGATTGGGATGTATCCTGTTAAACAAAATTAGCAGATCTT  
338951 TCATTTAAGGTGTTGGATTTAAAAAACTATGATAACACCCTGTCAAAGAT  
40 339001 TAACAAGCAAAAGGCTTTTTATGACAATGAGTGGGATAACTTCAAACAAC  
339051 AATTAAAAAAAATCTTAGCGCAAATCAGATAGAATACCAACTTGAAAGT  
339101 CGGATTAAAGGCATTTACTCTACATATAAAAACTAACTGTTTCATGAACA  
339151 GAACATCAGTAAGATCCATGATCTTTTGTATCCGCTTAATTACTAAAT  
45 339201 CAGAACTTGATTGTTATCACATCCTTGGTTTAATTCACCTTAATTTTTTA  
339251 ATTGACAGTAAATACTTCAAAGACTATATTGCCTCACCTAAACAAAACCT  
339301 TTACCAATCAATTCATACCACTGTTTCGTTTAAAAGGGTTAAATGTTGAGA  
339351 TCCAAATTAGAACCAACAGATGGACAATGTTAGTAAGTTTGGCTTAGCT  
50 339401 AGTCACTGGATCTACAAAGAACAGAAAGAGGGATTGTTAGCACCTGCTTT  
339451 GCAACTTAATTACCTAGTGACAAAACAAAAACACTCACATGATTTTCTAA

339501 AAAGGATTTTTGGGACTGATATTATCAAGATTAATGTTAGTGCTAGTCAT  
339551 GAACCTAATGTAATTAAGCAAATTAATGTTGATAGCAACAATAAACTCCT  
5 339601 TGATATTGCTTTTGAAGAACTATCCCAAGCAATTTGCTAAATTAACCAAAA  
339651 TTGAAATTGATGGGGTTGAGATCAATTCTTTTGATACTAGTGTTGAAAAAT  
339701 GAGATGCTGATTGAATTTTACTTTGGCAAGAATAACAATTTGAAATCAAA  
10 339751 GTGAATTAGGTATATGAATAACCCTATATACCGTGAAAAGGTAAAAAAGA  
339801 GCTTGGCTAACTAGCTAAATCTGGTAGATACAGTGAGTTAGCTTTTAT  
339851 GAAAAAGAAGCTGGGTGAAAAACAGTTAAACTTGCTAGTGAACTGAAAT  
339901 CCAAAAACGCTTAAACACCCTAAGAATTAAAAAATGAGTGATTACTTAG  
15 339951 CGTTAATTGAGTGTAATACTTTACTAATGATGAACATTTGTTGTTTCTA  
340001 GCTAAAAACAACGACAAGTGAAATAAACTAACAAAACCACTTAAGTTTGC  
340051 TTTTTCAAAGTAGTTTTTCCAACTCTTACTTTGAACAAATTGAAGGTA  
20 340101 TTTTTATACCAAAATAGTGATTGAACCATGTTGTAGTAAGATCCCTGAT  
340151 ATGCCTGAACAAGTAACTGGTATCTTAACTAAAAACATTTTAAGTGTTCA  
340201 CCGTTATGGTTGTAAGAATTTACAAAATAAAAAGCAGTTAAAAATATCC  
340251 CGTTATATTGAAATATCCAGCAGTTAAACTAAAACCAAGTTTCGC  
25 340301 AGTTACATTAACATTAACGGAGTGTTGGAGTGAAAAAACCATTAATAAAAT  
340351 CTGTCAAACAATTATTAATGGTGATGGTTATATTGAAAAATAATTCCCA  
340401 AGATCAACAAACAAAAAGATGAATTTGATTTAAACATCACCTTTTGT  
340451 AATAACTACCAACAACCTTCTCACCTTAATGGACCAAATTACCACTAAGAA  
30 340501 TATCAGCTTTAGTTGAAAATACCTTTAGTTACCAAAACACCGCATCATACA  
340551 CTTCTTCATCTCTTAAAGTAAACTAAGTGCTTTTTTAGTAGCCGTTGT  
340601 GGATTGAAACGTGATACTCTCACTCCATAAACTTTCTTTGTAAATAAAAT  
35 340651 TAATAAAAAACCAGAAACAAAAATGCCCAATAATTGAGATTCTGTAT  
340701 AGAAAAGGATTTGGGAACTTCAGTTAAATACCGCTTAAATCATCATTT  
340751 TGGTTTGATTTGGGAACTTTTCTAGCATTTGATCAACAAAGCTAGTTAT  
340801 GTTATTTAATGTGTGTTTAAATTTGGGTAAAAGCAGCATTACTATCAAAGT  
40 340851 TATTAATTTTTTCAATGAACCTTCAAGTGCATTTAAAGAACTATCTAAT  
340901 CCTGATGCAATGAATTGTTTTGCGTTAATTTTCGCCCTTCGTTTAAAGA  
340951 TTTTTCACTTCTGAAAGTGTTTAACTAGGTTATTTTGAAGATATTTT  
45 341001 GGGAGATCTTTTAATTTTCAAGTGTTATATTCACTAATCTTGTTATATCCC  
341051 TCTTTATAGTAGTTGTTAATAGGTTACGGTAAGTAAAAGCAAAATAACC  
341101 AGCAGTAGCAATTCCACCTAACAAATAAAATCCCTACCAAAATAATAAGAA  
341151 AAAGTGAAGTTTTTTAATAGTCTAATCATGGTCTAATGCTGTTATCAC  
50 341201 TTCCTCTTCCAAATCAGGATAACGATCTAAGATATCATTAACATGATCAG  
341251 CTAAGTTCAGTACTAATAAATCTTGAAACCTGATCAATCCTCTTTTT

341301 TTAGAAGTTAAAAAGGAAAAGACAATGGTTGTAATCAAAATTGCTAACAT  
341351 CCCACCTGATACAGCAACAATGGTTATCATTGTGACATCATAATAATTAT  
341401 TGAAGTGTTCAGAAGAAGGGATGTTGTTTTTGATCTTTTCATAGCTACTA  
341451 ACAATGCTTTGTGCTTGTGTAGAAAACCTACTAACTGCACTAATTACACC  
341501 ATCAGCTGTTGCTTGTTTTTTTACAGATGGAGATGAACTAGCAGTACCAT  
341551 TTTTATCAAGATTATTTTTAAAGTTGTCTAATTGTGTTTTACTGTTTTCC  
341601 AAGTCTTTTTTGGTTGCATCAAGTTCCTAATCTTTTCTTGACTAATATT  
341651 ACCTAGATTGTTCTGACTCTCTAAGTCTTTTTGTATTTCATCCACTTTTT  
341701 GTAAAGATTGCTCTAAGTCTTTTTTAACTTGATCTAAATTGTTAGTAATG  
341751 GAACTTTTGCTAAATTGGTTAGCACTATTTGCTAAAGCATTAGCAAAGGC  
341801 TTTAGCAGAATTGAAAGAACTATCAATGGAATTACGAGCTTGAACATAAA  
341851 GGTTAGCTGCTGTACTACGAAAATACAAAGCAGTAATACCAAACCTAAC  
341901 AGAAATACAAAACCAACATTCCAAAGAAAAGCAAGATGGTTTTCGAAAA  
341951 CCGATTAATAAAAAATAACCATTTAAATACTTGTACTTTTAACCAAATAA  
342001 TGGTTATAAAAGTGTTTTGAAAACAAAACCTACTAGAGTTTAAGTTTAACA  
342051 CCCAATGCGTTGGTTTTAAGTCTTTTTGCTAGTGATTTAACTTCATTTGT  
342101 ATCACTGGAAACACCAGTAATATCAACTGTTTCAAACCTTTCTTCACCAA  
342151 TTACAGTAACCAACCTTCAACTGCTTTAGTCATTCTTTCAAGACTACTA  
342201 TCTGTATCATTTTTCTAGTTTTTGGAAGTGTACACTGTATTTACCACTAGC  
342251 AGTAATTCTTTTGATGTTTTTCATCAAATGTTACTCCGTTTTGTTCAGCAC  
342301 GTTTTAAGATTTTCATTTTGAAACTCGCTGTCTCTGCTTGCGCGTTTCATTT  
342351 TCATAGATGCTAGCACCAGGGTAATAGTTTTTCATTAACCTGTAATAGGT  
342401 GTTATCTCCTTCTCTGTAAGCTTCTTCTAAGTGGAGGTTAAGTTCTTTTA  
342451 AAGAACGGTACACCAAATCATCATCACTATCCTTGTTGGTATTAACATTC  
342501 TTAAC TAAGTaCTTGCAATGTATCCCCAGCAAATAACCTTGGAAGTG  
342551 TCTTTCAAACCTTCTGTAGTTGTAAATATCACCAACTGCTTGTTTGAGCT  
342601 TATTAGCATCAATGGCTGAATTATCACTGTTTTGGAGTGTAACCTGGGTT  
342651 AAATCAATGTGGGTAAATGGTTTTTGAGGCAAACAGATCATAGATAACATT  
342701 AGTTTTACTTCCCAATACTAATGGGTTAAAACCAAACCTATTGCTTTAC  
342751 TGGTGAATAAAATTCCAACCTCAACTACGTTTGCAAAGATTGTTTAGCT  
342801 ACATTAACACCAGTGAATCACCATAAAGTGAAACTTTTTTAACTGATTC  
342851 TGGTAATTGCAATTCATTAAGTTGTGAACCATTACCACTTAAACCTCTAA  
342901 TAATTAGGTAAGTAGGTTTTCTGAATCTATTGTTGTTTTTAAAGCACTG  
342951 ATATCTTTAGCATCAATTGCGAGTGTTTTAACATCTTCAAAGAAGTGGTT  
343001 TGGGTATGAGTCATAAAGTGGTGAACCTTTAGCAGCAAATAAGTTCACCT  
343051 TATCATAAGTAAGGTTATTACTAGTTGAAACAGTTGTTGCTTTTGTGTTA

343101 CTCCATCCGCTGAAACTAGGAACTTGTCTAAACACATCATCATAACCACG  
343151 GTTGTGTTGCCATGAGAGTACCGTTAGTTGTTTGAAGATTGGCATCAACA  
5 343201 CGCGGTTATTGAAATATTCAGTTGATTGGTAATAGCTAAGCAGTGAACCA  
343251 TCACTAGCAACATGATCATAATAACCAGCTTTAAACTAGGAGTAATAAA  
343301 GTTATCACCTGTTTTAATTAAGCCACTAATTTTCAGTTTTAGGAACAGGAC  
10 343351 GGTCTAAACCCTTTGGACTGTTAGTGATCGCTTCTGATAACTCATTAGCA  
343401 AAGTTTCTAAATTTCTCACGGAAGTTAGCACCACCAGATAAATCAATCTC  
343451 ACTCTGATAGCTACCATCGTTTAAAGAAAGTGATTTCAACTTTACTTCTG  
343501 CACTAGGAGATTGTGTTGAGAACAACCTAAAACCGAGGTTACCACTCCTA  
15 343551 CCTGATGCAACCAAAGCATAACCACCTTTGATTAAGTTAGTTAGTGATCAT  
343601 AACTGCTGAGAATGTGGTTAACGCTCCAGCACCTAAAACACCAATAGTCC  
343651 AAAATAATTTACGCTTAAATTTTCACTATTTTTATGTTTTTTAAATTGC  
20 343701 ATTATTTTTTGTATTATTAGAACTTTTAAATTTGTAAACAGTAGTCTACT  
343751 TATCAATTTTAAATTAAATCCACTAGTAACTTCAATAACCCTTTCTCTG  
343801 AAAGAGCTTGGAATTTATTAAACAAATAAAAAACACCCTTAAATTGCTT  
343851 TAAGGATGTAATGAGTTTAAATCTTTAATTTTTGGAGCGAGTAATCGGAA  
25 343901 TCGAACCACACGATCAGCTTGAAGGCTGATGTTCTACCATTAAACTAT  
343951 ACTCGCACAAATTTGGTGCCCAAAGCCGACTTGAACCGGCACACCATTA  
344001 CTGGCGTGGGATCTTAAATCCCATGCGTCTACCATTCCGCCACTTGGGCT  
344051 GGTGACCCACCCGAGGATCGAACTCGGGACCCTTTGATTAAAAGTCAAAT  
30 344101 GCTCTACCGCTGAGCTAGTGAGTCTTTTTGATAGGGAGTTAACCTATCT  
344151 TTAGAAATTTAAGCTTTAACTGGCTGGGATGGATGGGATCGAACCATCGC  
344201 ATGATAGAGTCAAAGTCTATTGCCTTACCGCTTGGCTACATCCCAAAAT  
35 344251 GGTGGACAGGGAGAGATTCGAACTCCCGAAACCATAAAGGTGTCTGATCT  
344301 ACAGTCAGAAGCGTTTAGCCACTTCGCTACCTGTCCATTACTACCAGCAA  
344351 GATATTTTACAAATTATCTGTTGCTGATCTTCAGGATTTTAAACAGATAG  
344401 GGAACCTTCAATACCAACAACATCACATTCATCACCAATTAACGCCCATA  
40 344451 GATTGCAAGGGCAAGGGGTGATTCATTGGAATTTTGTGTTCTTCAGGAT  
344501 TTGCTTCAAGTGTACCTACAATTGTGTATTTTTCGTTTCGATTTAGAACTG  
344551 TAATCATAGATCTCAACAGTGCTCCCTAAGCTAACTTTTGTTACTTTGGT  
45 344601 TTTTGCTTGGTGGTCACTAATTAACCTAGCGTTGGCTAATATATCTTGAA  
344651 TTTGAGCAATCCTAGTTTCAATCTCACCTTGCTGTGCTTTAGCTGCATCA  
344701 TAATCAGCATTTTCACTTAAATCACCTGATCACGTGCTTCTTGTAAGAG  
344751 TCTGATAATCTCAGGACGTTTAACTTGGAATTAGGTTTCAAGTCTTTTT  
50 344801 CCAGTTGCTTAAATCCTTCTTGAGTTAGGTAATTTTATTTAGTTCCATG  
344851 ACAAATTAAGCAGCAAAACACTTTTATTATTTAATTATTTCCCTT

344901 TTTTGGCCAATTTTGTCTAAAAAATAGAAAATCAGTATTGCAGTAATAT  
344951 AGATATTAAATAGTAAATTTCTATTAACTTCGAAATAATAAACTCAAGA  
345001 TCAACAGAAGATTGTGAGTTTTAATACAGATGAGAGAAAACAATAGTAAT  
345051 GCTCAAAACAAAAAGAAGATCCGCTTTTAGCTTTGGGCATCATTATTCT  
345101 AATCGTACTAATTGCTTTAATTACTATGCTTTTTATCACTGGAGTAATTA  
345151 GTCGCAACCGTTAAGATTACTTTTTGTCTAGATGACAAAAAAACACAAGA  
345201 TCTCACTAGTTGGTATGACCAACTGCTAGTTAAAGCAAAGTTAATTTGTC  
345251 ATGGTGAAGTTAAAGGTACAGTTTGTTTTTTAAATAACAGTTGAGGCTTA  
345301 TGGATGGAAATCCAACAGCTTTACAATGATGCAATTGCAAATAAAAAATCA  
345351 ATTGTCTGCAATTGCTCTAACTAAATTCCAACCACTACTAGTTTTTGTT  
345401 ATCAAGTATTCCAAGTACAACCTCCCTACCCTTTCTTTTACAGTGAATAT  
345451 CAAAAGGAAAAAACCCATATCAAAGGTTTTAATCCTGAGCTTTTTTTAAT  
345501 TAATCAAGTTGGTCAAAAACAACTCAATGATCCTTTGGTTTTACGACCTA  
345551 CTAGTGAGATTGCTTTTTGCAACTTATGGAAAAACAAGAGTTATCTTAC  
345601 CATGATCTACCTTTAATTTATAACCAGTGAACTCAGGTTTTTCGTGCAGA  
345651 AAAAAACACCAGACCTTTTTTGAGAAACAGTGAGTTTACTGACAAGAAA  
345701 CTCATGGGCTTTTTGTGGATCAGAGCCAATCTGAACAAGCTGCTATTAGC  
345751 TTTTGAAATTTATATCAGGATTTAATTATTAACAACTTTGTATCCCTGC  
345801 TTTTGTGGTTTGAAAAGTGAAAGTGAAAAATTTGCAGGTGCTAAAAACA  
345851 CATGGACAATAGAAGCAATTATGCCTGATGGACAAAGTTTACAATGTGCC  
345901 ACTAGCCATGATTTAGGTGACACTTTTACAAAGAGTTTACTATCAGCTA  
345951 TCAGAGTAAACTAACCAAAAAATGACTCCAAGTAGTTTTAGTTGTGGGA  
346001 TGTCAACTAGGATCTTAGGAGCAATTTTTTTAACCACAGCGATGATTAT  
346051 GGTTTGGTTTTACCTTGGTATCTAGCAAGTAAACAAGTCAAGTTATACCT  
346101 GTTTGATAAAAAACAATAACCCTAAAACAAGAGCTTTAGCTTTTTTAGTGA  
346151 AGGATTTTTTAGAAAACTCAAAATTCGCTTTAGTTTTATAGAAATTAAC  
346201 AATCAACTAGGTAAACAACTTTTAAAAGGAGAAATAGAAGGTATTCCATT  
346251 ACAGATGATTGTTGATAATGAAAAACTATTAACATCTTCAACCGCTTAA  
346301 CACGTTTAAAACAGCTTAACATTTGCAAATCTCCAACTGAATTTGTT  
346351 AATTTAGTTAACAACCTACCATACAGAGATGTATAGAAAAGCAAATGATTT  
346401 AGTTGAACAAAACTAGCAAGAGTACAACTTTAAAGGAAATTGAACAAG  
346451 CATTCAAAAATAAAAAGGCTGTTTTATGTACCGTGAAGTTAACTGGTGAA  
346501 CTTGAACAACACTTAAAGACAAAATACCAAGTTAGTGTAGGTGTGTTTT  
346551 TAAAAAGTCAGATGTAACACAAAACGTCTTTTTACAAATCAACCTTGTT  
346601 TTGATTCAAGTTTTAATTGCACGTGCTTACTAACAAAGTACTGTCAATCAC  
346651 TACCCAATAAAACCCTTGATTATTTGGTTTTATTTAATTTATTTCTAAAT

346701 ATTTTTTACCAGTAATTTTGTGTTAAAAACAACTCGTTTTGTAAAAGAA  
346751 AAAAGTTAGAGTTGTTGTATTTCAATAACGATTATTTAGCCTCTAAAATC  
5 346801 GATTAGACGATCTTCTGATCGTTTAAGATTATTCAAATTCAACATGACT  
346851 TTATGACTTTTACAAACAAAGAAAAAATTGCAAACAAAGCAAATCATT  
346901 GCAGCGTTGATGACAAAATTTAAGCGCTCGCAATTAATCTTGAAACACCA  
10 346951 AGCTAATAACATAGCACTGGAGTTGTGAAATGAAATGATATTAACCTAT  
347001 CAAACAGCTTATTGAGTTAATAGAAGATACTTTTTCAATGCTTAAAAA  
347051 GAAACTGTTGATTTTATCTATGACATCTATATTTATGGCAAAAAGCCGTG  
347101 TGATATTGGTTATTCTAATTCCACCTATTACAAAAACTAAACAAAGCAG  
15 347151 CTAATAGTTTTTTTGACCATTTGTTTGAGATTTCGTCAATATTAGACAAA  
347201 AGGATCATAACTAATGGCAGCAATTCTCAACGTACAACGAATTCAAATA  
347251 ACCAAGTCACTGAGTACACAATGAGTCCAGTGCCTAATTTTGCAAACACA  
20 347301 AAAGATGTATATTTTGATGCGCAATTAACAAATATAGAAAGCAAATTGA  
347351 TAGTAGTAGGGCTCAAATTCACCTTACTATTGCACTAAAATACAACACTA  
347401 ATCTCCCTGATAATATCTTTCAAGCCCCTTCAGTTTAGGCAATTGACAA  
347451 AGTGATAAGATTCAACTTCAAAAAGCTCCTGATAAAAAACACGATAGTTT  
25 347501 AAACAGCATTAAATATTTTTATGCATTTCTAGATGTACCCCGTTCAGCAC  
347551 TAGCAAAAAAGAAATTAATAGGTTTAGTAATGTGGTTGCTAGAGTATTG  
347601 AGAATAAGTTTTCGCTTGCAAGATCAATCTGAAAAAGGAATTGAAGTGA  
347651 CTATCATTTGTTTGATACTGTAGCTAGTGAATTGTATGCAACAGTAATTA  
30 347701 AAGAAACAATCAACTTTGGCAACATGATTAAGATTAATGCACTTGATGGT  
347751 AGTAAACAGCTAACTAGTAGCCAAGGAAGTTTTAAATACAGTTGAACAAT  
347801 GTATGACTATAGGAATTTAGAACAACCTTGATGAGGTGAGAACTTGATCA  
347851 ATATCAGTTTTGACAAACCAGTTCAAATAGTAAATGTTGATGTCAAAT  
35 347901 CACTATGTTCCAATAAGGTAGGTTACAAGAGATAAAACAACAAGGTGA  
347951 GTTTGAAAATAACCTTGATGTAAATGAAAAGCTTAACTCAATTTAATAG  
348001 GCAATTGAAATTTTGACAAACATAACAAGAAGCTAATCAGTGATATTTCA  
40 348051 GGTACTGGAATCTTTTACCCCAGGGTGGTTATGGAAGTTATGAAATAAT  
348101 GATTGGCGCTACAGTAGGTAATGATTTCTACACAATTATAGCCAACAACC  
348151 AGTTTAAGTACGAAACACCTTTAGATGATCTTGAACAAAATGACTTTTTT  
45 348201 GAGGTAAATTATTTACCTGTTTACAGTACATACAACCTTAGTGATTAAAC  
348251 TCAGTAAGTATGATTTTTTCAATTAGTAAACGAAAGTTAATTTGCGGATT  
348301 TTTGCTAGTTATTTTAAACAATAGGTGGGGTTTTGGGTGGTGTATTTAG  
348351 TTAATAAAAAACAAGGATAACTACCAAAATGAAAGTAATTTCAACAAT  
50 348401 CAAGAACAAATTAGTAAATCCCTAATTTCAAAGCTATTGGTCCTGAAAC  
348451 ACAACGTATCTTAAGAGAAAGAACTATCCTTTAGATGATAGTGGTTATT

348501 ATGTTTATAAGTATGGTGAAATTAATAGGTATCTAAGAAATGAAAGTGAA  
348551 CTAGATGAATTAATTAAGTATAGAGTGATGGTACCTTCACTTAAATTACA  
348601 TCACAAAAGGGTTAATTTTGATAAGGCATTTCTTGAAAGTAAATTAAGAA  
348651 AATGGATTATCAAAGCAATTAAGCAACATAACTATTTCCAACACTTTTGAA  
348701 AATGAACCAAATTTAAGAGTTCAATATAACATGAATATTCAGCACAAAA  
348751 AATTGATGTTAATGCTGTTTGATCTTATAAAAAGATAATGATGCTGCTA  
348801 CTGGTAAGCCAATCCGATATTGAGATCAATTTGAGCTTAAACTTAAATAA  
348851 TAAATCTTTATAATTTTACTAGATTTACTAATGCAACGCATGAAATTC  
348901 TTTTAAAAATTAAAGAAATTGCTAAATCAAAAACTTTAATCTTAATTTA  
348951 GATGAAAAGACAATAAATCAACCACTTCGTGAGTTGAAAATCGATTCACT  
349001 TGATATGTTTAGTATTGTTGTTAGTCTAGAAAATGAATTTGGGATTAGTT  
349051 TTGATGATGAAAAGTTAATGAATCTAAAAATCTTGCTGACTTGGTTTTA  
349101 GAAGTTAAAAACCTTTTAGCAAAAAAGGGGTATAGTTCAAAGGTAGAAC  
349151 ATCTGTCTTCAAAATAGAGTGTTGTGGGTTGAGTCCTGCTACCCCTGCC  
349201 ATAAAATATAAAAGCTTAGTAAGTTTACTAAGCTTTTTTCAATCCCCC  
349251 CATTCCCCCAACCTCTATTTTGTGTTACTAGTGCCTAAGGTGGTATTGGA  
349301 GTATCACAACCTGAATAACCAAGTAGTCAAAGAGAGTTTGGAAGTGGAAG  
349351 CAACTGATTCTTTTGATCCCACCCAAAGGTTGCAAAAAGATAGTCCAATG  
349401 AAGGATACAGGAAAGATGGGGGAGAACTCCAAGAGACCATGTGCATCAAT  
349451 GAGTGGTGGTGGGGCTACATCTCCTCGCAAAGCCCTCACCATTGAGGTGG  
349501 AAAGGGGGAGTCAAAGTGATTCACTTTTAAAAACGACTTTGCCAAAAAG  
349551 CCACTGAAACATAAGAACAGTAGTGGGGAGGTGAAGTTGGATGCGAGTGG  
349601 GGAGTTTACTGAGGCCCTGAAAACCATTTGTTGACTACTGATCAAATAGCAA  
349651 GAGAGAAGGGGATGGGGGCGACTTAGACTTTCTCCCCTGAATCGGCAACA  
349701 ACAAACCCTTCTCCAACCTCCCACTGCTTCCCTTTCTTCTTCTTCTCT  
349751 TCCCCACTCCCCACTTTTTCTAACATCAATGTCGGGGTTAAATCAATGAT  
349801 CACTCATCTCAACAAAGAAAACACCCGGTGGGTGTTTACCCCTAACTCTT  
349851 CACCAGACATTTGAACGGGAGCAGGTTATAGAAAAGCTAATAACAACAAT  
349901 AACGGCATCTCCTTGACAAGTGTTGCCTAGTAGCAATAGTAGTCAACA  
349951 GTTTAATCCCAATTCAGATGATAATAAAGTCACTCAAGGTGGTGGCTCCC  
350001 CAGCCAAAAAACAACCACCTATTCCTTTTTACCCAATTCATCAGTCCC  
350051 ACCAGTGAAGTGGATCAACGCATTGACTTTTACTAACAAAAATAACCCGCA  
350101 GCGCAATCAACTGTTGCTCAGAAGCTTACTAGGAACTATCCCGGTATTGA  
350151 TCAATAAGAGTGGAACGGGAGATGAGTTTACCCATACGAGTGAGCAGAAA  
350201 TGGGATAAAACGAATGAAAAAGATGGGAATTTACCTGGGTTTGGGGAGGT  
350251 GAATGGTGGTTTTTATCAACTAAATAAAAACTTATTAGCTTATTTTTAT

350301 TAGGTTTTTACTTATTTAATAGTTAAAAAAGTTTTGAATTTTTCTTAGTT  
350351 TTTTATTTGTTTAAATAGTTAAAAAACACTAGGCTTTACCTTTATTTAATT  
5 350401 AATAAAACCTTTACCCCTATTACCAAACCATCCATAACACCAACTTGTTT  
350451 GTGTTGTTCAAGTCTAGGGATGTAAAAGTTAAGTATGACAGTTCAAGTGG  
350501 CTCAAATAACCAGATTAGTTTTGATTCAACTAGTCAAGCTAACAAACCCG  
350551 CCTACATCGTTGAATTTACTAATTCCACCAACATTGGCATCAAGTGAAGG  
10 350601 GTAGTGAAAAAATATCAGTTAGATGTACCGAATGTTTCTAGCAACATGAA  
350651 CGAAGTACTGAAAAATTTAATTCTTGAACAACCTTTGACTAAGTATACCT  
350701 TAAACAGTAGTTTGGCTAAAGAGAAGGGTAAAACGCAAAGGGAGGTGCAT  
15 350751 CTGGGTAGTGGGCAAGCAAATCAGTGACGATCGATGCGTAATCAACATGG  
350801 CCTAAACAACAATCCCAGTCCCAATGCATCAACCGGATTTAAACTCACTA  
350851 CCGGCAACGCATATAGAAAATTAATGAGTCCTGACCAATTTATCAACCA  
350901 ATTGATGGGACCAAGCAGGGCAAAGGGAAGGATAGTAGTGGGTGGAGTTC  
20 350951 AACAGAAGCAACAACGGCAAAAAATGATGCGCCAGTGTTTCTGGAGGGG  
351001 GATCAGACACCACTTCAAAATTTAAAAGTTACCTCAACACCAAGCAAGCG  
351051 TTAGAGAGCATCGGCATCTTGTTTGATGGGGATGGAATGAGGAATGTGGT  
25 351101 TACCCAGCTCTATTATGCTTCTACTAGCAAGCTAGCAGTCACCAACAACC  
351151 ACATTGTCGTGATGGGTAACAGCTTTCTACCCAGCTTGTTGGTACTGGGTG  
351201 GTGGAGCGGAGTGCAACAACCTGATTCATCATCAAAACCCACCTGGTTTGC  
351251 TAATACCAATTTAAACTGAGGGGAAGATAAACAAAAACAATTTGTTGAGA  
30 351301 ACCAGTTGGGGTATAAGGAAACTACCAGTACCAATTTCCACAACCTCCAT  
351351 TCCAAATCTTTCACCCAACCTGCATATCTGATCAGTGGCATTGACAGTGT  
351401 CAATGATCAGTTGATCTTCAGTGGCTTTAAAGCGGGGAGTGTGGGGTATG  
35 351451 ATAGTAGTAGTAGTAGTAGTAGTAGTAGTACCAAAGACCAAGCACTT  
351501 GCTTGATCAACAACAACCTAGCTTAGATAGTAAACGGGGTATAGGGATCT  
351551 AGTGACCAACGACACGGGGCTAAATGGTCCGATCAATGGGAGTTTTTCAA  
351601 TCCAAGACACCTTCAGCTTTGTGTTTCTTATTCGGGGAATCATACAAAT  
40 351651 TCAAGTGGTTCATCAGGAACCATTAACCGGCTTATCCGGTGAAAAACAC  
351701 AGAAAAATCAACTGTCAAGATCAATTCTTTGATCAACGCTACGCCGTGTA  
351751 ATAGTTATGGGGATGAGGGGATTGGGGTTAGAAATATTTTATGAGTTTA  
45 351801 AAACAAGGTAATGCAGATAACTAGCTAAATCAACAACCTGGAGGTTTTGTA  
351851 GCCCCATTTCTTAAATCCAAATTATGTAAGTTTTGCTGTTTAAGTAAATC  
351901 CATAAATTTACCATCTTGAACCTTTATCTGTTCTTTTACGTGTAAAGTGA  
351951 AAAGTAGTTGATTGTCTTTAAATTGAAATAGAGAACCTGGATAATCAGTA  
50 352001 TTTTGAACATAAGTTATAATCCAAATCACCATCAACTATGAACTTGACATC  
352051 CATTTCAACATTCATGATGAAGGGATACCAGAAAAAGGTGCAAATCAAC



352101 TAAATAACCCAGTTAATTTGTATCCACCTTGGTACTTTATGTCAATTTCA  
352151 AATTTAAATTTGTATGGATAATGTTGCCTAAATTCAATTCATTATTTTTT  
352201 TCAATCAATGGTTGGATTATTTTCCTTGTTTTCAATTTTATGCTTGTTA  
352251 AGTTTAGTTTTATGTCAGTATAGGAAGTTAGCTTTCCTCTTAATCAGTCA  
352301 GACATATAAAGACCTTCAAGCCCTTGTCTAGGAACTGAATTCCTTTTTTC  
352351 ACTAAAGGCTTTCTTTGCATTTtCACTTTCATCTTTTTTATTATTTTTGT  
352401 AATAATCTGACGTTGCTTTAGTAAAGCTATTAATTAAGTGAAAAAGTT  
352451 TTATTTTTTATCAGCAGCAAAAGAAGTTTTAGAGCATCTATTAGTTGAGT  
352501 CTTATCAGTAACATCTTTCTTTTGATTTTTTCAATAATCTTAAATCTT  
352551 TAGCATTTTCAAATGATTTATTAAATTGTTCTTGTTGTTCTTTTAAGCGC  
352601 TTAGCTTCTCTTCTTTTCGCTTAAGTTCTTCTTCTGTTTTCTTCTTTC  
352651 CTCAGCTAAAATTCGTTGTTGTTCTTCATAATCAGCTTTAGCTTTTTTAC  
352701 GTTCTTTTTTGAATGGTTCAATTATTTCTTTTTCAAATTTGTTTTAGCT  
352751 AAATCTAGTTGTTCAATTTTTTAAACTGAATTAAGATATTTGTATT  
352801 GGAAAGAAAAGTGAATCACTTACAGCAGTTTTAGCTATTGAAGTGAGAT  
352851 CATTTTGATTTTTATCAACAAGTTTATTAATTAGAGGTTTTCAAACAAT  
352901 TGGGTATTTAGATCGTTACCATTAAAGCTATTTTGCAACTCTTGTAATTT  
352951 CAAAAAATTAGAAGTTTGGGCTTTTAAATCAAATTGCAAGTTAACAGTGT  
353001 TGTTACCACCTTCATAATCAACTTCAAAATCCATTTTGATTTCAAAGCTA  
353051 TAACGAATCTTATCTTTAATAACAATGTCATTTTTTTAACCAATTCAAGA  
353101 TTAAAGTCTTTTAAATGAATTTTCTTTAAGTTGTATTGATTAAATATTTT  
353151 AACAACTTTTCGGTAATGTTTAAACCTTTTGGATGCAATTGTGGAAAGA  
353201 AATTTTCATTAAGGAATTTAAAAAATTCTGTGGAACCTTAGGCAATTTA  
353251 TCTTCATCATTAATTGGAAAAATTTTGTTAGTTTCATTAATGCTTGATTA  
353301 CAGCCTATTTAATAAATCAACTGTTTTTTAATACCTGATTTAAACCAC  
353351 TTAAAAGATGAAAAATATCTATAACATTAAAGTTCCTAGGATAAAATTC  
353401 TTCTTAAATTTCTCTTGAAATAAGTCAAAGTTTTTATCATAATCTTCTC  
353451 TTTAGCAATATAGTTTTCTTCTTGCTCTGTTATAGCTGTTTGCTGTTGGA  
353501 GTAGAATACTATTTCTCTACTATTTGTTGTACTTGATTTCTTAGACTA  
353551 GGTTGACTTAAATTTGCAGCTGAGCCATTATAGATAGAAGGGACAATAAG  
353601 TACACCAGCAGTTAAAGTTGATGCAAAAGAGACAAAGAGAAAAGTTTTAA  
353651 TTTTAAACGAGATTTTTTGATAGCTTCAAAGTTAATAATTAATATTGA  
353701 AAATAATTAGCTAAACTAAAAAGTTACAAACGAAATTGAATTTGTTTA  
353751 AAATAAAACAGACAGGAAAATTTAACATTATATTCTAACTCTGAATAG  
353801 CAAAAAATATAAGAATAGCTTTAATTCAAAAAAGTAATTCGGATCTTAAA  
353851 AAATATTTTTTAATAAAGATTAATTGCCAGCAACTGAATCTAAGTAATA

353901 AAGTGAATATTTATTTTTATTAAAACTTATATTCAAATTTGTAGTCTAT  
353951 TTTTAACTAATATAAAAAAGTTGAATATTTAAAAACAATTAATTTTGATA  
5 354001 ATTAATAATCCAGGATTAATAAGTGCTTTTCAAAAAATTACTTGGGTCA  
354051 TTCCAAGTTTGTTTTTAACAATTATTTCAACATCTTTACTTATTAGTTGT  
354101 GCAACTAAAAGCGATAACACCTTAATATTTAATATTTCACTTGATCATAA  
10 354151 CGCTGATACATCAATAGAAAAATTCTTTACTGTTTTTTCAAAAAACTTA  
354201 GTGGAAAATTGAATAAAAAAATTAATGTTAACTTTAATATAGTTGATGAT  
354251 TCCTTTACAAAAATTAACAATATTCAAGCTAATAAAGCAGATTTTGCTTT  
354301 TGTTAATTCACAAGCTATTGCTTCAAATAATTGGTTTGGCTATACGCCAT  
15 354351 TGATACAACTTTAACAACAGCTTTTAAAGAAGATTTGGAGCTTGATTAT  
354401 TATGAAGATGGTAATTTACAAAAAAAGCTGAAAAACGAATTTGCTTTT  
354451 TCTAAGTCCaCCTTACAAAGAATGAGATGATATCAAACAAAAATGAAGT  
20 354501 GAAATCGTTATGACTTTCTTTATGAACCTTCGAAGTTAGTTTCTTTTTAC  
354551 AGATCAATGATTTTAATAACTGGTTCAGCTAGTGAAATTACAGCTATTAA  
354601 AAAAGCGTGAAATGAAAAAACTGAAATCAGTTTATGAAATTGGAATTG  
354651 GTCATGGACAAACAAATTCAGCTTCACGTTTTGAGCTACCTGATCTTTTA  
25 354701 TTTAGAAAACATTTTGCTAAAAATTATCCCGGATTACAAATGCAATTAA  
354751 TTCTGATCCCGATAAATTTGCCGTAGTTAGAGGAAGAGAGATAGGTATAA  
354801 ATAAAAACATCAAGATTGTTTTTGATGATGCTAATTCATTTTCTTGAACA  
354851 CAAATATTTAAAGGTTCAAAAAGACCTTTTTTACTCTCAATTGATCCTAA  
30 354901 CGATAGATTAGAAATCTCACTTATAGTGATCCGCTTTTGTATGACATTG  
354951 GTATTGTTAGCAACAATTTATCAAGGATATATCAAAAAGCTATTGGTGAA  
355001 ATTTTTATTGAGTTAGCACAAATCAAGTGAAGATCTATATGGGCCTTCAAT  
35 355051 TGGTTATAACGGCTATAAAATGATTAATGATTTTGAGAAAGAAGTTGTTG  
355101 AAATAATTGAAAAAACCTATGGAAAATAAACCAATTCTTTCTTTTGAAAA  
355151 AGTATCAATAATATACAAAAAGCTCCACTTTTGCAAAACATTAGTTTTTA  
355201 AAGTAATGGCAAAGGAAAATGTTTGCTTATTAGGTAAGTCTGGAGTTGGA  
40 355251 AAATCGAGCCTTTTAAACAGTGTTACTAATACAAAAATAGTTAAAAGTGG  
355301 GTTAGTTTATTTTGATGGTGTTGCTTCAAACAAAAAGGAATACAAAAAC  
355351 TGAAAAAACAGTGCAGTTATCTGGATCAAATACCAAATTTAATTGACACT  
45 355401 GATTATGTATATGAAGCAATTTTAAGATCTGCTAAACAAAAATTAACCTG  
355451 ATTACAAAAATTAATTTGTTTTGAACCTAAATGAATTAAGATAAGATCT  
355501 TAGCAATACTAAAAGAAGTTAATCTTAATGATTATGTTAGTTGTATTATT  
355551 AAAGATCTTTCTGCTGGACAAAAACAAAGAGTTGAAATTGCTAAGCTTTT  
50 355601 TTTTAAATCACCAAAGCTACTTTTAGTTGATGAACCAACCACAGGATTAG  
355651 ATCCTTTAACCGCTTCTAAAATAATGGATTTAATTACTGATTTTGTGAAA

355701 AGAGAAAAAATAACTTTGGTTTTTGTAAACACATGATATAGATTTAGCACT  
355751 GAAATATAGCACCAGAATTATAGCACTTAAAAATCATGCTTTAGTGTTAG  
5 355801 ATAGATTAACAGAAAACTAACAAAAGAACAACTTTATAAAATTTATGAT  
355851 AACTAAGTTGTTTTTTCACCAAGTTGGCGATAATAAAAAACGCTTAATTT  
355901 GGTATTGAAAACATTAATAATAATTGCTGTTTTGGCTATTGTCATTTAC  
10 355951 AGTTGAATAGATAACTTTTCTAGCTTTAATCAGTTTGGTTTAAATGTTTT  
356001 TATTAATAACATTACAAGCTTATTTACCCCCAATCTTAACCACGAATATA  
356051 CACTAGTAAGATTCCTAGCACAACTGCTTTTTTTGTTACAGGAGGTAGC  
356101 TTTTTAGGATTTATTTTTGCGATCCTATTTTCTATTGAACTGCATTTAA  
15 356151 AATTCAACCCTTTTACATTGCTCTACCGATCAGGTTAATAACTATAGTTT  
356201 TAAGAGCATTTCCCGTACTTTTATTTGGTTTTTTATTTAGTAATTTATTT  
356251 AATAAACAACTAGCAGCTACACTAACGATTAGCTGGTTTAGCTTTTTATG  
20 356301 GAATACAAAATACATTACTACATTTTTTGAAAACAGCAATTTAAAGTATT  
356351 TTTTAAACAAAAAATTAGAGAAGGAAGTGGTTTTAAAGCTTTTTGAAC  
356401 ACTATTTTTCTTAGTGAAAATGAGCGACTATGGTTGTTTTTCTTTATAG  
356451 TTTAGAAGCAAATTTTCGTTGAACTACGCTTCTAAGTATATTTGGCATTG  
25 356501 GTGGCATAGGACAATAATTGTTGATCCTTTAAGTATAAGGGTGCAGTTT  
356551 GATCTTGTATTAATTCCATTAGTTGTTTTAATAACCTTTCTAATTTTTAT  
356601 AGAAGTTGTTGTTTTTTTATTATCAAGTTTTGTTTTTGAGAAAAATAGTG  
356651 AAGATTTAAGACCAATTTTAAAAACAACAGTTATTGAAAAACGAAAGTGA  
30 356701 AAAAGAATTATATTTATTTTGTTTATTGTAGTACTAATTAGTCTTAGTTT  
356751 AGCCAATTTAGTGACTATTGATTACAGAATTAACGATGCTGAATTTTTAC  
356801 AAGATTTTTTTAACCAGTTTTTTCAGTTAAAAAGTAATCTTTTTCAAGT  
35 356851 AATGATCCTAATATAAAaCCCAATTTTAATGTTAGTTAACTTACAACCTCA  
356901 AGCTATTAGTTTAATTAGCTTGGTTGTAATCTTTTCTATTCTCTTGGTT  
356951 TTATATCATGTAATTTATTTAAAAAGAGATTTTCAATTAGTTTAAAGATC  
40 357001 TTATTACTTTTTGTTAGAGTAGTTCCTAGTATTCTGTTGTTTAGGCTACT  
357051 AGATCCTTTATTTCTAGAAGCAAAAACAACTATTATTTTAGTCTTACTAA  
357101 TTAATCATGGTTCAAGTTATGGCCAATTGATGTCAATTAACCTTAATAAG  
357151 GCAAATCAAAATATCATCAATAACTATAAAAAATCATGGTATGACAAAAGG  
45 357201 TTTTATTTTATGAACTATTTGTTAGTTGAAAATAAACCTAATTTAATAA  
357251 ACATTACCAGTGATGCTTATGATAGTGAATTAGGGATTAATTTTGTTT  
357301 GGTAGTTTGGCGGTTCAATTATTGGTAGTAGAATTACTAATTTTTTGA  
357351 AAGAGCTCAATTTGATAATCTAGGTTCTGTTACAATCCCATTAATGGTTT  
50 357401 ATCTAATTGCAATAGAAATAATTTTCCTTTCAGTTAGATTAAGTAGAATT  
357451 TCAGTTTTTAAGAACTACCTTTACTAATGATAGTTTTTGAAAGAAGCGCTC

357501 TAATATTAAACTGCAGCTAATGTATCTTTAGCCTTTTAAAAATCCTTAT  
357551 GTTTTAAATCCATTGTTATAAGCTTATCTTTAACAGCACTTGTAGTATTA  
5 357601 CTTTCATCAACCAAAATTATTGGCAAATTAAAAACGTTTTCTAAAAGTTG  
357651 TTTAAATGATTTAATTGCCTTTTGAATATCAGAATAATAGTGAAATTTGG  
357701 GAAAACCTATCACTATTTTTCAAGTTCATACCCATCGTTTTTAATTCGC  
10 357751 AAAAATAAGTTGTTAACAGCAGTTTTGAAATTATTTTTTACTTCAAAAAC  
357801 ATGAAATGCAGAAGGATATTTATCTAGTGTATTGGCAATTGCTGTACCTA  
357851 TTTTTTTCAAGCCAAAATCAATTGCTAATATATATTTCACTATTTATTTT  
357901 GAAACAATTCATTAAGCTTTTGAGGGGTAACATTATCCTGAAAAGAACCT  
15 357951 CTAAATAACTTATCATTGCCTCCGCCCTTTAAATTAAACTATTTCTTAA  
358001 TTTTTCATAATGGTGGTAGTTTTATTTCTATAACAATAAATGAATTAC  
358051 TTTCAATTGAATTGATTAATTATCAAGAAATTTTAGTTTGATTTTGATTG  
20 358101 AAAACATCATGTAGTGTGTGTAGCAATAGTTTAGGTTCTACGTCATTAAA  
358151 AGTGGCAATTACATAACTTTTATTTTCATCTACTAAGGATAATAATTGCT  
358201 TTTTAATTGATAAAGCTAAAGCTTGCTGTGATACTTTATAGTTTTTTGTT  
358251 TTTAACTGGTTAATATCATTTTTTAAAGCTAATAAAGTATCAGATGCATC  
25 358301 TCTTAATTGGGTAATTTTTTCAGGTAAGATAAATTTATCTAGCCTTTGTT  
358351 GCAATTCTTTTAACTCACTTTAAAAATTGAACTATCAATCAAAGATAGA  
358401 ACTTTTTCAAGTTCTGATTTTAATTGGATTAATTTTTGATTTTCTGCTTT  
30 358451 TAAATAGTTGTTAATAGTTTCATTACTGCTAATGATTTCAATCCTTCATC  
358501 TTCCAGCTCCTAAAGAATAGAAATCAGTAATAAAACAATCTTCAATTGAA  
358551 GCAGTGTTAGCTACATGAGTGCCACCACACAACCTCAACACTATAATCACC  
358601 AAAGCGGATCACTCTTAATATTTTCATGTTGAGAATATTCCTCTTCAAAAT  
35 358651 AAGCAATTGCATTTAGTTTTTGGACTCCCTTCAAATCAGTAAAAATCTCT  
358701 TTTGAGCTTATTTTTTGTTTAATCAAAGAGCGAATTTTATTTTCTACTTT  
358751 CTCAAGTTCATTCTTGTTAAATGACGATTCAAATTAAAGTCAATAGTTG  
358801 CTTTTTGCGCAGATTTAAAGCACCCTTTGTTTAATAAGTGGATCAATT  
40 358851 TCTTTTTGTAAAGCTGCATGTAAAAGGTGTTCTAAACTATGGTTGTTAGC  
358901 AGCAAGTTTTCTTCAAGTTTCATCATGTGATAAAGTTACTTGATCATTGA  
358951 GTTTAAACTACCTACTAAAAAGTAGTGGAAGTGTGTTTATTAGGTCCT  
45 359001 TTAAATACACCTTGAAAACCTGATTTTTTGATCATTATTATTAGAATGATT  
359051 AATGCAACTtCCTTCATCATATCTCTGTCTCCAGAAGTAGCATATAAAA  
359101 CTGTTTGGTCAAAAACCTACATAACCACTTTGATTATTAAGTTCTTTAACT  
359151 GGTAAATAATTTTCATCAAAAAGACCAATTACCTTAGCATTAAATTTTATT  
50 359201 TTTGTGATAaAAAAAAGTACTTTTAGTTTTGAAATTAACTAAATTAATAT  
359251 TTTGTTTTTCAAATTTATAGTTTGGTTATTTTGCTTAGAGATAGAACGA

359301 TGT TTGGCCATTA ACTGATCAA AACTGTTCAATCAATAGTTAAACCTTT  
359351 TTGATTAACTAGTTCTCTTATTATTTCAACAGGAAAACCGTATGTTTCGT  
359401 TCAATTGAAATGTTAATTGGGGAGTTAGAGTATTGTTTTTAACACTTTTT  
359451 TCAAACAGCACTAAACCTAAATCAATCGTTTTATTAAATGCATTAATCTC  
359501 TTTTAAACTACCTGTTTAAACAGTTTCATTTTTAGCTTTTAAATGTTGAT  
359551 AATAATTCTCATATGAAGCGATGATTCATCTATTATCTTTTCAATAAAT  
359601 GCTAAGTTTAATTGCAATTTCTTACAAGCTATTAAAGCACGTCTTAAAAG  
359651 TCTTCTTACTACATAATTTCTCTCATTAGGACCAGGTAAACTCCTTCTG  
359701 AAATGGTAAAAGTGATTGCTTTAAAGTGATCAGCAATAATCCGAAAATAA  
359751 CTCTGTTCTTTCACTTTTGTAGGATCGAATGTAAAGTAAGAGTTGGGATC  
359801 ATATTTAAATGGACAAAAAGCTTCAATTATTTTGATTAGCTTTAAAAAGA  
359851 TGTCAGTATCAAAATTGGTTGGACTATTTTGTAATACTGAAACAAGTCTT  
359901 TCTATTCCAGCACCTGTATCAATATTTTTTGAGCAAGTTCTGTATAGTT  
359951 GCCATTACCATCATTATTAAATTGACTAAAAACAATGTTTCATATCTCAA  
360001 CATAACGATCATTTTCAATGTCCTCAAAGAAAAGTTTTTCACCAATTTTT  
360051 TTAGGATCAAAATTTCTCACCACGATCATAATAGATTTTCAGTGCAAGGTCC  
360101 ACAAGGTCTTAAACCTAAGTCTCAAAGTTACGACTTTTGTACACTTAA  
360151 TAATGTGATTTTTATCAATTTTATGCTTAATTCATCTTTTATAAGTAGTT  
360201 TCATCATCTTCATAAACAGTGATATAAAAACGCTTAGGATCTAGCTGATA  
360251 ATAATTAACTAAAAGATCAAAGCAAAATCAATTGCTTCTGTTTTAAAT  
360301 AATCACCGATTGAAAAATTTCCAAGCATCTCAAACAAAGTTTGATGTCTT  
360351 GAAGTAAAACCCACATTTTCAATATCATTTACCCTTAAACATATCTGTGC  
360401 ATTAACAAGGCGTTTAGATGGTGGTGTCTTCTAGCACTGAAATAATCTT  
360451 TTAAAGTAGCAACTCCTGAATTGATTCAATAATGATGGGTCGTTGATC  
360501 GGAATTAGTGATTTTGAAGCTAAAACCAGATGGTCTTTCTTTGCAAAATA  
360551 ATCTAATCAGGTTTGCCTTACTTTATCAGTTGTTCAATTCATTGCTTAAT  
360601 TTTAAATGCAATTTACCAGTGATAAAAATAACTATAGTTCTTTTATTTGC  
360651 TAATTTATTTTTATTTCAAACCTTTTGTAGCAATTTGTGCATAAACATG  
360701 ATTATCAGCTAAGAACTGCTGAAACTTATTTTGAAGTTTACTGTTTCATA  
360751 AATTTAAAGGTAAGTTAAGTTTTTTGATCATTTGGGGATACTTTTCATAT  
360801 ATTTTGGTTCATGGGTGGAGGAATTGACAAATCTTTTGGATTCTAGCTGT  
360851 ACTAATGTTTCAAACGTTTTTTTAGTCCAAAATAAAAAACCTTTTTTGT  
360901 AACTATTATCTAAATCATAACTTTTTGCAAAGATTCAAAGTTAAAGGAT  
360951 GAAACAAGATCTTATCTATTGCTTTTTTACCATAACCTTTAACTAGGTC  
361001 AACAAGCTTCTTTTCAATTCCTAAATATGGTTTTTGATCAGTTTAAATCT  
361051 CAATATTGATTAACTTAAATTTATCTAAATAAGATCTAAGAACTCTTTT

361101 AAAGTTAGGATCGATTGAAATTGAATTTTAAGGTGAAAAAAGCACTATG  
361151 ATCATCTCTTTTTAACTAACTAATGATTCAAACCTCAACCTCCTTATTAA  
5 361201 CTAATGCGGTTCTCAATGTTGTCTCATCATGAATGATAACTAACTGTTCA  
361251 TCTTTAGTTAAATGAACATCAAGCTCTATTCCATCAAACAATATTCAA  
361301 AGCTAAATCAAATGCTAGTTTGGTGTCTTCTGGAGCAATGAATGAATAAC  
10 361351 CCCTATGTGCTAAAAGCAATTGCTTGTTATGCATTATCAAGATCTCTTCA  
361401 ACGGTATGAAGCTTTATTTAATCGTTTAATTTCCATGCTATTTGAGATAA  
361451 AAACAATTGATCCACATATCAAACCAAACAAGCAATGGATAAAACAAATA  
361501 GCAGCGATAATTTGATAACCAGTGTTACTAGTATTACTTTGTCCTGCAAC  
15 361551 TGTATATTTCTTACCAACTTCAGCAGTCACAGTGTAAGTCATCCATCAG  
361601 TAGAAAAACCAATAAACTAAGTAAACCAACTAGATGCATAGTTATTT  
361651 TTACCAATATCAATTTACCTATTTGGTTATATCTGACTGTAACCATTCC  
20 361701 CCATGATAAGATACCAGTAAAGATATAGAGAATGGAAGAGAAAGTAATTA  
361751 AAGTGATGTTAGCAGAATTTGTTTGTACAAAACCAAGTAGAATAAATGCT  
361801 AGAACAAATACAATACCAAGAACAGTACATATCATTAAAAACAAGATATA  
361851 GCTTTTACACTTATCTGCTAATCTACAAAGATAAACTAACAGCACTTC  
25 361901 TCAGTGCATAAGTTCTAATTCCTTCAATTACAGTTACTAATACTACAGGC  
361951 GCTAAAAATGCATTTTGTCAACATCTGTAAAAGGTAATAAGCAAAAGTGCT  
362001 TTGAAACACATACATCCCCATTAAAAAGAAGGATAGTAACCATAACTTTC  
30 362051 AGTTTTTTAAGGTCACTAAAATCTGGTTTAAATTGCGTTTAAAACTTACT  
362101 AAAGTGGTTTGACTTTGTTTTCAATTGGTTTTCCTTAACAAAAACAA  
362151 AACTGTAAATCCAGTAATTACTAGCATTATGGCAATGATAAAAGCGTATG  
362201 CAGCAAATGGTTTGAATCAGCATTCTCACTACCTCCTGATGGATAGAAA  
35 362251 ATGCTGGTAATTATCAATGCAATTAGAAAGATAAATATTAAACCTCATAT  
362301 TCCATTAGCAGCTCCCTGAATTCAAAACCAAGTGCTTGGTTTCTTTTG  
362351 TTGCTTGTGACTAGCTAGTTTTCATAATGGTGTTCAAAAGATTAAAGTA  
362401 CTTGTTATCCCTCATAACCCTCATATTACACAATACTGAATAAATAAAGC  
40 362451 ATCATGGCTTTGTTGGTTTTTAGTTAAGATGTTGGCTGCTAATCAAAAAG  
362501 TAATTGCTCCAGTAGTAATTGCTGATAGAAATAACAATTTTCTAGAACTG  
362551 AAGCGATTTGTTAAAAACCTCCTGGTAGTTGAGTGGCAAGTGTTACATA  
45 362601 ACCAATGATAGAAGTAACAGTAGCAACTTCATCCTCTGTAATTCCTAAGT  
362651 ACAAGTGGAGGTTAGGAACAACATTCTTAACATAATAGGGTGCAGCAATT  
362701 ACAAATACATCAATTGCTCCCAAATAATTAAGGCAAGAATTTGTGTTT  
362751 TGAAAAATCCTTTAAGCGTTTTTTAAATCCTTTTTTGTGTCACATATCA  
50 362801 CTAATGATAAAGTGGGATAAATTAATATACATCTAATAATAAAGTGGA  
362851 TGGAAGTGAAACGTTCTTCACTTACTTTTAAAAAGAAAAATAATGTTTAC

362901 TAGAAAACTATTTTTCTTAAATTAATCCTGCTCCTAAACAAATTTGAT  
362951 CAAGTGTATATAATACACCAAACTGTCCAGATGCAACACTTATAACAGGA  
5 363001 TTTTAAATGTTATTTCAGTTTATTATCTGATAATAATTTCAACTTTGC  
363051 AATTTCTGGTTTTTTGAGCATGTCTAATTCCTACCAGAAGTTGACTAGGAA  
363101 GTTGCTTTGGTGTATACAACCAGTTAAATTGATCCAATAAAATTGTTGTT  
10 363151 TTCAATAATTCTTCTTTGTGCACAAGAAACAAATAATTCATTAGTTTCAAT  
363201 ATCCTTAGCAACAACAAAATGACGTTGTTTAAACCCCTTAAATTTAATC  
363251 CACTGCGTTGACCAATCGTATAAAACCAACACCATCATGTTCACTAATA  
363301 GTTTGTTTGGTTTTTCAATCCTTAATTAATCCTTTTTTTTACAGGTAAATA  
15 363351 GTTTTTTAAAAATCACTGAAATGTCTTTCACCAATAAAACAAATTCAG  
363401 TTGAATCTTTTTTATCTGCAACTTCTCAATTATTTCTCTAGCAATATTT  
363451 CTCACTGTTATTTTTTTTAAATCTGCTAAAGGAAAAATAACATTCTGAAA  
20 363501 TTGTTCTTTTTTAACATTTGCTAAAAATAAGTTTGATCTTTATTGGTAT  
363551 CTTTAGGAATAGAAAGCAAAGGCTGATTTTCTATCATGTTTATTTTGGCA  
363601 TAATGACCAGTTGCAAAAAGAGAATTAGGGTTAATTTGCTTACAAAAATC  
363651 ATGCAATAAACCAACTTAATAAACGATTACACCAGATGTCTGGATTTG  
25 363701 GGGTTAACCCTTTTTTGAACTTTGAATCATAGGTAAAAAACTTTGTTT  
363751 CAATAAGCTTCAATTAAGTTTTTTTTTATTAACCTAATTCCTAAAGAATT  
363801 AGCGATTTTTTTAGCCTGTTGGAAGTCTTGAAAAGATGAACAACCTGATT  
30 363851 TGTTATTATTTATTTTCTTATGACCATAAAAAATCATTATTAAGTGTCTCA  
363901 TCCCAACATTCCATAAAAAACACCAATAACTTCTTGGTATTGCTTTTTTAA  
363951 AAGTAAAGCACTAACAGCAGAATCAACACCACCGCTTAAACCTATAAAAA  
364001 CTGTTTTTGCAATAATTGACATTTTTTAATAAACAGCGTGAATAGCAAACC  
35 364051 TGTTTACTAATCTTTGGTGAAATCTATTAGGATTAATGCCTTTTGTAATA  
364101 GCAAGTGCAGAAATAAACACTATTAATGCTTCATAAAAATTTTGACAGCA  
364151 CTGTTGATCACTATCTTTAGGATTTTCTACAACTTTTGCTAGATAATCTA  
364201 GCTGTTTAATTACTTCAGTTTGGATAAAAAAACCATCACTTAACATTGGT  
40 364251 TTGAAAAAAATGGTTGGTCATCATAATCATCATCTTCATAAATAACAAT  
364301 ATTGTCTTGTTCTCGTTTTAAACACAAATTAAAGTTAATGCGAAAAGTCT  
364351 CAAAATCAACCGCTTGAAATTCAGTTTGTAAAAATTTTTTAAAGCTATA  
45 364401 AGTTGTGGTTTCATTACACCAGTCTAAAAAGTTTTAACACTTCTTGTTCA  
364451 AGATAGCAATCCTTAAACAGTTTATTTTCAGTATTACTTAAATAAACTACT  
364501 AACCAAAATACTGTAAAAGGTTTAATTTAAAACTAATTTTCTTTATTAT  
364551 CTAAGTTTAAGTTATTAAGTAAACCTAAAACATATTTTTCCAGATCAAAG  
50 364601 ATAGCTAAATCACTAGTTTTTTCACCAAAACCTATCAGTTTAAACAGGCAG  
364651 GTTAAACATATCTTTAATAGCTAAAATAATTCCACCCTTAGCAGAACCAT

364701 CCATTTTAGTTAAAACAATCCCTGTTAGTTTGGAAAATTCATTAAATACC  
364751 TTTGCTTGTGATAGTCCTGTTTGACCTACTGTACCATCTAAAACATAAAG  
5 364801 TGTTTCACTAGGTTCACTTCCACTTACCTTTTGAATAATTTGATAAATTT  
364851 TTTGCAATTCATTCAATTAAGTTAAGCTTGTTTTGCAATCTTCCTGATGTA  
364901 TCACATAAAACAAAGTCATATTTATCATCAATCCCTTTCTTTACGCCACG  
10 364951 AAAGATAACAGCTGGAGTTTGTCTTTAGGGTTTGGAAGTACAATGTCAC  
365001 AGTTTAAACAGCTTTGCTCACTGATTAAGTTGTTCAATGGCTCCTGCTCTA  
365051 AAAGTATCACCTGCAACAAGTAGAACACGTTTATTTGTTTTATGAAAAA  
365101 ATCCGCTATCTTAGCTAAAGTAGTTGTTTTACCAACTCCATTAACACCAA  
15 365151 CAAAGAGATAAACATTTGTAAAGTTAGGTTTAACTATTAAATCAGTATCA  
365201 AAGAGTTTATCTTGGATGTAATAAACAATAATTTGGTCAATAATTAGCTC  
365251 TTTAATGAGCTGAAAATCTGTAATTCTGTTTAGCTTGATCTGTTCAATAA  
20 365301 TAGCATCACAAATTTGTTTGCAGCATGATAACCAACATCAAGCAAACT  
365351 AGCCCTTCAAATAGATTTTCTTTAACTGTTTCGTC AACATTAACATATCG  
365401 TTTTGACAGTTCATTAATAGTTTGTAGCGAAAGTTGTAGCAGATTTTTC  
365451 AACCTGATAGTAAGTTTATTATTGGTTTGGAAAAGGCTTTGTTTTTC  
25 365501 ACTTCTTCTTTAAGCTGTTTAGCAACTGATTTTTTTGGTTTTAGTTTGGC  
365551 AATTAACCTTGCTTAAAAAGCCCATTATTAGTTAATTAGAATCATTTTCAG  
365601 ATACATATTTTTTCAAGTTTCAAGTTCAACTGCAAAGGTTTTAGTTACA  
365651 CCTTTAGTTTGCATTGCAGCACCCCAATAACATGTCACATTTTCATCATTGT  
30 365701 ACCTTGACGATGGGTAATAATTAATAAATTGGGTGTTTTTGCTAGCAGTTT  
365751 TAATGATGTTAGCAAAGCGCTCCACATTAGCAGGATCAAGTGCACTTTCC  
365801 GCTTCATCTAAAATAACAAGTGGAAGCACTTACTTTCAAATACTAAA  
35 365851 TAAACAGAAAGTGCAACTAAAGTTTTTCCCCGCCTGATAACAACATTA  
365901 AGTTGGCAATATTTTTTACCAGGAGGATTGCAAAGACATCTATCCCTGAA  
365951 ACCAATACATTACTAGGATCAGTGTAAACGAATTTGGCAAGAACCACCACC  
366001 AAATAGATATTTGAAAGTTTTTGGCAACTCTTGATTTAATTTTTGGATCA  
40 366051 GTTGATCAAACCTATTGCTAGCAATTTTCATCAATTTTCAGTAATAGCTTTT  
366101 TGCAATTTTCAACTGCTTGTTGAGCTGATTCATATTCAGCGTTAATATC  
366151 ATCAAAGCGCTTTTGCTTTTCACTTATCTCAGCAATTGATTCCATGTTAA  
45 366201 TTACCCCATTTTCATTCAATTGATTTTGTAGTTTAGCAATCTTGTTATGG  
366251 GCTTGATAGAAGAGAGTTTAACTGGTTTGTGTGATTAGCAATAGCAAA  
366301 CTCCATTGTCATTTTGTAAACACTGTTAATCTTTTCAGTGATATTTGGGA  
366351 TTGTATTTTCAAACCTAATTTTCTTCCCGCGCTGAACTAATTTAGCA  
50 366401 CGTTGTTTCATCTAACAATGCCCTAAGATCAACTATCTTCTCTCACTTTG  
366451 TTTAATTGTTTTTGCTAGTTGTAACCTAAGTTCTTGATTAAGCTTTAACT



366501 TAGAGTTAATTTTCATCACGTTTGTAGCTCAAGCACTATTTAATGAATGGATT  
366551 AATTCAGCTTCACTAGCAACAGCTTTTACCATCAAAAGTTGTGTTAGT  
5 366601 AAGTTGTTTCATATTCCATTTTGAGCTCTAAAATAATTTTTTAATTTGAA  
366651 CAATACGCTCTATAAACTTGGCTTGTAACTCTTCATACTTGAGTTT  
366701 CTGTTCAATTCATCTAGCTTTACTTCTAGTTCTGTAAGCTCCTTTTTTAA  
10 366751 CTCTCGTTTCGTTGTTTCTAGTTTGTAAATGTTCTGTTCAATTATCAAGTG  
366801 AAGCTGATGATAAATACCCATCACTAAGATTTGTTTTTCAAATCCACCA  
366851 TTGATAATTCCCCCTGCATAAACTGTCTCACCATCTAAAGTAACGATCCT  
366901 ATATAACTTGTAAGTATAGTTAGAAAGGTTAATGGCACTATTTAAATCTT  
15 366951 TAGCAATAATAACTTGTGCTAAAAGAGTATTTACAACCTGGTTGAAACAAT  
367001 GGATCACACTTAACATGATCACTACAAACACCAAGAAAACCATCAAGCTG  
367051 CTTTAAAATTTCCATGTGTTTCGTTTGTGATTTTAGTATCACTAGCAACAT  
20 367101 CATCTAAAGGTAAAAAGTTACTTTACCTATCTCATTTTGGACTAAAAAA  
367151 TCTATTGCTTGGATGGCAGCATTATTGTTGTTAACAACCTAGGTAACCAAT  
367201 TGATTTTCCAAGTGCTTTTAAGATAGCTTTTTCATACTGCTTATCAAATT  
367251 TAAGAAATGTTCCCTAGTGTATTTAAATTCCTGTAAAGCATTAGCATT  
25 367301 TTAACATAAGATATTGGCATTGTTAGTTTTTTAAGCTCATTAGTTTGGAG  
367351 TTCAATAATTGTTTTTAAGGAACGTTGGTAAATTAAATCAGCAGTATTTT  
367401 TTTCAATCTGTAACCTTATCTGATCAACAAGTGATTTTGTTCGTTAATT  
367451 AGTTTTTCAAGATCAGTGATGGTTGTTTGGAAATTTGATAGTTGGTTTTT  
30 367501 AAAACCATCAAGCTGGGTTTGATCAACTAAAATTAGTTTTTTAAAGCTG  
367551 CAGCTTTTTGCTTTTCATCTTTTTGTGAAAAACCTGTCTTAAGTGCACA  
367601 TCAATAATGACTTTACGTTGTTCCAATTCATTGATCTTTTGGTAAATATC  
35 367651 TTGTAACCTTTTTTGCAATTCATTAGATTGCATATCAGCACTATGAAAGC  
367701 GACTATTAAAGATAACAATCTGTTCTTCTAACAACCTCTAGTTGGGGTTCTG  
367751 TGTATTTTAAAGTCATGTTCACTACTGTTAATCTGAAAATTAAACTTATC  
40 367801 AAGTTCAGTTTGTGCTTGGAGATATCCCCAACC AAAACAGCAAGTTCCA  
367851 ACTCTTTCAATTGTTTTTAACCTAATGAATTGTTGTGCTTTTTTCAAGCT  
367901 TGTAATGTAAGCTTTTTTAAATCTTTTTTCAAGTTCAATTTAAACAACGCT  
367951 AACTTGTTTTAAGTTAATTAAGGTTTCGATTTAACTGGTTAACAACCTCTT  
45 368001 CTTTACGCTTGGTATATCTACCAATTCCTGACGCATCTTCAAAGATCTTT  
368051 CTGCGTTCTTCTGGCTTAGCTTCTACAAATCAAGAGACACTCCCTTGTGA  
368101 AATAATTCCAAGTGAACCTTTTTCAAGACCAATATCAGCAAAAATACCGC  
368151 TAATTTCTTTTAAAGTTGCTGGATTGGAGTTAATAAAATATTTCACTCTGG  
50 368201 CCACTCCCTCTATAAACCTACGCATCACGCTTATCTCTTTCTTGAATC  
368251 ATGTAATAAACGGTTGGAATTATCAAAGGTTAGCTCTATTTCAAGCTAACT

368301 TACTAGCAGGTTTGTCTTTAGAGCCAAAAAAGATCATATCATCACCTGAT  
368351 TTACTACGGAGATGTTTCATACTTCTCTCCCTAAAACCCACTTTAATGC  
5 368401 ATCAACAACATTGGATTGCCCCGATCCATTAGGACCAACAATACCAGTCA  
368451 TTGAATGGGTAAATCAATTGTGATTTTCATCAGCATATGATTTAAACCA  
368501 TATGCGCGAAAACGTTTTAGAAAAACCATTGTCTCTAAAAAGCTTTAATT  
10 368551 TGGATGTTGTTATTAGATTATACTAGTTGAAGTAAACTAACTAGGCTAA  
368601 TTATTAGGTTACTAAAAAATAAGCTAATAACGCTTCATTTAAAAAAGCTT  
368651 CTATGTTTTAATAGTAAGTAGTTTATTTAATTAAAAATTACATTAATTG  
368701 CTTTTAGAAAAGCAATATCATTTAAAGTTTTTATTTAATTGCTTGAGCG  
15 368751 GCAGTGATAATTCCAACATTAAAAATGTCAGTACACTAGCTCCCTTGA  
368801 AAGATCATTCAGTGGACTTGAAAGTCCAAGAACAATAGGACCAATTGCAT  
368851 CATACCCTCCAAGTCTTTGGGCGATTTTATAAGCAATGTTACCAGCATCT  
20 368901 AAATTAGGAAAAACATAGATATTAGCACTATTTTTTCAAGTTAGTTGAGG  
368951 TGCTTTTTGTAACTAACCTTTTCAACAAAAGCAGCATCAAACCTGGAGCT  
369001 CACCACAAACACTTTGATGCAATTCAGGGTGTTTTTCTAAAAATAGTTTA  
369051 GTTGCTAAAACAACTTTATCCACCATTTCACCCTTACCAGTCCAAGCGT  
25 369101 TGAATAGCTTAAAAAGCCATTTTATCTCATCCTCATTTAACTTTTGG  
369151 CAAAATTGAAGGTGTTTTTCAAGCAATTGTTGCTAACTCTTGGGAGTTAGGA  
369201 TAAACAGCAAAAGCACAAATCAGTGAAGTACAAACGTTCTTCACCTTTTTC  
369251 CATGATGAAAACACTAGAAACAAAATTACCAGTTGCTAGTAAGTAAAG  
30 369301 CTGGTCTTAAAGTATCTTTTGTAGCATATTCTTTACCACAAACCTCACCA  
369351 TCAACAACCTTTAGAGCAACTAAGGTAGCAGCTAAAGAACTAGGATCACG  
369401 TACAACTTTTGTGCTTCTTTTAAATCCATCCCCTTATGCTTACGTTTTT  
35 369451 CATAGACAAAGTTAGCATAGCTAGTTAAATCCATCTCATCAATCACATAA  
369501 TGAGTTATTTTTTATCAAAATTTGCAGGGATTTCTGACGATTATGAAA  
369551 GATAACTGCAGGTTGGATCAGCTTAGATTCAATTAAGCATTTCAACTGCTT  
40 369601 TTAAACACTTGCTGATCAACCTTCTGGAAAGATAATTACAGGTTTTTTA  
369651 CTAACAGCTTGTAATCGTTTTTTTAAAAATATCAATAACACTCATTGTTTT  
369701 ATTAATTTGGTTTAAAGATTTTTTTGAATATCGCTAATACCTACTAACTC  
369751 TTCCCCACCAATTAGTGCTAAAGAAGCACCACCAGTGGAGATAAAAC  
45 369801 TAACTGATCAGATAGTTGCATTTGCTTAACTGCTGCAGCTGAATCCCCA  
369851 CCACCAATAACGCTAAAAGCAGTTTTTATTTTAGCAATAATCTCACCGAT  
369901 TTTTGAAGTTCCTTTAGCAAAGTTAGTAAATTCAAAAACCTCCAAGGGGAC  
369951 CGTTTCAAAAGATAGTTTGGCTGTTTTTAAATAACTTTCAAATAAAGCA  
50 370001 ATTGTTTTAGATCCAACATCTAGAGACATATAGGATTGATATTGTTCTTG  
370051 AATTTTGTCACTAACATCTAAAGTAATGCCAGTTTGATCTTTAAATTGAG

370101 AACCCATTACCTGATCAATTGCCAGCACAATCTTATTATGAGTATCTTTA  
370151 TCCAAGATTTGCTTAGCAACATCAATTAACTCTTTTCAACTAGGGAATT  
370201 AGCAGTAGCTTTGCCTTTTGCTTTAAGAAAGGTATTTACCATCCCTCCGC  
370251 CAATTAAGATATTATCAGCAAGTTTITAGTAAGTTTTCAACTACCTTTAGT  
370301 TTATCTGATACTTTCGCACCACCCAAAACAACAAGGGTTTTTGTGG  
370351 GCTTTGAATTAGGTAAGAGAGGTTCTTTAGTTCTTTTTCCATTAAAAACC  
370401 CAATACAGGATTTTGCAACATACTTTGCAATTCCTGCATTAGAAGCATGT  
370451 TTTCTATGGGCAGTACCAAATGCATCATTAAACAAAAATTTCCCCTAAACT  
370501 AGCCCAGAATTTGCTAGTTCAGGATCATTTTTACTTTCTAATTTAACAA  
370551 TTTCTCCTTTATCGTTTACATCACAATAGCGAGTGTTTTCAAGGAGAAGG  
370601 ATTTCAACGAATGCTAATGCTTGCACTTTTTGTTTAACTTCAGCACCAGT  
370651 GTTTTTACAAGAAAATTGAACCTTTACAGTTGGTAAGAGTTGTTGGAGTA  
370701 ATTCAGCAACCGGCTTTAAAGATTTTGTGTTGTTTAGTTATCTTCTAA  
370751 CTCTTAATCCTTGAAAGGTGTGATAGTAGCACTATCTTGCAAGTTCTTTTT  
370801 AACTAAGAACTTAATAGTATCCAAACCAGCTAAAATCTTTCACATCAC  
370851 TAATAACCCCATGATCATTGGGACATTAAAATCACTTCTTAAACAAACG  
370901 GTTTTGTTTTGAAAATCAATTGCTTGAGTGTTTTGAAATTAAGCATATT  
370951 AGAGCTTAGCACATAGCTAACTACTCTCACTAGTTGGGTACATAGGAA  
371001 GATTCAATTATCATACCATGCATACACCTTATAAAGTTTCATGCCATCAAC  
371051 TTCAACAATATTGGTTAGTTTAGAATCGAAAATTGAACCATATTCAGAAC  
371101 TTACCACATCGCTAGATACAATAGGATCTTCACAATATTTAAAGAAGCG  
371151 GAAGCAAATCGCTTCATGGCTTGATTTACTTGTTCAACAGATGGACTTTT  
371201 TTCAAGTACAACACTTAACTCTACAATAGAACCAGTTAACTGGAACAC  
371251 GGAGTGACATCCCATTAAAGTTTGCCATTTGCTTCTGGAACAACAAGCCCA  
371301 ATTGCTTTAGCTGCTCCTGTTGTTGTTGGCACAATGTTAACAGCTGCAGC  
371351 ACGAGCACGACGTAAGTCATTATGAGGAGCATCTTGTAAGCGTTGATCTG  
371401 CAGTATATGCATGAACTGTTAGCATCGTTCCATAAACAATCCCAAAGTTC  
371451 TTTTCAAGTACATGAACTAATGGTGCTAAACAGTTAGTAGTACAGCTAGC  
371501 TGCTGAGATGATCTTATCATCGCTACTAATGGTTTTGTGATTAACTTGT  
371551 AAACAACGTCTGATAGTTTTTTCTTTAGCGGGTGCGGAAATAATTACT  
371601 CTTTTAGCACCTGCTTTTAAATGGAGAGAAGCACCTCTTCACTTACAAA  
371651 CCTACCAGTTGATTCAATTACTACATCAATATCATGTTTATCCCAAGGTA  
371701 AATTTTGGGGATCTTTTCACTAAAAACATAAACCTTTTTCTATCAATT  
371751 TGCAAGATGTTTTGTTTAAACAGTAATCTTTCTTTTCAATTCACCATGAGC  
371801 TGAATCATATTTCAACAGGTGCGCTAAAACCTTCAGGTTGGGTCAAATCAT  
371851 TAATTGCTACAACCTCAACATTTGCCTTACTGAGAAGAGAACGAAAAACA

371901 AGTCTTCCAATTCTTCCAAAACCATTGATTGCAACCTTAATGGTTCTATT  
371951 CTTTGCTGCCATACTTTAATTTAATAATTAGATTTTAATACTTTaGCCTA  
5 372001 TTGCAATTAATTCTATCTGTCAAAAATACAgCAAATTATTGCTATTAATT  
372051 GCTCTtAAAAAAATAAAGTTTTGCTTATCAAAATTGAAACTATAATTAGG  
372101 ATTTTCTCAGTAAACTAAATTCCAGTTATTAGCAATTAATAAAATACTAA  
10 372151 ATAAAAGTAAACCCACTAATAAAAATACCCCGTTTAATAAGTTGTATTTT  
372201 AAAGGATAATGAGTTCTGTTAGTGTTATTTAAATCATAACCTTTAGCTTG  
372251 TAGAGCAAACGCTGTTGTTTCTGTTTTTTAACTGTTGAAAGTAATACGG  
372301 GAATAAAAAGGGTTTTAATCTTGAAAGGATTTAAAAACGAACACTTGTTA  
15 372351 TAGATAAAACCTCTAGTAGCTTGAGCTTGTTTTAATTCTTATAATTTCACT  
372401 TTTAACAGTTGGGAGTAATTTAAATATAACTGCAAGCAAGATACTAATTG  
372451 GTTGAACCTTAATATGAAATAACTTAAGAACTTAAAAAACCTCTCAACT  
20 372501 GCTCAAGCCAATTTCATAGATAGAAGTTGAAGTTGTCAGTAAAAAGAAGC  
372551 ACTGAAAAGCATACTAATCCTTAATGCAATTACAAAGGATCGTAAAAATG  
372601 AACGTAGATTAAACTTCACCAGCTAACACCACCAAATTTATTACCACCT  
372651 GAATAGATAAAACTTCCTAAAAAATTATGGTTCTGATCAACGCTTAAAGC  
25 372701 AGTATTTGGTAAAAAGATAAAACCGTTAACAATTACATTAAACCACAAGA  
372751 AAAATAACATCCAACCTCAAATAATTAATGCACCTTTTAACCCTTTTCTCA  
372801 CTAATTACAACCTAGGGTTAAAAAACTAAGTTAATAATTACAAGACCATA  
30 372851 TAATCCTAGCGGTAGAAAAGCAACAACCTAACTAATTAGTCAAAACCACA  
372901 ATTTTAGAAGTGGGTCAATTTTGTTTAAAAAACTGGTTTTTTGCATGAAA  
372951 ATAAGTTTTTTAGTTCACTAATAAGATCATCAAGGTTTTTAATTTCTGCT  
373001 TGGTTTTTTAAAGCTATTCCCTTTTCATTAAACATCTTAACCTGCTTGGAT  
35 373051 AATTACTGGAGGGGTGATTCCATATTGCATCAACCAACTGGTGTTTGAAA  
373101 AAAAATCATTAACAGTGGTTTGATGAATTATCTTTCCCTGGTGGAGATGG  
373151 ATGATTTTATCAGCAGTTTCAAAGATAAAATCAACATCATGGCTAACAAT  
373201 AACAATCCTTGTTGTTTGTTCATTGCTACTAGCATTTTGCTTAAGTTGC  
40 373251 TAATCGCCATTTGATCTAACCCAACAGTAGGTTTCATCAAGGATTAAAAAC  
373301 TTAACCTGCATTGCTAACACACTAGCTAATGCCAAACGCTTCTTCTGTCC  
373351 ATCGCTTAATTCAATGGGATTTTTTATTAAACGGGATGTTTTCCAATCCAC  
45 373401 ATAGATCAAGGTATTTTTTGGCATAATTAACATCTTTTTTATGACAAAGT  
373451 TTAAGGTTCACTGCTCCTGTTAAAACTTCTTCTAAAATAGAATCACAAAA  
373501 AAAGTATCTTCTGCTTTTTTGCAAAATATAACCAATTTTTTGCTTAAAGT  
373551 TTTTGTATCTTTTGTGGTATGGTTTGCAAAATAACAATAATTAGCA  
50 373601 CAATTTATATAGCCAAAACCTAGGTTTTTCAAATAAACCTAACTGTTTTAT  
373651 TAGTGTAGTTTTACCCTACCCTTTTACCACAAAATAACTGTAATTTTAT

373701 TAGGtTCTATTACCCCTGAACaACATTTAATGATCTGACCATCATTATGC  
373751 TTATTGACAAAAGACACTAATATTGTTAAAAACAATGGATCTTGTTC AAT  
373801 GTTCAGTAATTTGCTATTAAAAAATGGAATGCTTTTTTTACTGTTTAAAA  
373851 AGTAAAAAGGATTAATGATTTTATCAACCTTTTTATAAAAAAGAAAACAGT  
373901 TTTTTTGAATCTAATTTTGTCTAGTTTAAGATTGCTTTTTTGAGCTTGAAG  
373951 ATGGTATTTTTGTTCAATTAAATCTAGTTTTATTTGAGGTGTTTGCATAT  
374001 CCAGTTAACTACATCATTCAATTCAAACTTAACTTGGTGTTTTTTTGT  
374051 TTATTTGTTTAGCCACCTTATGGGCCAATAAAAGTGGAAGGGAGATTA  
374101 AAGTGGTGGTTATGAAACAAATCAAGCTGCTCATATATCGCTTCAGGAGC  
374151 AAACTTTTTAATTAGCGATCCTTTACTTAAAAAGATAATCTCATCTGCTA  
374201 GAAACAGATCATTAATAATCATGGGTAATATTGATAACTATTTTGTTTTGT  
374251 TTTTGTATGGTATCAAACACAAATTTTTTAAGTTTATTGCTGATCTTATT  
374301 ATCAAGCATACTAAATGCCTCATCAAGCAGATAAATTTGTGGTTTGACAG  
374351 CCAATAAACAAAGCAAAACAGCACGTTGTTTTTCACCAAATGAAAGTTTT  
374401 TTAAGTGGTGTAATTTGTTTATCTTTCAATTCAACAACAGTTAAACTTC  
374451 ATTAATAATCTTATCCATTTCACTAGCTAAACTCCATGGTTTTCCAAAG  
374501 TAAAAATCAATTCTGGTGGAGTGTATCAGCAAGTAATTGCACATCAGGG  
374551 TCCTGTAATAAGATTCCAATCTTATTAACCAACAGAAAGTCAACTCCTT  
374601 ATCATTGAAAAAGATAGTTCCTTTTTTAGCTTTTAGAAATCCGCCAAGGA  
374651 GTTTAACTAGGGTTGATTTACCTGAACCGTTATGACCTATTACTGCTAAA  
374701 TGACACCCATCTTGAACATTAAACTAATCTGATTTAACACATTGTTTTG  
374751 GTGTTTTGGGTATTTAAACTGAGGTTTTTAAGTTGTAGCAAAGTAAAGCT  
374801 TATTTATAAATTTTAAAAATAAGTCAGAGCTAAAAATCTGTTTTTTGGTA  
374851 GATAAAAAACAAAAAGCAGCTGTTGTGCTGCTCTTTTTTATTTGGAATA  
374901 TGTTCTATATGAACAGGTTATTTTGCTTGTGGACCTTGTTCCAGGTTGG  
374951 GTTATATTTTTTTGCCATCTCTTCTCTTCACTTCTTAAAGTTTTCAATTT  
375001 CCACCTTGAGTTTGGCATAGTCATTAGCTTTAATAGCAGCATCAATGTTA  
375051 CCTGTTAGCTTTTCTAATTCTCTTTTCTTCTTTAGGGAAATCTTAGC  
375101 ATCAGGACTTGCTAATATCTCTTTGATGGTATTAACAATACCTTCCCCTT  
375151 CATTACGTAATTCAATACGTTACGGATGATGTTATCCCGTTCCTTGTTA  
375201 GCTTCAGCATCACGGATCATCTTTTGGATCTCCTCCTCAGAAAGATTACC  
375251 GTTGTCACTAATGGTAATACTGTTTTCTTTTGCCTGGTTAAATCCTTAG  
375301 CTTTAACATTTAAGATCCCATTTGGCATCCAACTAAAGGTAATCTCAATT  
375351 TGGGGTTTACCTTTAGGTGCTGGTTGAATACCACCTAAGTTAAATCTTCC  
375401 TAATGACTTATTATCTCTAGACATTGGTCTTCCCTTGACATACAACCA  
375451 CATCAACTGATTCTTGGTTATCTTGAGCAGTTGAAAAGATTTGACTTTTA

375501 CTTACTGGGATAGTTGTATTTCTCTTAATTAAAGGAGTAGCCACACCACC  
375551 TAAAGTTTCAATAGAAAAGGGTTAATGGAGTTACATCTAAAAGTAAAACAT  
375601 CCTTAACATCACCACGTAAAACCCACCTTGAATAGCAGCGCCAATAGCA  
375651 ACAACTTCATCAGGATTAATAGAACGGTTTGGTTTTTTTACCTGGTACCAT  
375701 TGATTCAACTAGCTTTTGAAGTGCAGGCATCCTTGTAGAACCACCAACTA  
375751 AAAGAATTTTCATTAATCTCTTCAGGTTTAATCTTAGCTTCCTTGATAACA  
375801 TCTGAAATAGGGTTTCTTGTCTTTCAAGTAGTGGTTTTGTAACTCCTC  
375851 AAACCTTAGCACGGGTTAGTTTAACTCAACGTTAACAGGACCTTTTTGGG  
375901 TAACAGTTAAAAATGGTAGAGAAATAATCGTTTCAAGTTGAGCGGAAAGT  
375951 TCAATCTTAGCACGTTTCAGCTGCTTCTTTAAGCCGTTGCATTGCCATCTT  
376001 ATCTTTTGATAAGTTTAAACCCTGGTGTCTTTGGCAATGTAGGCTGAGA  
376051 TATATTCAATGATCTTGTATCCCAATCATCACCTCCCAAACGGTTGTCC  
376101 CCAGCAGTTGCAAGTACTTCAAAGTACCTTCTGCAATGTCAAGTAAAGA  
376151 TACATCAAAGTTCCACCACCCAAGTCATAAACCAAGACTTTCATCTCTC  
376201 TTGATGCTTTATCAATCCCATAGCTAAAGCAGCAGCAGTTGGTTCGTTA  
376251 ATGATCCTTTCAACATTTAAACCAGCAATCTTACCTGCGGTTTGTAGTGC  
376301 GTTTCCTTTCCGCATCATTAAAGTATGCAGGAACAGTAATAACTGCTCTTG  
376351 AAATCTTTTTACCAATCTTTTTTTCAGCAAAGTCCTTAAGATAACTAAGG  
376401 ATTTGCGCTGAAACTTGTTTCAGGACTTAATTCCTTAGTTGTACCATCAGC  
376451 ATTTTGGACTTTTACTTTATTTGAGGTACCCATCAACCTCTTGATGGAGA  
376501 CAATGGTATTTGGGTTTGTAAACCATCTGTCTTTTAGCAGCATCACCTACT  
376551 ATAATTTCAATTGTTTTTATAGGAAACAATGGAAGGTGTTGTTCTTTTACC  
376601 TTCAGGATTTTCTAATACAACAGGTCTCCACCTTCCATTACAGAAACAC  
376651 AAGAATTGGTAGTTCCAAGGTCAATGCCAATAATTAAACCATTGTCTGCA  
376701 CTCATACTTTTTTTTAGATCAATAACAATTACTCAGTAATTATAAACAA  
376751 AAATTAGCACTCAAACACTAAAAGTGCTAATTAAAGTTTGTTTTATTAT  
376801 CTTTTTTAGTTTCTAAGCTAACAGTGTTAACTGTTTTCAACGGTACATTA  
376851 ACGGTCTTTTTTAAATTCCCATATAACTTGAACAATTACACAACAAAACA  
376901 AATCCAGTGAAAATAGCAGGTAGATAAACAGATAAAAGTCTTCATAAAA  
376951 AAACACCATCTTTAATCTGATCATGGAGGAATTGATCAGTTGGTTTGAAT  
377001 GCATTGAGAAAAGTAGTCATCACAATTTGTGTTGCACCTTCCCCACTAGC  
377051 AACTGGAATAAAGTTAGAAGCGGTAACAGCAATATTAGTAATGTTAAAAA  
377101 GATCAATTAAGCTGTATTGATCAATAACGTTATTAGTTGTGTTGACAGTT  
377151 TTTGTGATCATAAAAAACCAAACAACTAAAGTAGGAACAATTGCTAC  
377201 AACCATGTTAGCTAGTAATTTAAAGATTGTTAACCTTCACCTTCGCATCT  
377251 CAATTCCATACAACCTATTAAATTCAGCTTTTTCTATAAAAACGTTGGTAG

377301 ATCTGCTCTTTAGTTAAATAAGGACGTTTAAAGTCACTTTCGAAACTGGTT  
377351 TACAAGTGAATAGATCAAAACATGCATCTTTTATTGAAAGCAATAACAA  
5 377401 TAAATAAGATAGCAACAACAACATCAAAGATCATCCCAGTAAGACTTAGT  
377451 CAGTAAGAGACAAAGCTATTATGGTTATTTGCTAACAATTGATAGTTTTT  
377501 AGAAAGAACAAAAAAGAAGGTCAAGTTATTAACGCTTGCGATAGATTTT  
10 377551 AAAATGCTCCTGTAGAAAGTGACAATTAAGTGCAGTTTGTTTTTCATC  
377601 CCCTTTTAAATGAATCAATACAAGCGAAATGGATCTTGTCTAGTGATAA  
377651 GGGGGTTACAATTTGAAAAAAGTACTACAAAACCAAATAAACCCT  
377701 CTCACCAACTAGCATAAAAACAAATCTCCTTGATACCCACCAATTAATG  
15 377751 ATTACATTCCACAAAAGTAAACTAAAAACCTAAGATAACAACAAATAT  
377801 CCAACCCCAATTCTGATAGTTAATTGCAGTGATAATAGTTTTACATCAT  
377851 CAACACTAACACCTAAAAAAGATAGTAACAATAACACTAATAACGATT  
377901 AGAAAAACAAAAAAGCTAAAAGCAACGATGTTTTTAGTGTTAAAAA  
20 377951 GGTATTGGTGGTTAACTTTGCCATTACTTAAGCAAGTTTAAAGCCTGATTG  
378001 AATTCTTTTATCACCATCCTAAATTGGGGTTTTTCAATTGCACTTAAAG  
378051 CAAGTTGTTGGGTGCCTGTATCACTAGCTTGAAATAAACTAAAGCTGCT  
25 378101 ACTATATCACTTTCAATATTGGTAGAACTTGTTAAACTAAGTGAATCAAT  
378151 GTCACTTTTAGTGAAGTGAAGATAGTTGTAAGTATCACCACCAAAGTTAA  
378201 ATTCACTAAATTTTTGGTTGGTTTGGGTACTTCTTTTTGAAATACTTGGA  
378251 CTATTTGATGAATTAAAAAAGTGAATATTGGTCTAAAACAGCTAATAA  
30 378301 CAACGCTTGTTTAGCTTTGAAATCTAAAGCAGAATTGTTAATTGCATCGA  
378351 CCTGAAAATAAGCTGAAAGTGTTTTGCCATTACTACTACTACTTGGA  
378401 GTTAGTCTACTTAGCTGTGCGGCAATGTTATCTAAACTAATTGGTCTTT  
35 378451 TGTTTCACTAATAAAATTTTTTAAGATCATCCTTTGAACCATATTGTTTTA  
378501 AGGAATTGGCAGCGATATGGTTTAAAAGTGCCTGGTTAGTATTGTTTTCT  
378551 AACATGGAAGTGTAGTTGTATTCAAACCAGTAAAACCATAAGTACCATT  
378601 ATTACTTGTTGATACTGCTTGTCTGGTGCTTAACATCGTAGTAGCAGGTG  
40 378651 TAGTGTTAGGACTTGTTTTGGTTTTAAAAAGAAATTATTAGGATCAATA  
378701 GTTTGGTTGGCATTAGCTGTTGTAGCATGTTTCATCATTTTCATAGTTAAA  
378751 AACAGAGCCAAATATCCCTGAGGATTATTGGTGTTGTTACTGATAATAT  
45 378801 TCTTATCATAAGCAATATAGGCAATTTACCATACTTTAAGTTAGCTTGT  
378851 AAAATATCTTTAAAGTTTTTTAGGTTGTTTTCAATTAACCATTGCAAAGT  
378901 AAAAAAGAAAGCGATAATGGTCAATAACTGCTTTAAAGTTAACATTAAAAAC  
378951 CTGATTCATCAACACTCTCTAAAAAAGCTTTTTTAAACAATTCATCAATA  
50 379001 TTGCCATTATTAGGATTACCATACATGGCTTTATTGGTTAATTGCTTCA  
379051 TGTCAATGTAATAGTAATTGCTAATTACTTTAGCTAAACTATCTGCATCAC

379101 TACTTGATGAAGTTGATGAAGATCCATTTTTAGATTTAATCTCTTCAAAT  
379151 AACTTTTTAGCTTTTTCAAAGTGTGATTGCTAGTAAAAGCATTTTTTTAA  
5 379201 CAATGCAAAGGAAAGAGGGTTTACAGTTGTTACATCTAACAACGCATTTA  
379251 AACTCCAATTGGCACTGTTAGTAAGTGATTGATCATTGTTAATATCAACT  
379301 AGAATAATGTTGCTAAAGTTAGGTTTTGATTTTTCTGTAACTTTCAATTG  
10 379351 GTTAACAAATTCTGTTACTTTGTTATTTATGTCGCTCAGAATTTTCATCTC  
379401 TTATCTTATCAACATCAGCTTTTGTAGTTTTTAACTTATTGTTGTTTTCA  
379451 CTAATATTTATTTTTTCACTACCTACTTTTTTCCAAAGTGTTTAGTAAT  
379501 TAAAAACAAGAAATAGTTATTGAGTTTTTCATAATGACCAGACTTGCGAA  
15 379551 CATATGGCAAATGGGAAGATAAGCCATTTAACCAAGGGGTTGGATTAATT  
379601 TGGTTAACATTGGTATTAAGTTCAGTTGTTCTACTTGTAGTTTGTATC  
379651 TAATGCATCCATTTGTAAAAACAAATCTCTGATTACATTTGTTGCTAATG  
20 379701 CAACTGGTGCAAATTTTTGCATTAGTTCCTTTGTAATCATTGAATGCTTTT  
379751 TGCATCGCATCACTACCTTTATCTTTTTTTTGAAAATCAGTATTTATTAG  
379801 TCGCTTTACTAATATTAATTCCTGATTTTTTTCAAACCAAGTTTTTCAGTG  
379851 TTTCAATTTAATGGAAAACATAAGGAATATAAACTGTTTTTAAAGGTGTTT  
25 379901 GTTTTGGCTTGAAAAGCTCTTCACATTA AAAACTGCTTTTGCTTTTCAAT  
379951 GTCTCTTTAGTTTTGCTACTACTATTTTTTGTGAGATAATAACTACCTC  
380001 CATCAATTCCAATTACAGCAACTCCCTCTCCGTTTCTAACTAGTCTTAGC  
30 380051 TTCAATTGGTTATTAGAGTTATGGCTTGTTATTTGAACAGTAGCATTGTC  
380101 ACAGTTTGCACTAACAGTGCTAGCACCATTATTTGTTTTGTTATTAGGAA  
380151 TAGCTGCATCCCAAACAAGATAACTGCTTGTTGTTGATGAAGTAGCTTTA  
380201 GTTGAAACCATCATATCACTTGTAGTTGTTTGGTGGATTGCTTTGCTAG  
35 380251 TTTTCCTAAATTGGAACATCATTAGAACTTATAAAAGCATCTTAATAA  
380301 GACTCTTTAAATTGTTTTGTGAACTGTCTGTTGTATTGTGTTACAGAAC  
380351 AATGTATTACTCTTAGTATGGTTTTCAATTTTAGTTGATTCAACAACAAT  
380401 GGTATTGTTAAGTTCCTTTATTAAGCTCTTTAATTGTGGGAAGTTGATCTT  
40 380451 TATCTTGATTTAAAAGATCTAGTTTTAAATTTAACTAGCACCTAAATTA  
380501 GCTGCTTCTAGTTGATCAACAATGTTTAGACTATCTACTATTTGCTTGGT  
380551 TTGAGTGTTATCAGAAAGAGTTGTTGGAAAATCAATCAGGTTGCCTTGAT  
45 380601 TTTGATCTAAGATGATTTTTCTAAACCTGTTTTTGCTGTATTTAATCCG  
380651 TCTTTCCCTCAATTAAGTCTCTCAGCGTTTGTGGCAACATTCTGGTT  
380701 CTGAGGAATTTCCCATCTTTAGGAAAGAAAGGAAACGCATAAGAAGGGG  
380751 TTAATTTATCTTTTAGTTTTTCAAGTGTGTAAACTTGACCCAAACCTTGT  
50 380801 TGTGGTGCTGCATATTTAAAAGTAGCTTGACTGATTAAAGTAGGATCGGT  
380851 ATATTCAACCCAGAGATTAAAGATTGTGCTTGTAACCTTGCAAACAATG



380901 CATCATTAGTTTCACTAAAAACGTGGTTCTTGAAAACCAAAGTCCTTTCAT  
380951 TTTTCAGGTTGGGATAGTTCATCATAGATATAAGGACCAGTTGAGAGTTG  
5 381001 TCCATTAGGTTTATAAACTAAGAAATCCTTAGCGAATAATTTAGCGGTAA  
381051 AATCACTAATAAGTTGATTGAAAAGTTGTTGGGATTTTCACTAGCCTCA  
381101 CTGCCACCACTTTTATCTAATAGATCTTGTTGAATAAATACTGCTCTGTT  
10 381151 TCTGGGTGGTGATATTAACCCATTACAGTATTTTTATATTGATCATCAA  
381201 CATTCTTTTTAGTGTCTTTTAAAACTTGTTTATGGCTTTGTCTTCATTG  
381251 TTTTCATACCAAGCCTCAAGTGCTTTTAAAAGTGGTCCTATAACAAAATG  
381301 TTTGTTTGCTGAAGGAGTTTTTAAAGCAGTAATAAGTCCTTCTTTTAAAC  
15 381351 TACCCTTTTGACCATGAAAAAAATTAGTTGAGGTTGGTGAAAAAACTGTT  
381401 TGCAAAGCACTGTTTGTGGAGTTGAACAAGCTACAAGTATTGTGCTTAC  
381451 TGACAAACCACAAAGTAAAAACCACCAGAACTTTGATTTTTTAAAAGtT  
20 381501 TTTTCATGATCTTGGTTTTTTCTTATTAATTAAGGTTTGAATCTGTT  
381551 GTTTTTGGTATTTTTTGTAGTTAGGTTTAACTTTTTATATTAGCTTTG  
381601 ATAGCTTTAATTTTCTAATTTGTAAAGTTGAAAGCGGTTTTTGGTAGT  
381651 TTTTTGGTTATTTTCAGTCAAAAACCTCAAATCACCATTACTAGTTAAAC  
25 381701 TAACGTTTTGAAATTTAATTCCTTTTGCTATTAGTTTATTAAATTTACTT  
381751 TGATTTTGGTCATTTCAAAAAAGATATGATCTGCCCAACTGTAAAGTCG  
381801 TGCTACACGACCAGAACGGTGGATGTAAAAACTATCAATTTTAGGTAGAT  
381851 CTCAAGAAATCACCACACTGAAATAATTTAAATCTATCCCACGTGAAAAT  
30 381901 AGATCAGAAACAAC TAGTAATTTCAATTTATTATTAGTTGCTTTTGTGAA  
381951 ATTATTTTTACGTTCTTGATAGGTTAACTACCATAAATTGAACCAAAAC  
382001 TAATATTGTTATTTGAAAGCAATTGTGTTAATTGTTTTAAAGATTTTTGA  
35 382051 TTAGAACAGAAAACAATAATTTGCTGATTTTGGTGGTGTTTAATAAGGC  
382101 TAATAAACAGAAAAACGGTTTTTCAGTATTGAGATGAACAACAAAATGCT  
382151 TAACTAAGGGGTGAATCCATTGCTTTGGATGGAGATTAATAACTTTAGTA  
382201 TTAATTACTTGTTTTTTAATTATTTGGAGTTGTTGATTGAATAAAGTAGC  
40 382251 ACTAAAAAGGCAACAAGGGCTTTGCTTTTTGAAAAAGATGAACACATT  
382301 CAAGTCACTGCTGGATTGAACTTTGCTCTAAAAACATGTCAATTTTCATCA  
382351 AAAACAACGTATCTAACTTTGCTAGTAAAAAGGTATTTTTCGTTTAGTAA  
45 382401 ACTAACAATTAGTTGTGCTTTTGAACATAATGAAGTGGCAAAAGTAAAGG  
382451 TTTTAAAGTACTTTTTGATTTTCAGTTAAGATGTTGATAATTTGTCATTGT  
382501 AACTCTTTGGTTGGTACAAAAATAACTGCTTGAGGTTGATCTAAACTGGT  
382551 GTTAATCTTATCTAATAGAGGTAAAAGATAAGCAAAGGTTTGGCCACTAC  
50 382601 CAGTTTCAGCAATACCAATGATATTTTGAATGGTCATAATTTAAAAACT  
382651 GCTTGCTGAATTTTGGTAAATTCAACAATGCGTTTCTTATCTAAAAACTG

382701 CCTAATAGAAGAGGAAAAATTGCATCTTAACTAGAAATTTACGCACTCACT  
382751 GTGAACTGATTGCTGAAAACAATCTGTTATCACCAACTCTAACTAAGCCA  
382801 TTTTGGCATTGCTATCAATGCATTAATAGCTTGGGTTTGATTATTAGG  
382851 ATTAAGCGCTTCAAGCGCAACTGTACTTAAAAATCTTCAAGTGAAAGAT  
382901 CAAGTCTTTTGAATTATTTGAATCTGTACTATTCAAACCTATCACTACCA  
382951 AGCATACTTACATCTTCAAGGTTAATCTGTTTTGCATAAACTGCATGATA  
383001 GATCTGGTTATCTTGTAATAAGTTATAACTGCTATAATTACTGGTTTTAT  
383051 TTGTACCTATATACCTTCAAACCTACTAAACACATCATTAAAGTTACTA  
383101 TTATTAGTTTTACTTTGAGCTTGTTTTAATTGAACAGTTTGAGTATTGTT  
383151 AAAGTTTGAATTAGCAAAATCTTCAAATTAGTTTTTGTCTTGTAAGG  
383201 ATTTTGATCTATCAACACCAGTAACGTTAATATTAAGGTTACTTGTAA  
383251 TGGTTATAAAGTGCATCAAACCTCAGCTTGGGTTGGGATGTTATCAATTGT  
383301 TTCTATAAGTTTGTAGAGAACCAAACTAAATAAAGCACCTTTGTAA  
383351 TTGTTTCATTACTACCACTTGATTGAGTAGATTGTAATTGTGCTTGACCA  
383401 CCATTAGAACTTGATTTTTTCTAGATTGGGAAACAAACTTGTAAGAGGCG  
383451 ATTTCTAACTGCATCTGGTAAGTTGTTGGATGAAGTGTGGTAACAATAC  
383501 CATGGAAACCAACCTTCTTTGCTGGTTATTGGTTTGCTGTGCACTTTTT  
383551 TGCATTAAAGTTAATGATGTACTGCTACTACCATGTTCTTTGTATAGTA  
383601 AAGACTTGAAATATCATTTGCAGCACTGTTAACTGTTGGGGTTTTGTTGT  
383651 TGGTTCAATTATAAGCACTCGAACCAAAATACATAGTTAGGATTTGTTGT  
383701 TCTTGCTTGGTAAAGTCTTGATTAGTTTGAGAAGCAACGTTGTTAGCCAT  
383751 TTTTACTAATACAGATTTAGAAGAACTTCACTCATTGCTTGACTAGCAG  
383801 TATTATTTCTGTCTTTATCACTAGCTAAACTTCAAACCAAGAACTATTT  
383851 GTTGTTCTTGATAGTTTAGCTTGCAAGTCTGTTTTAGGTTTTTAAGGTT  
383901 ATCTTTTAATAGCCATTGAACTGTATAAAGATAAGAATAGTAATTGATTA  
383951 AGTCATTGCTATCCAAGCGTCTTCTAAGTTTAAGCTGTTGTATAAACTA  
384001 TCTAAAACCCCATTAATTTTGGGTTTATTATCAGTTGAACTTTTCAATTAAC  
384051 ACCATTACCAAAAAATAGAAGGATTAGCTTGTTTTTGAAAAAGATCAAATA  
384101 GGTAGGTATATTTAAAGATATTTTCAAGTTTTCATTATTGAGACTGTTTCAG  
384151 TTTTTAAAGTTAATTTATCTAAATCAATCGCTTGTTTAACTGATCATC  
384201 ATTGACAAAATAATCTCGTCTAATGGTATTTTGTAACTCATCACTTGATA  
384251 AAACAGCATTTAAAGCTAAATTAAGTGCTAGAGAAGTGTTCAGGATCA  
384301 GATGAAAGTTTGGTATCAACAAGGATAATTTGTGAATATTGCGGTGAGGG  
384351 AATTACCGAACTTTTAGTTCATCAACATGCTTTTTAACTGCTGCTTCAA  
384401 CTTTCTTTTATTCTCTTTTAACTTGTCATTAATTATCTTTTTTGAAAAAGGA  
384451 TCACTACTACTACTATTACTATTACTATTACTATTACTTGATTTGAACT

384501 AACCTTTATCAATGATGTCTTTATAGTAAATACCAAGTTCATTGTAGTGTC  
384551 CTGTTTTACTATCTTGTTTCATAAGGTAAAAACAGCAGCTAAACCGTTCATC  
5 384601 CATATTTGTTTATTTCGCTCATTATCAATGAAAGGTTGGTTACGTTCTGC  
384651 TAGTTTTAAAGCAACTTTGTTTTCTGCAGTAGCAACTTCATTA AAAACAA  
384701 TTTGTTGATATTGACTTTCAACTAAATCCTTCAACTCGTTTTTAACAGTG  
10 384751 ATAATGCTATCACTAAACTTTTTAAACTGAGGGAACTTAAAAAGTTACT  
384801 TTCTTTGCTGTCTACTAATTTAAAAAGGGCATTAAATAAAAAATAAACTC  
384851 TGTTCTTATCAAAGTGTTTTTTCACCTTCATCAAACAACCTAAAGTCATAA  
384901 GTAGTGTTTGTATCAATTAAGCCATATTTGGTTTGTAGTGCACGGAATAA  
15 384951 TAAGAATTGTTTTTGTATTATTACATCACGTCTGATTCAGAGAGATAAT  
385001 AACCACCACCATCAACACCCATTAGATGGATACCATCTTACCACGTGCT  
385051 AAGATTAAATCAGGTTGACTATTGTtATCTTTTTTAAGTTCTTTTAGATC  
20 385101 AACGATTGCAGAATTATTACTACTATCACTGTTACTTGTACTAGTAGCAT  
385151 TACTGAACTTTTTTTGATATTACCTTTAAAAACATCTGTTGATTTAGTA  
385201 GTTTCATTTTCTTTAAAGATCTTAGCTAGATCTGTTTTATGAACAGTAGT  
385251 TGTTTGTGAAC TACTACTTGCAC TTTTCATTGCAGCCTTAGCTGAATTAT  
25 385301 TTTCAACAAAGAAATTTTCAATGATTGATTTATCTTTTCTAATTTAGTG  
385351 TATTCAGTTTGTCTGCACCTTTGGATTTTTTTTGTAAGCTAAATAGCC  
385401 CTGGATAAAAGCTGCTGAAAAGCTAGGATCAAAGGTATCAAACATATCAC  
385451 TAGCTTTTAAACAACAATTTACCACCCTATCACTAGAAAACCTTATTAGGG  
30 385501 ATGTCAATGGTTTTATTGTTAGTATTACATAGCTTTGTAAATTACTAGC  
385551 TAGGATATGAAAACCATTTGCTCCTTTTATGGAGTTATCTTGTTGGTTAT  
385601 ATTTGTTAAATACTTGAAATTGATAGGAAGGGGTTGGAGATTTAATTAGA  
35 385651 TCAGGATTAAAATAGTTATCAAACCCATCATTAGGAGTTTCATTAGTAAA  
385701 TACTACTCTTGAACTAAGTTAGGGTTTTTCATTAGTAACGAACTGATCTA  
385751 ATAATTTATCTTGAATGGCAGCATAACTGCATCATTATTGATCCTAAGT  
385801 CTTTTATTTTTATCAACAAACTTAGCTTGATTTTGATATTATTCCAATT  
40 385851 ACTTTGGTTTTCAATTAAACCTTTTAAATGGAGTTGATAATACGCCAACAC  
385901 TTTTATCAACATATTCAACAAAGTTCTTTGTAAAAAGCTTATTGATAAAA  
385951 TCATCAACAATTTTGTGTTAACATCACGGAGCTTTCAGTTGGCTTGATT  
45 386001 TCCACCAGTGTTATCTAAATATCAGTTTGTAACCTAACTAAATAATCAC  
386051 CCCGATACTGATTTCTTAAGTTTTGTCTTGATTAAACAAAACCTATTGTCT  
386101 GTATCAGTATTAAGtTCTTAAATTTCTCTTAATGTCATCATCAACATT  
386151 TTCTTCATAAAAATTGCGCAATACTGGCGCTAGGCGCATCGTTAAATATT  
50 386201 GCGTTAGTCCTTCTCTATTTTCAAGTGCTTTATAAAGTGTTGGCATTAA  
386251 CTACCATCATTTTTATCAGTAAAAGCACTACTGGGTCTAAAGAGATTTTC

386301 AATGGTTCTGGAGTTTGGTTGTGCACAGGCAACAGCAACAATTCCCAAAC  
386351 TTACAGCTATGCTTGAAAGCAGCAATGGTCATTTTACTCGGTGTAAAAAA  
5 386401 CGTTTCATTGCACAGTCAAAAATTTCAATAATTTTAAAATTTATATTTTT  
386451 ATTATTACCACATGCGACTTGAAATAGAAAACGGGCTTGAATTTGTCAAT  
386501 GATCCTGTGGTAAATGAACTTGGCAAGATCTGTTTTTTTCATCCTTTTAC  
10 386551 AGGTAATTTAACAACAACTTAGTTTCAGAAGTCATTTCAATAGATACA  
386601 GTTTTTATGCCATTAACACCCAGGGCATGGTAATAGTGTATTAAACAAT  
386651 CCAAAGCAACTTGAATTTAGTTACTGATTGGAAATTACAAAACAGTTTTT  
386701 TGATAAACATAACTTAAAGGATGTAATCTTATTTGGTCATTCTATTGGCG  
15 386751 GTGGTTTAGCAGTTGCTTTAACTAACTATTTAAGCAGTGATCAATATAAA  
386801 GCAGTCTTGTTAGAAGCACCATTAAATCCTGCTATTGTTGAACTCCTTT  
386851 AAATATTGTTCAAAATCTCATTCTGATCCTGATAGTGATTTTGCTGTTA  
20 386901 TTCAAAGTGCTTGTTTACAATATTGAGAAAAAACTTGGGGCAAACTTT  
386951 AAAGAATATTGTGAAAGAGAAAAGCAAAAATCAATTCACCAAACCAACG  
387001 CCTTAAAGTGATGTTAGAACCTTCTACACTCAAACAAAACATAGTTTTAA  
387051 TCAATGCAGCTTTTTTAAAGTTAAATTGTCCTGCTTTGTGAATCCATGGT  
25 387101 AAGCAGGATGGAATTATTAAGTACCTTCCATCCAAGGCTTATTATGAATC  
387151 ATTAAACAATAAGCAAATTCAATTTAAAGCCATAGAAGCAGCGGCTCATA  
387201 CCCCTTACTTTGAACAACCACAAAAGTTTTTAAGTTTAGTTAATGATTTT  
387251 TTTCAATTAATAAGTTAAAGCAGTTTATTTAACTAAACGCTTGATCACT  
30 387301 CAACAACGTAAGATTCATTTATTCCAGCAGGTAGTTCGCTACGCTCTGGG  
387351 AATCTTATATAAGTACCTTCAAATGCCTTTTTTGTGGTTTCCACAAATGA  
387401 TGAGATAACACTGTTTTCAATAAAATTTTTAACTAATGGGGATTAGTTA  
35 387451 TTCTTGCTTTTAAACGGACTTTATCCCCGGGATTAATGATGATTGAAGGG  
387501 GTGTCAACAGTTTGATCATTTAAAAATCACATGACCGTGGTTTACCATTG  
387551 TCTTGCACTCTTCTTGTTGGTGCAAAACCCATTCTGTAACTATGTTAT  
40 387601 CCAAACGTGATTCTAAACTCTAAATAAATTAAGTTAAGTTACCTTTT  
387651 TGTTTTAAACAAAGCGAAATAACCTACGAAATTGTTTATCAGTAATACC  
387701 ATACATGTATTGCATCCTTTGTTTTCTTGAGTTGTTGGGCATAACCTG  
387751 ATAAAGTTGAGGAACGAAACCTATTTCCATGTTGACCGGAATAGATTTA  
45 387801 CGTTTTTTTCTTTGGAAAACCTTTGTTGTTTTCAAGTAAAGAAAAACC  
387851 TAAACGTCTTGATCGTTTGAAAATACTACCAGTATATTTATGTGTTTTT  
387901 GATTTTAAATTATCTTAATAATCAAGGCTAAAATCACCCTGCTTTCAA  
387951 TAAGTCTTCATCTAATAATGAACTGAAATTGGAAGTACGATCAGGAATA  
50 388001 GTGTTTCTATATCCAAATCATTAACACTAAAAGCACTCATTGAATCCATT  
388051 ACTTTGGCATCAATGTCAACAAAATCATTGTTAAACCTTCAAATTCAAA

5

10

15

20

25

30

35

40

45

50

55

388101 ATCGATGTTACGATCCATGTTTTTCATAGATAAAATCATCTAACTGTTTCAT  
388151 TGGAGATGTTATCAAAAGTGTGGAAAAATCTATTAAATCATCCATTAAC  
388201 TGATTAGGTTCTACTAACCATTATCTGTTACACTATCAAAATTGCTTAA  
388251 AAGTAAAGGATCTTTTTCTTTCTTTGCAAAGCGGAGCGTATTATCAAGCT  
388301 TATTAATGTTGTTTCATAATAGTTTCACAACAAGAGTTATAAACAGTTTTTA  
388351 AGTTGTTTTAACTACCTTGAATGCTTTCTATCTTTCTTTTCATTTTCAGT  
388401 GATAGCACGTTGAACATGACGCATAATTTCTCCAGATTTTTGCAGTTGTT  
388451 CATACTATTACTTGGTTTTGTAAGCAATAGCAAAATCACTAGCTAATGAT  
388501 CTGATCATTTCTTCTTTTTGAAGTGTGTAGATTCTTAGCGTTATTAAA  
388551 TTGAACGTTAAGGTTCTCATTTTGATCAATTAAACGGGAAAGTTCACTTT  
388601 GTAATTCCTTTTAAATTATTAAGTAACGtTCACTAATTTGGTTCTTATAG  
388651 TTGGTAACAAAATCATTGAGATGGATAAATGATTGTTTAACAGACATCTG  
388701 ATAATCATTCAATTTGAAAGATTGCATCAAAGTTAATTGTAGGGTTTAATT  
388751 CACCACGTTTCAATTCACTAATAATCTTGTAAGATCTGATTTTTTTATTG  
388801 AAATTATCAAGTTCACTTTTATCTTCAACCGATTGCTTATTTTGAGTAAT  
388851 TGAGTGTCTTCAACAGGTTCTTTTGCTTTGACAAAACTTCAATTTTAG  
388901 GTTGTTGGTCTTCGCTATTAACAGTATTGATAGTTAGTTGATCATCTTTT  
388951 TTATCGAGTCTTACTGATTCACTAGTAACAATTGATTGATTATTTAAGCT  
389001 ATTAATTTGTTGCAATTGGACAGATAATGTTTTTGCAAGTGTGTTGGAAT  
389051 CTTCAAGTTATGGAATTAATGGTAATTTGTTCTTGCTGACTTTCTTTATTA  
389101 TCTAAAGCTAAAGTTTCAACTGGTTTATATTCAATACGGTTGGATACAAA  
389151 ACTAATAGGTAAAGTTGTAGGGATTTGGGGTGAACTTTTTTTGGTAGTGA  
389201 TAGTTATCTTATTATCAGACTGAATATCAAATTTCTGTAAATTATTAGTG  
389251 TAGTTACTAGTTTCAACTACATCTTGTTTATTGAAACTACTTTCTAAAAC  
389301 TGGCTCCTTAGTTATTTTCAAGTTTGAATTGATCGTTAACTTCGCTATTTA  
389351 CTTGATCAAACTGCTCAACTGTTGGTTGAGTTTCAAATGAAGAAGAAAAA  
389401 GTTGTTTGGTCTTGTTGATCTGTATCAATTGGTAATTGGTAACATCAAC  
389451 TACTTGGGCTTGTTTACTTTCAAATCAGTAGTTACTTCTTTTTTCAGCAG  
389501 TTGGTTGTATTTCTCATTATTATCAAGATTAGCTTGAACCTTGATCAAAT  
389551 CCAACTGATAATTATTTTGTCTTTCAGCAACTGGTTTGAGCTCTTCATG  
389601 GTGATCAAAGTTGTACTGAACATGATCATCTAAAGAAGGTTGGTCAAGGG  
389651 TTGGTTGAGGTAAATCACTGTCAAAGCTGTAGCTATCAGTTGTTGATTCA  
389701 GGTGTTTTTGCAAATGATCATCTGAAGAAGGCTGGTCAACAACTGATTC  
389751 AGGTTGTTTTACTTCTGGTGGTAGGTCGTTATCAAAACCATAGTTTTTCAT  
389801 CAGTTGGTTGTTTTGCAAATAATCATCTGAAGAAGGCTGGTCAAGAGTT  
389851 GGTTTTAGCTCTTCATTTTGATAAATGTCGTATTGAACCTTGATCAACTGG

389901 TTCAGATTGACTTTCAAAGTGTGCATCAGGTGCAGtTTCACTATTAACT  
389951 TAACAGGTTTCAGACTCTAACGAATTATTGCTGTTTGATTGAGATAAATCA  
5 390001 CTCCCAAATTTATAGTCATGAATTGGTTCAGATTTACTTTCATAATGCAC  
390051 ATCATCAGATGCAGTTTCACTATTACTATTAAGTTGAATGAATTCAGAAT  
390101 TTAATGAATCATTGTTAGTTGCATCTTTGTTGTTTTTCAGAGTAAAGATTA  
10 390151 GATTGAGAATTTAAGTCACTAGTTTCAACTACATCTTGTTTATTGAACT  
390201 ACTTCTAAAACTGGCTCCTTAGTTATTTTCAGGTTTGAATTGATCGTTAA  
390251 CTTGCTATTTACTTGATCAAACCTGCTCAACTGTTGGTTGAGTTTCAAAT  
390301 GAAGAAGAAAAAGTTGTTTGGTCTTGTTGATCTGTATCAATTGGTAATTG  
15 390351 GTAACATCAACTACTTGGGCTTGTTTACTTTCAAATCAGTAGTTACTT  
390401 TTTTTTCAGCAGTTGGTTGTATTTCTCATTATTATCAAGATTAGCTTGA  
390451 ACTTGATCAAATCCAACCTGATAATTATTTTGTCTTCAGCAACTGGTTT  
390501 GAGCTCTTCATGGTGATCAAAGTTGTACTGAACATGATCATCTAAAGAAG  
20 390551 GTTGGTCAAGGGTTGGTTGAGGTAAATCACTGTCAAAGCTGTAGCTATCA  
390601 GTTGTGATTTCAGGTTGTTTTGCAAATGATCATCTGAAGAAGGTTGGTC  
390651 AACAACTGATTTCAGGTTGTTTTACTTCTGGTGGTAGGTCGTTATCAAAAC  
25 390701 CATAGTTTTTCATCAGTTGGTTGTTTTGCAAAATAATCATCTGAAGAAGGC  
390751 TGGTCAACAACTGATTTCAGGTTGTTTTACTTCTGGTGGTAGGTCGTTATC  
390801 AAAACCATAGTTATCTTCAACTGATTTCAGGTTGTTTTACTTCTGGTGGTA  
390851 AATCGTTATCAAAACCATAGTTATCTTCAACTGATTTCAGGTTGTTTTACT  
30 390901 TCTGGTGGTAAATCACTGTCAAAACCATAGTTTTTCATCAGTTGGTTGAGA  
390951 TTCTTTAGTGGAGATCCACTGGTCATTTTCAAAGTAACCAGATCAAACCC  
391001 ACTCACCATTTTCATCATAAGAACCATAGTCAGGGTTACCAACATACTTT  
35 391051 AAATAATCATTTCTCTTCTGCTTTTCATCAAAAACAAACGGATTCCCATT  
391101 TTCATCAAAGAGTTGGGAGATATCATATTTCAGTATCTCCATAAGGATCAT  
391151 AGTAAACCCCTGTTTCTTTGTTAAAGCTATATAATAGCCATTACCATCA  
391201 GCATCATATGCTACCTTAATATTAGGGTCTTCTTCAACAGTGGATTTACC  
40 391251 ATCATAAAGATCACCAAAAATGTTTTTCAGGTTTCGGTTTGGGTATAGTTTT  
391301 TTTCTTCAAAAACCGATTGCTTGTTTTTAGCCATCAAGAAAAGTTATTTA  
391351 TGCCAGTTTAGTCAAGCTTGATTATAAACTTATCGCTTCGCTCTAACTC  
45 391401 TTCCATGAAAGCGTAAATAGTAATAAATAATTTTTTAAATTATTTTCCAC  
391451 AATCCCTATTAAAGGGTAAACAAAGCTACATAGATAGGTAATAATAACG  
391501 CTGCAACCAATACTCTTGGTAAAAGAAAGAAATAAACCCCATACAAAACA  
391551 AAGTTATTACTTGGTCTGCCATTATTAATAAAAGTAATAAACTCAATGGC  
50 391601 AGCAATTGTCCCCAAAAGGATAGAAACAACTACTGACATTAAACCATTA  
391651 GAACCAAGCTATAAATAGTTAAAGTGCTTGTTCTTTATTTCTCTTTTTT

391701 ACATAAAACAAACCCTAAAAATCCTTCTGTTACTAAAAAGAAAAATAACAAA  
391751 GCTAACTAAAGTTATGATTTGTAAAACAACAACATTAACACTAAGATCAG  
391801 CAGTTTGAAAATTTTTTGTTCGAATTTGCTGAAACTCATTATTAGTTAGA  
391851 TAAAGTAAAAGCAGTGTACACTAACACAAAAAAAGTTACTAATAGTGT  
391901 TTGTAACACCCAAAAATCAACCTTGTAATTACTGGCATTTTTTCTAACTA  
391951 GATAAATCCCTTTAACTATGCCAGCAAGaAAAAGCAAAGAGTGGCTTTTGC  
392001 AATGCAAACATCCAAAACCACACATAACCCTTTGTTAACCAATCAATAGT  
392051 ATCAGATAAAAATCCAAAAATAAAACCCCAAATAGGACCAAAGATCCATC  
392101 CGAACAAATGCAAAGGGAATCCTTAGAAAATAATGCTTAATACATTAGTA  
392151 AACTAATTGAAAAGATAGAAAAGATAAAGGTTAGTGCTAATAAAACACT  
392201 AGCTCAAACCTAACAGTTGTAAACTCTTTAAAAGTCTCAACGGATAGTAAG  
392251 GAAACAAAAAGTTTCAAAACAGTTTTTTAGATTGAAGCTTGAATGTGAAT  
392301 TTTAACCAAAAATAGTAGGTGGGGGGATATCTAAAGTAGTTTTACTTTCA  
392351 TCACTAGTAATTGGTTTTTGCCAATTCCTCTTGAAAGTACTTATTAAATAT  
392401 CTCATTAGTTTGTCTAAGTTTAATTTAGGACTTAATGAAAAAGCAATTA  
392451 CACTAATGATGCTAAAAGGAACAATGCTAAAAACAAACAATCAGGCGATT  
392501 CCTATCAGATAACTTGCAAATAATGGTGAAACACTAATTAGTTGGTTTTTC  
392551 ACTAAATAAGCGGATGATTAAAGCTGCATTTCAAAGCCACTTCTTACTA  
392601 TATTACCAGGGATACAATTTAAAAAGACAAAGATAAAGATAGTCCAAAAG  
392651 ATCCATTTTATTCTTACCTTATAACGGTAGTTATCATTAATTTTGGGAAA  
392701 CTCCTTGACCCCAAATTCACTACGTAAATACCGCATTGCTCTATTGGTTT  
392751 GACCTCTAGTTGCAAAGCTATAGGGTTTACCCTGAAAAGCAAAGAAAAAA  
392801 GAAGCACCACCAAAGCCAGGAAGATCATGGTAATCAAGTTAGATGAACT  
392851 TAAAGCAAAAAGCGGTTTAGATTTGTGTATCTGCATTACTTTGCTGAA  
392901 CAGTATTTTGGTCAATTATTAACATTGAAAAGTGGACTGTTCTTATCAACA  
392951 AAGTGGGTAAAAAGACATTGACCATCACAACGTATGCTATCGAAATGAA  
393001 AAAGATGGCAATCATAGAGATGAAAATCGCTAGTTGTGCTCATTTAATCC  
393051 ACTGACTCTTAACTGAAACTCAAAGATCTTACCAACTAGTTTTTCAGAG  
393101 GTAAACCTACCAAAGGCACGATCTCTGGCACGAACTTGAGGGGTTTGTG  
393151 CAAAATATTATTCTCAAGTCCTGAGTTTAGCTGTTGAGAATTGTTTATAG  
393201 TTTGAAAACCTGGGTTATCTTTAACTGTTTTATTGTTTTCTTGTAECTA  
393251 CTAACGGGTTTAACTTGAGTTTCAGCAAGTTTGGTAAAGCTATTCAACTC  
393301 TTTATTAAACAAGTTTTTAACAGCAACATTAAGATAATTAGCTAAATCTA  
393351 ACGCATCAGTTAGATCAAACCTTAGCAGCTTTAAGTTCTTTTTCACTTAAT  
393401 TGGTTTTGCCCTAATTGGATAAACTTATCATGAAAACCTACCAAAAAGAAA  
393451 GTGGTCTGGTTTTTTTTGTTTTAACTCTTTTTTGTTCCTCTAAAAAAT

393501 AAAGTAATTTGAGTTGTGCCAAAATTGTTTTGGCAAAATCACTATCAGTT  
393551 TTTATCCTTGTTCTTAAAGTTTCGTTATTA AAAACAATGTCAAGATTATT  
5 393601 TTGTACCTTAGTTAGAATTTCACTAAACGTCATTTTGATAAGTAATTTTA  
393651 GAGAGGTTAGTTAGTAAAAAGCTTAAAGCAAAGTTTTTTAACAACGGAA  
393701 TGGCAAAGCCATCATTTGTGCTTTAATTTAATATCCAATTTTTGAATTGCA  
10 393751 TTAATTATATTTACTAAAACTTTGCTAGTAAAGTTATGGTACTGACTTTG  
393801 AATAGCAATTAAGCGAACTGATTAACATTTAGATTAATGTTAGTTAGTT  
393851 GCTTTGGATTACAACTTTAAACCATCAATGCTAATAACAACCTCCCCACTA  
393901 AAAAATTTCTAAAAATTGGGTGGCAAAATTGGTTTTGTACTTGCCAATTC  
15 393951 ATCAATATATTTAAATGCCTTTACAATTTGTGAATTTGTTAGAGCTTTGG  
394001 TTAATTTGTAAATTTGAACAGGTTGATAATCACAAATAACTGTTTCAACT  
394051 AATTTGTTATCTTTGATTTTCATTTTTACCTAACAAGCTAAGTTTGTTAAT  
20 394101 TTCTTGGTAAATTACCCCATATTTAAAGGTAAAGCATTGCTAATCAAT  
394151 CAATTATTTCCAAATCAAGTTTTAAGTTAAGTTCTCTACAACTTCACCA  
394201 ATTGCTTTATGCATTGATTTTCAATCCAATTTATCACAAAAACAGTTGT  
394251 GATTGATTTAATGGTTTTAATCCCACTAAAAGGATTGTCAGTATAAACAG  
25 394301 TTAAACTACATCAGTTGTTTTTAGTTTTCTAAACACAAGTTTTCTTGT  
394351 CTAGTTAAGCTTGTTTTTTCCAAAAACTGCAATTATTGACAATAAACTT  
394401 TTCATTATTAGAACCAATAATGGTTGTGAAAAGAGATCATAAAGTTGCT  
394451 TAAGATCTTTAAACCAATAGTTTTATATGGAGAATTGCTTTTGATTTGA  
30 394501 CTTAATTTTTGGTGAATTAGCCCAATATCTTGACCATAAATTATTGTCAT  
394551 AATAAGCTACTGTAAAAATAGTATATAAAAGTCCCAATAAGCCATAATAA  
394601 ACAAAAAAGAAAATCAGATTAGGTTTAGGTATTTGTAGAAAACTGTTAC  
35 394651 TTTTAATGATCATTCACTTAGCATTTTAAGTGGGAGATAAATACCAAAAC  
394701 TAGCTTGACCAAAAACACCAATAAAGGGTAAAATAATTCACTAACACAA  
394751 AAATAAAATAAGGCAATTGGGCTAAACAAAAGGTTAAACAAGACACTAAA  
394801 AGCATTTAGTCTTGAATTTAAATACAAGCTTAAGGGGCTGATAACAATCA  
40 394851 AGATTAACTAGAACTGACAAGCGGTTTTAAAGCTTTTAATACTTTAGT  
394901 TTGTTGACAAATAACAATACAAAACAAGCTAGAAAAGAAAAATTAAAAAC  
394951 AAAGTTATTTAAAGCATGGTTACTAATAAGAATGATTAAGTGCAGTTA  
45 395001 AACTTAAGTTATCTTCTGGTAACTGTTTTTTAAAAACCTGTTTTAACAGT  
395051 GTTGAGATAAAAACTCTTAGTGCTGAAAAGGCAAATCCTACTAAAAACAG  
395101 GTAAATCAATAAAACAGCAAAACCACTAAGTTTGTTTAAGTACCATCTTT  
395151 TTCATAAAAACCGTTCCATTAAATTAAACAAGAACTTAAGTGAAAACCA  
50 395201 CTGATAACAAACAAATGGACAATGTTTAGTTTTAAAGCATTTTGGTACAA  
395251 ATTGTTTTTAGTGGTTTCATTAATTAAAAATAGTTTTAAATACTGATTTA



395301 ACTCACCTTTAGTGGTCTGATCAATTCAATTAATGAAAGGGGTACGAATA  
395351 AAGTTATTTTAAACAATTGATTTATCTTGACTGCTGGAACAAAATAACA  
395401 AAAAGCAATAAAAAAACCAACAATTGTTAAGTTCAATAAACAAAACTTTC  
395451 AGTCATACCAAAGACTAAAAAGCGTTATCAAAATGATCCAAATTGACAGT  
395501 GCAACAAACTGTTCTTGTGTACTAAAAAGAAGCCTGGGATAAAACTGAG  
395551 TAAACAAAAAAATAAAACAGCTTTGTTTGCATGCTGTTTTATTAATAGA  
395601 TTTATTTTGAACTTTTTAAACAAATTAAAAGT CCTTAGATCAATATGATCT  
395651 TGATGGATAACGTCTAAGTCCATCATAGCTAGAACTAAATGGTAAACTAG  
395701 TTCTTCTAAAACTTGATAGTCTTGTGGTGAATGGAATGATGAACGGTAT  
395751 GAACTGATATTAGTTAATCTTCATGGTCTTCTTGTTAAGGGATAATAACT  
395801 ACTTGGTGTCTGCTAAAACGATAGTTAGAAATAGCATTATTTTGGAAT  
395851 TAGTTGATCTTAATGGTGTGTAATTGTTGACTCTAGATTTTGGTGTGTAG  
395901 TCAAAATCAAGAGAAAAACGATCACTAGTTAAACTTTGATTGGTATCGCT  
395951 GTAAAGTGGATCACTGTATTTAGTTGCAACATACTCATTTTCAGGATAAA  
396001 AACGGCTGAAATTGCTACTTTTTATAGTGTATCACTCTTTAGAGCAATA  
396051 TCACTCATTATCCTTTGGTGGTTTAAAGCATTAAATTTCTCTAGAAGAGA  
396101 AGCGTGGGAAGAGACACTAACAGTGATATCTGAATCAGTTGTGCGTTCAA  
396151 CTTGTCTAGGTTGAAAACAGTGTCTAATTTTGATTGAAGTAAAGCTGCT  
396201 GATCTTGGTACAACTTTAATTTGTAAACCTGAAGTTGGCAATGGTTGTTG  
396251 GGGTTGATATTCAGTTTTTACTTCTGGTTTTTCAGTGGTGAACCTCAACTT  
396301 GAGGAGTTGATTCTACTTGAGGGATGTATTTGTTTCAGGTTTGGTTCA  
396351 ATTCTTGGTTCAACCATTGAGCTTTCGGTTGAACTTCAACTTGAGGAAT  
396401 ATGTTTTATTACTTCTGGTTTTGATTCAATTCTTGGTTCAATCCTTTGAG  
396451 GTTTTAAATCAACAACAGGTTTTGGTTGAACTTCAACATGTGGTACATGT  
396501 TTTACTTCAGGTTGTTTAACTTCTGGTACTGAATCAACAACAGGTTTCAC  
396551 TTCTGGTTTTGGTTGAATTTCAACATGTGATACATGTTTCACTTCTGGTT  
396601 TTGGTTCAATTTTGGGTTCAACTATTTGAGGTTTCGGTTGAACTTCAACT  
396651 TGAGGAATATGTTTTACTTCAGGTTGAACTAACTTTGCTGGTTTATTAAC  
396701 TAGTGGTGGTTTTAAAGAAGGGGAATTATTAAACTATGGTTTTGAGATC  
396751 CACTATCAACTTGAACGGGTTGTTGGTGGACTAAATCCTGATGGAGCTGT  
396801 TGAGTAGGTGGCACTTCTTTTTCAACAACTGGTCATCACCCAAGTTTTTC  
396851 TGTAGGTTGTTGGGTTGATTTAACTGTCATTTAATTCAAAGACATCAG  
396901 GTTCACTTTCAGTTTCTAGAGTAGTGTGTGAGCTGCTTTTGGTTGGTCA  
396951 TCAACTTCTATCTTAGGAAGACCTGCATCAATACTAGGATAATCTTGTTG  
397001 GGTGGTTGTTCTTGAGAAGTTTGAGTACTGCTTAAATAGTTAATTAAAG  
397051 GGACCTTTTTCTCATCAGTATAGCTAGAAACATCCAAACATTACCATT

397101 TGGTCATAGAAAGTGTGTTATCCTGATCATATTGAACAGTTACCAAGTT  
397151 GTTCTTATCATCATAAGCATTTAAGCTAACAATGTTATTTGTAAAGCTAA  
5 397201 TAGGGTTATCTGAAGTTAATTCAAACAAAGGATAGTTACTAGCTAACTGC  
397251 TTTCTTTTTTCTAAAGAGAAGATATTACCTGATTCAGGATCTTGGTATAG  
397301 AGCATGAACCTTATTTTTATGATCACGGGCATAAACAACACTAACATCAG  
10 397351 GATATCTTTTGTTAATCTTTTTTAAAAGCTTGTTATAGGCTTTGTTTATT  
397401 TTAGCTTTCTGTTTATCGTTCATAAAAAATTACTAAATTAGGGTTTAAA  
397451 CCGCCTTTTGGCATCAATTGTGATGGGTTAGGACGTTGTTGCATATTTGG  
397501 ATTAAACCCAGGGCGTTGTTGCATGTTTGGATTAAAGTTATTTGGTTGTG  
15 397551 CAAATTGGTTAGGATGGGGTTGGTTAAATCCAGGGCGTTGCATGTTTGGG  
397601 TTCATCCTTGGGTTGAAATTATTGTGTGGTTGGAAGTGTGTTTGGTTG  
397651 GTTAAACCCAGGGCGTTGTTGCATGTTTGGATTAAACCCAGGGCGCTGCA  
20 397701 TGTTTGGGTTTCATCCTTGGGTTGAAATTATTGTGTGGTTGGAAGTGTG  
397751 TTTGGTTGGTTAAAACCCAGGGCGTTGTTGCATGTTTGGATTAAATGCAGG  
397801 TCTTAAAGCGGAACACGCTGTTGAACTGTGGTTGAAGGGGTTGTTGAA  
397851 CTTGGGGTTGGGAAGGCTGAGCTTGGGATTGTTGAGGATCAATTTCAACT  
25 397901 GTTTGTGTTCTTGTGATCTGAGATTCTTTGTAATTGCTCAGCAATCTG  
397951 TTCTTGGCGTTCTTCTCTTCAAGTAAACGTTTTTCTTTGCGCTTTACAA  
398001 TAGGTAAACCTATCGCAAGTCCAAGGATAATAGCTAAAGCACTAAAACCA  
30 398051 AATGAACCTGCTACTGTAGGGATAAATCAGGGCTGTTCAACAATTGATCT  
398101 GCCCTGAATTACAGTTGTATTATCTTCTGTTTGATGAAAAACAACCCCTA  
398151 GTTCACTACCATTAGTTTTCACAACAAGTGCAAATGCTAGTAACGATAAA  
398201 CTAACAATTAGGATTGTTGTAAAAAGTAAAGCAAGAACTATAAAAAGTTT  
35 398251 TTTGTATCTCAAAAATCCATTTAACTCCATCTTTATCAAACTTAATTAG  
398301 TTCCTTTTTCTTCTTGATCTTGAATCATCATAATACTCTTCTTGTTCTTG  
398351 CTTTTTCATGTTCTTTTTCTTCTTTTAATTGAACGAGTGATTTTATTGA  
398401 GAAAGAAGTTAACAATTAAAGTACCTATTAAACCACTAACAATGCCATT  
40 398451 CCTAGGGGAATTACATACTTAGTTAGATAAGGTGTAACTGTTCAACAAA  
398501 TCCAGGCAACTTAGCATTTTTCAAAAATCTACATATCCTGGGATAGCAT  
398551 AAAATGCACTTTTTTTCAGTTGGAAAACGGTTATCCAAACCATTACTTGAA  
45 398601 CCTTCTAAAAGTTGTAATAAGCTACTTGTTTGAGCAGTTGCAGTTGCACC  
398651 ATTGTTTGAAGAGATGTTATCCAACGCTTCTTTTGAAAAGAACCTGTTGA  
398701 AAACATCCATTGGTTGTGCTAACTCAAATGGGTTTAGAGAACCAAAGTAA  
398751 AAGATAGCTAAGAAAAGATAAGCAAAGCCTACCAATACCAATAAAAGAAA  
50 398801 GCAAAGCTTAAAGAGAAATCGAAACAAGCGCATTTGTATTAGTCAAAAAT  
398851 AAAACTACTCTGTGAATTTAACTTTATTTAGTTAAGCAAATGGTTTATG

398901 TAATTAATTAAATTAAGTATAGAGCTTTAGAAAGCTCTAAACTCTAGAAA  
398951 AATTTTTAGTAATTAGGATGATTCTTAGGATGAAATAGACCAAATTCATG  
399001 AAGCTGCTAATTAATCAAGCCCCAAAGAATAAAGCAGATCTTCAGCTCTG  
399051 TCTTCTTGCCATTTTATAATCTTCACCTTCATAGTATTTAATCAAATCTT  
399101 GTTCATTACGGATCTGTAAACTCACAAAATAAACTGAAATTAATGAAAAG  
399151 ATTCCCCCTACTATTAAAGATAAGCCAGGGATAATTCTATCAAGTAGGTT  
399201 TGTGTAGAGAAGCAAACACTGTAAAGTTCAAAATAAAGCTCAATAAGCTCG  
399251 CTACAATACTAATTACAAAAGCCCATAATAAGATGTGAACAAAGTTTGG  
399301 GTTTGTTGATATCGCCTTTTTTGACTTGGTAGCGCACTTAATCCTCACAC  
399351 TGAACCAAACACCAAAGTAGCACCTAAAAAGCATAAACAATGTCATTAG  
399401 CTTCAAAGTTAACTTGTGTTTGAAGATGTCGTTGCTAAAGTTAATAAGATC  
399451 CCAAGGGTTATCCCATAACTAATCACATCAGTAATGATTAAGGCCCAAAA  
399501 CCATGTCAAAGTAGTGTGGGATTCCTTAATTTAAAGCAGTAACAAAAT  
399551 AAAGAATTAAAGAGACAAAAGTAGTAATAACTGCAATAGTACTAAGTGTT  
399601 CTAAAATCACTAGCTAAATCAATTAGTGTGCTTCTTGAAAGCAATTGTTG  
399651 TACTGTTAATGCAACAAGAAAGATAAAAAAGATCCCAAAGCAGCTACCA  
399701 TAAAAGTTAAACGGATTACAGAAAGCTGTTTTGTTGTACAAAGCTTTT  
399751 GCTGCTAAACCGTTTTGATCAATATAGCCTTTTGTTGAATTAATCATGAC  
399801 AATTTGACTTGTTAAATTTTAATTTGTCAATATAAAAAACTAATAATTG  
399851 CAAAATATATAGATAAGGATACTTACCCAAGTGGCTGAAGGGGTAGGCTT  
399901 GGAAAGCTTATAGATGGGTAAAACCATGCGAGGGTTCGAATCCCTCAGTA  
399951 TCCGCCAGGGAGATTTACCCAAGTGGCTGAAGGGGGCGCTCTCGAAAAGC  
400001 GTTAGGTGGTTATCCACGCGTGGGTCAAATCCACAATCTCCGCCAAAT  
400051 TCTTAAGTGTATAAACAAAAACACACCATTTTGGTGTGTTTTTTATGT  
400101 CCATAAGTTAGTTGAATTTACTCATCAATGTAACCTGAATCACGCATTGT  
400151 AGCAATCCCTGAAGGGGCATTACGGAGTGAAAATCATGGTTTTAAAGCG  
400201 AAGGAATAGTTTCATTTAACCAGGAGCGGAGACTGGTAGAACAGGAAAG  
400251 TAACTATCTACTACAGTAATTAAGAACTTAGCATTATCAGTGTCTGTTC  
400301 AGCTCAAATGCTGTTAAATCGGTTAAGTTGAGCAGCGTTGTCATAAAGAT  
400351 CTTTCAATTCATAACCAATGTGGATATCTGATACATTTGCTGGTTTGTG  
400401 TCATCTATCTTGCTTCTTTTTGATAGATATTTATCAGGATCTTTAATTGC  
400451 TTCTTTAACTTTATCAGCTTTCAATACCTTATTATCAACTAAAAATTTCA  
400501 GTAAGCTTAATGCTTTTGTAGTGAATGCTAATGAAGCGGATGTACCGTTA  
400551 TTACCATTAGTACCAAAGTTCTTAATGACATAGGGATCATCTTTAAAAAG  
400601 ATCAGCACTTGTTATGCAACTACACCAGTCTTTTCCGTTAGTTGTTGTG  
400651 TATTTGAAGTTTATTTTCAATTTGATTAAAGACATTGTTTGGGATGCA

400701 GCTAACAATAAAGTTCTGACAATATGACTACCTGAATTGTAAGTAATTAC  
400751 TTCACCAATACCCTCACTGTTAAGCTGTGTAGCAGCATCAAGTCAGGTAC  
5 400801 CAACCCCATCATAATCAGGACTCCAATAAGAAAAACCAAGTACACTTGAT  
400851 AAACCTATGTATCATTCGTTTCTTGTTGGACCTTGTGCATCTCCTAAGAT  
400901 AATCTCAGGGATAATTAAATTTTCACCATTATCATTACCAAGTTCAGTTA  
10 400951 AAGCTTGTTTTAAAGCGTTATAGTAATCAACTTGGTTAGAGGAGAGTGAT  
401001 GCATTTCTAGTTTAAATGTTGAAGTGTAAATGGATTGTTACCAGTAAACCC  
401051 AACTTTTTTTAATGCACTGATAAACTTTGCTTGGTAACACTTACTTGTT  
401101 TTGAAGAACTTGACTAGTTTGACTACTGCTGCCACTAGTAGAAGCTGTT  
15 401151 CTTACTTGAGCACCATTAGTTTTTGTAGAGCTATAGTAACTTAACTTAAC  
401201 AGTTGCAGTATCAAGAACATTCTTATCCTTTTGAAAAGTTCAGTTTGT  
401251 CAGGGATTAAACCAAGTCTTGGTTGTTGTTAATCTTGTAAATAATAATCA  
401301 TTCTCAATTCCATCTGTATTTGTACCACTACTAGTTCATTGCTGGTTT  
20 401351 TTCTTTAAAGATCCCAAAGGAACAGTAGAATAGTTAACATCTCCTGAGT  
401401 TGGGCAGATCAATGATTGCTAAGTTCTTTCAGTTGATCAAACCATTAAAT  
401451 CCAGCACGGATAGTCAACGCTTCTTCAGATTCACTGTTATATAAGAACTT  
25 401501 AGCTTCTGTCTCAGTGATGTTTGCAATTTAGTTGAACAGTACTGTCATTAG  
401551 CAACATAAGGTTTACCTGAATAAGTTACTTGAGCACTTTGCGCAGTTTTT  
401601 TGGATTTTTAATCACCTCAGATCCCCTGTACCATTAAACCTTGATCTTGC  
401651 ATCTTGTTGTTGGGAATAGGGAACAGCTGAAGCTGATAAGCCCCCAGCGA  
30 401701 TATACTAGAATAGAACACTTCAGGAGTAGCTCCTGGTTGGAAATAACTA  
401751 ACTATAGCAGGGATAGGTTTTTCGTTTTCTGTCTTGTGTTTAGGAAGATT  
401801 AGGGGTGATAATTGCATCATAAATCTGGTTGCGTTTAAAGACAATTTGTG  
35 401851 CTTGGTTAAACTCTCAACATAGTAAGGGCCAACTGATCAAGTGTCTTTT  
401901 CAAGCATTAACCCCCCTCCATAGATACCATCAAAGTTAGTATTTGCTTG  
401951 ATCTAAAATCTTCTGTTGTTATTTTGGTTATATTTAAGCGGTGAATCTT  
402001 TACCTAGTTTAAAGGGCTTTTACCTTAGGATGGGTGTGAGGAATTGGAAAG  
40 402051 AAGAATTCCTTTGACATCATTGATAGAAAGAAAGGAAAAGGAGAAGTTAG  
402101 ATAAACATTAAACTTGTTATCATCTACACTTCTATAGTTTTCAACATCAT  
402151 AATTTTCATCAGTGATCTCAATACCTTTACCATGCCATCACTAGAACCG  
45 402201 TTGGTTTTATCCATACCAACGGTTTTTTCAACATCAAGACCCATTAGGTC  
402251 AATGAAATAACCATTCCGGTTAAACCTAAGTTAGAAGAGAGAATATAGG  
402301 TCTCAAAACCCCTTTCAAAGTCTTTAGAGGAGAGTTTAACTGGTTGGTTG  
402351 TTTTGTGTTGACTTCTCTACCAGCATTATCAACCCAGCTCAAACCTAGTGTT  
50 402401 AATGGTAAATTCATATCTGGTTGCTTCTTGGGTATCTTGTGATAGTTAG  
402451 GATCTTCAGTAATAGACTTTGAACTATCACGATAAATTGTGCCTATTGCA

402501 TCCCACTCATTGAACTTAGTGTAATCATTCTTACTAGATCCATCAGAAGA  
402551 ATCTGTTGAACCGTTTTTTTTGTGCTCTACCTTTAAGGCCACTGTGTGTTG  
5 402601 TCTTTTTATAGCCAGTAACCTGATAAAGCAAGTTCTAACACTAATTTTTCT  
402651 TTAATTTGGTCAGTAACATTAACCCCATCATCACGGTTTGTACCAGTAGC  
402701 AACATAGTTAGTTAACCTGCATAAGCATTACCAAAAAAGATGAAGTGG  
10 402751 GTGAAACGTTAAACATGCTCAATGGAACAGAGTTGTTCTTTAACAAATCT  
402801 GCTGAAGAAGAGGTGAAAAACACCCCTTTGTTTAACTGTGAGGATGCACA  
402851 AGCACTTAGGATTAGTGCTGCACTAACTGTCAGTGTAGAACCAGCAACA  
402901 AGTATCTTTTTTTTAAATTCATTGTGTCTTTTCATAAATAAATCGGTAA  
15 402951 TTGATTGCTGATTAGTAAAAAGAGTTAAAAACAGCAATTTACCCTTAG  
403001 TTA AAAA ACTAAAAGTAGTTTTATTCTAGTTTGCAATCACATTAGATTGCA  
403051 AAATCAAAA ACTAATGTTTTTATCAATTGCTCACTTTTTTAAACAAGAAAA  
20 403101 TGCTTAATACAAAGTTAGCAAACTAAAAACATGGTGCACCCGAAGGGAC  
403151 TTGAACCCCACTTCTAGATGAACTAGATCCTAAGTCTAGCGCGTCTAC  
403201 CATTCGCCACGAGTGCATTATTGGTGCATCTTGAGGGGATCGAACCAC  
403251 GACCCAATGATTAAGAGTCATTTGCTCTACCAACTGAGCTAAAGATGCAG  
25 403301 ATAGTGGTGCCGACTATAGGATTTGAACCTACGACCTATTGATTACAAGT  
403351 CAATTGCTCTACCAACTGAGCTAAGTCGGCATGGTGGATTGTGAGGGGAT  
403401 CGAACCCCACTTATGCTTGTAAGGCATATGCTCTCCAGCTGAGCTA  
403451 ACAATCCATCACTTATGGTGCCGAATACAGGAATTGAACCTGTAGCCTAT  
30 403501 GCATTACGAGTGCATCGCTCTGCCCTTGAGCTAATTCGGCATTGGTGACG  
403551 CGTACGGGATTCAAACCCGTGAATGCACGCGTGAAAGGCGTGTGTGTTAA  
403601 GTCTCTTCACCAACGCGCCAAATAATGGCGGCCACAACAGGGATCGAACC  
35 403651 TGTGACCAACCGGTTAACAGCCGGTTGCTCTACCGCTGAGCTATGTGGCC  
403701 TGAGAATAAATTCTAGAATTTCTAGCCAATTTTAAACAGCTTCCTTAGGAT  
403751 ATGAATAACTATTTGCTTTGGGATGTTTTCTAACAAAAGTTAGCACAGAA  
403801 CTGGACACACCAACCTGTCCCATACCATTAATAGACATAAAGCAAGGAA  
40 403851 ATTAAAGGTATTTCTATTTGGATCTAAAGCAATGTTAACAGTAGCTCCAC  
403901 TTGAAAGTCCAACCTGTTCCAAAAGCACTAGTTGTTTCAAATAAAGCATCA  
403951 ATGAAACTAACTGGTTGTTCCATACTTAAAGGTAGAAGAACAGCTGTTAG  
45 404001 TAAAACTGCAATTAAGCTTATGATTAGTACTAAAAAGCATCTATTACTG  
404051 TAGTTTGATCGATTGAACGCTTAAATGCTTTTACTTCCTTTTGACCTTTA  
404101 AACTTAGCAACTAGAGCTAAAAAGATTACTGCTAGCGTAGTTGTTCTAAT  
404151 CCCCCAGCAGTAGAAGAGGGACTAGCACCAATAAACATTGCCAATGCAA  
50 404201 TAATTATTTTTGTAGTTTGAATCTCACTAGCAACAGGGAAAACTAAAA  
404251 CCTGCTGAACGGGATGAAATAACCATAAAAAAGAGCTGCATTACCCTACT

404301 TGCATTAGGGTTATTACCAAAAACCTGACGCATGGATTGCTTGGTTAGATT  
404351 GTGATTGCAATTGGGTATTTATTAACTCTTTTTTTCATCACTAAAATTA  
5 404401 ACAATAGTGTTAGTTAACTATCACTAGCAATAAATTCCACCATTAAAAG  
404451 TAAGGTGAAAAAAGCAGGATTACAACGATATTAGTAATTACTGTCAACT  
404501 TGGTAAATAGACTAAATTGGTGTTTTGTGTGTCTACCATACTTAATCTTT  
10 404551 TTTTAAATGGCTTCAAAGCCATCAAACAAACAAGGATAACCAATTCCCCC  
404601 AAAGATAATTTGGCTAATAGTTAACCCTGAATAATAATACCAAGTCCAT  
404651 TTCTATAAGGAACAAAAGAACTACCCCTATCAGATCTATCCCAGCATT  
404701 TTAAGTGTGATAAGGAATGGAAAAACCTGCTTGAAAAGCCTTATTAAT  
15 404751 ATCATTAAAAGCTGCTATTGTTTGGTTTGAATCAACTACTAAAGCTTTTA  
404801 ATTGAGTTGAAACTTTTGCATGATCTGCAACAAGTTAGCAGGTTCAAAG  
404851 CCTGGGATGAAATAAAACaAAATACCATATAAAAATCCATAAATTAGTTC  
20 404901 AACGATAAAAAGAAAGATGATAGATACTAAGATCATCTCACTAGTATTAC  
404951 CTAGCTTAGAACCACCTCGTTCTGATTGCAACATTAACCTTTTCATAAAAA  
405001 CTGTATTGTTCTTCTTGTGAAAGTTAAACAATCGTCATGCTAAAAAAGC  
405051 AATAACAACAAATCCAATCCCTCCTAACTGGAGTAATACTGCTAAAACTA  
25 405101 TCTGGCCAAAGATACTGTATGTTTTTGATACAACAACAGTAGAAAGTCCT  
405151 GTATCACTAAAAGCACTGGTTGATAAAAATAATGCATCTAAAAAGTTGTA  
405201 ATCAGTTTTCTGTTCAAATCTTTTTCCCTGTCAATCAATCCATAACTAA  
30 405251 CCACTTTTTGGTAGTTATCTTGGAGTGCAATTGGCAAAAATAACAGCAAA  
405301 CTTCCAAACAAGATGCAATAGATATAAAAACAAAAAATTCGTTGGGTAAT  
405351 AGTCTCACCTCAGCCAATTTTTTTTAACCAAGTGGTGAGTTTACCATCT  
405401 GGTTTTGTCTTCTTGTCAATTAAGAAGCGTATCAAATATAATTTTACCA  
35 405451 AGGTATGAAACGTGCAGATTTTGCATTATTGGTTTAGGTAGATTGGGA  
405501 TGCAGGTTGCACAATCACTAAAAGAAAACAACTTTAACTTACTTTTAATT  
405551 GATCTTGATGATAAAAAAAGCTGACACCGCCTCGCAACAGTTTGATTATGT  
40 405601 TATTTGTTGTGATGCTAGTAATCTAACTGCTTTAGAAGAGTTACAAATTG  
405651 ATGAATTTGCTGGGGTTATTGTTGGGGTTACCAACATAGAAGCGAGCATC  
405701 ATGATATGTGCTAATTTAAGGGAATTAGGACAAAAAACATTATGCTAA  
405751 AGCCAAAAATGAAGTACATAAAAGGGTGTTAAGCACAATGGGAATTAGAG  
45 405801 AAGCTTTGATCCCTGAAAAGATTGTTGGTAAAAATCTGGTTATCCGCTTA  
405851 ATCCATGGGCTTGAAAATGAAATTATCAACCTTGGTAATGAGATAATTTT  
405901 CATCCGTTTCAAGCAGTTAACAACAAGGCTTTTTTTTAAACAAAAGGTTAGAAG  
405951 AGATTAACCTTTAGGCAAAACACCGATGCTAACATTATCTCCATCATGCGC  
50 406001 AGTAATAAACTGTTGTTTTTCTTTAGGACCAAATACTGAGATCCAACC  
406051 AGGGGATATTATCACTGCAGTTTGTCAACAAAAAAGTTTAAATAAGTACT

406101 TAAATTACATCAATCCTAAAACCAAAAATAAAAAATAAAAAAGGATCAT  
406151 CATGATCCTTTTTTTTAGATAGCATGCTGTCAATAAGCCATGTTCTGTTTT  
5 406201 AAAGTCAGTTATTTATCTACAGCAATTGCTGTCTTACTTTAATTATTTG  
406251 TTCTTAAAGCAACATTCCCTTACCAAAATTTAGGTTTCTTGCTTGTGGAG  
406301 TTTACCGCGTTTCATACCTGGTTTTTCACCAAGCTCGTCTCTGTGGCACTT  
10 406351 TCAAAACATCATCATAGTATTAACCTTAGACTAGTTATGTCGTTATGGCT  
406401 ATCACATCCTAAATCTTATCGCTTTGATTTACACAAACACTACTTGCATT  
406451 CCAGCAAGTGCAAGCATGGACTTTCCTCTACTTTAAATATATCTTTAAAG  
406501 CAGCAACTAACCGACAGCGTCAAAATTATAATTTGGTGTGGGGATGTTT  
15 406551 TGGGTTTGACATAATGCTGATAGACAAACAGTAGCATTGGGGTATGCCCC  
406601 TTACAGCGCTAGGTTCAATAACCGACAAAGAAAATAACGAAGTGTGGTA  
406651 GAACCAAAATTTGATCATTAAACCAACAAGCAAGTGTTAACTTTGCTTTTGC  
20 406701 ATAAGTAGATACTAAAGCTACAGCTGGTGAATAGTCATAGTTTGCTAGCT  
406751 GTCATAGTTTATGACTCGAGGTTAAATCGTTCAATTTAACCTTTAAAAAT  
406801 AGAACTTGTTGTTTCCATGATTGTTTTGTGATCAATTGGAAACAAGACAA  
406851 AAATCCACAAAACATAAATGTAGAAGCTGTTTGTGTGTCCTTTATGGAA  
25 406901 ACGGGTTCGATTCCCGTCATCTCCACCATTTATCAACTTTAAGTTGGCCT  
406951 TACACTCCCCTAGTTGGGAGTTTTTATTTTGCCTTACTCTTTTAAAGAG  
407001 TTGTTTAAATTTGGTTTGTGTAATTAAGCAAAGATAGCTATAAAAA  
30 407051 AGAAAGAATAAAAAACTAAGCTAATCGCTCAAGCGGTAGCAAATACACCA  
407101 AAATATTTAATTTAGAGAGATAAACACCATTGTTATTTTCAACATTAAA  
407151 AAACAAGCTAAACCGCGTTGCTGATTGAATTTTTTGTGTATCTCTTTCAA  
407201 AAACTGTTGGTCTAATAACACCAAAAATAAAACCATTAGCAAGATCCAT  
35 407251 AAGAGATAAACAACAATACTGATAAAAAATCCAGTAGTATAGCCAATGCG  
407301 CTCTCACTTAGTAGTCTGACTTTTTAAAAAATAATGAAACAGTTCATCTAA  
407351 AACTTAGaAAAACTAATAATGCTAAACTAATTAACCAAAAACTAAGTTA  
407401 GCAATTCCATATTGACTAATCTGATAAGTAATACTAGCTTGAATAATATC  
40 407451 AGTTGGTTTTTCAACAGTTCAAAAAAGGTAAAACTGATTAAGCCGTAA  
407501 CTTGTTAAAAAGTGAATTGTTTAGTGTGAAAAACGCCAGCTAAAAACAAA  
407551 ACGTTGTTTAGAAAAAGCAGAGAAAAATAAAAAAGTAAACAAAAGTATC  
45 407601 AAGTAAGCCAAACCTGCTGTAAAAACAGATAGTTACTGTGTTTGGAAACAA  
407651 CTTGATACTCAGCGACATTTATTTCACTGAGTTTATCAGATATCTTATTA  
407701 ATCCAACCACCACCCTATTTTTCTTTTTAGAAAGCACGTGGGATAGATT  
407751 TAGATAATCAAACCTGATTTTTCTTTTTTAACAAGTACCATATCTTCTATC  
50 407801 CTAATTCCACCAAGGTTAGGAATATAGATCCAGGTTCAATGGTTACAAC  
407851 CCCATTTTCACACAATAACTTGTTGTAAGATTGGGAAACATTGGGCATTT

5

10

15

20

25

30

35

40

45

50

55

407901 CATGGATATCaATACCAACGCCATGACCAGTACTATGCACAAAAAAGTCT  
407951 TTAAACTCAGAGTTTTCAATAATATCGCGGCACACCTTATCAACTTGTGA  
408001 ACCTGTTAAAGTAGTGTCTTACTGCATTTATACCAGCCAAATTAGCCTCTT  
408051 CAACTTTTTTGTATGCAGATAATAACTTTGCACTTTTAGGTTTTTTACCA  
408101 ACTAAAAAGGTTCTTGTAATATCAGAGCAATAACCGTTGTAAATGGTGCC  
408151 AAAATCACAAGTGATAAAATCACCTTCCTTAACTATTGTTTTGGTTGGTT  
408201 TGTGATGTGGGTTAGCACCGTTTTTACCAGTAGCTACTATAGGATCAAAT  
408251 GAGTTTTTAGCCCCACCCTGCTTCACAAGCTCATTAGTAATCCATTGTGA  
408301 AATGAAAAGCTCAGTCATTTTGGTTTAATAAAACGCTTTAACTTAACTG  
408351 CTACTTTTCTTGTAATATCAACTGCTTTTTCAATGGCTTGAATCTCACTA  
408401 GGCAACTTTACTCTTCTAATCTCTTGGGCATTAATTACTGTGTATTGTTT  
408451 ACAAATAGCTTGAATTCAATCCTGATAGTTAAAGGTAAGATAGTCACCCT  
408501 CAATTAAGGTTGATTGATACCATTAGATTCAAAAAAGCTTTAACTTGT  
408551 TTAAACTTAACAAATAATTCAACTTCAACAATAGGATTAATAAGTTCCT  
408601 TGCTGCTTCATAATACCTACCATCAATAACAATTTTGCTTTATTGCTGG  
408651 TGATGATTAACCACCCTGCACTACTTGGAATAAGTTAATCAAAAGCGG  
408701 TTTTGATCAGAACCAATTAGGATAGCATCAGCTTTATTGGTTTTTAAAG  
408751 ATCTTTAAGAACTGTAATTTTTTGTTGTAATCACTAATCATTATTTACG  
408801 TTTTACCTCTTGTGCAATACTACCTTACGACAACGTGAACAAAACCTTAT  
408851 TAAGTGCTAGTTTTCTGGATTTTTCTTGACGTTTTTAAAGGTTAAATAA  
408901 TTAATCTCAGAACATTATTACAACCTAGTCGTGTGCTTCTTTAACAGC  
408951 CATAATTAAATTATCTTAATTATTTATTGTCAATAAGTAACTAATAGAA  
409001 AAAGCATCAATGCCAGTGTGAACAATAATCACACTTGTAATGAAAGCATT  
409051 TTCAATTTTCAATTTGAAAGTTAATCTTATTATGCTCAATGAAATCAGTAA  
409101 TTATTTTTTTAATTTTATTAGCGTAATTTTTACAAAAAGAATAGCAAAAA  
409151 CCGATCCGTTTAAATTTGTAGTTATCACCAAACCTTAGTTTTAACAAAACC  
409201 AAATATCTTCTCAACCGCTTGACTAAAACCTTTTGCTCCTAGAG  
409251 TATTAACCTCCCTGTCAAACAAGATAATAGGTTTAACTCTTAGTAAAGTA  
409301 GTAATGAACTTTTTCAAACCAGAGATTCTCCACCTTTACGCATTGTCAC  
409351 TAGGTTTTTTAAAGTAACTGCAGAAAGGATATTTGTTTATGTGATTCAA  
409401 CCTTGCTTTAATTGTTTGATTATCACAACCTTGTCACCAATGCCTTT  
409451 ATATCTTCGACCAATCATTTTAGAGAAATAGCAATATCACTAGTTTCAAA  
409501 CACTAAAAATCTTTGTCTTTATTTGTTCACTAAGCTCTTTTGCTAATT  
409551 GAACCAACATATCATAAGTACCACTTAAACCTTTACTTAAAGGCAGAAAA  
409601 ATAAAGCGATCATACTTAGTTTTAATCTCTTCAAAGATCTTAAGAAGATC  
409651 ACTTTGACGTGGTAAGGAAGTTGAGATGTTAAGTCCATGTGGGTTTTCTT



409701 TTAGAAGTTTATGAACATGATCATAATCAATTTCTATCCCATCACGAAAG  
409751 CTTTTTTCACCATCAACAATTACTTGTAAGGCAAGATGTAAACGCCGTT  
5 409801 AATCTCCCCAGGTTTAATAGAAGCAGTTGAATCAGTGATGATAGCTGTTT  
409851 TCTTCATGAATTAATCTCCTTAGTACCTTTGTTTCTTTAAATTATCTAGA  
409901 AACTCTAGCACATAATCAAAAAAAGTTTAGGCGCTGAGTCGTGTGGTGA  
10 409951 ATGACCAACACCATCAATAACCTTAAAAATAATCTTGTCACCTTTTATTAG  
410001 CTAGATAGTCTACAGAAGCTTTGGTTGGCGTGACAATATCATTAGCTCCT  
410051 AAAATAACTAAGGTAGGTTTATTACCAATCATTTTATAAGCCCTTTCAAG  
410101 TGAGTCATTACCATATTTAGCGTTTGAACCATATCACTGTAAAGTGTTT  
15 410151 TAAAGGTAGTTCTTTTTTAAATGCATTGATAGCTATTTTCAAAAGTGAT  
410201 TTACGTTTTTCTTCATGTTCAACAAAATCCTTATGGTTGCTGTTATTACG  
410251 CTTAAAAAAGTATCTAAATCCGCTTTTTATTAACTGAGAAAGAAGTTT  
410301 GATTCATAGGAGCTACTAATATTAAAGCCTTAATTTTTAGTGGTATAACT  
20 410351 TTGTTAACTAAACAGCCACAGCACCTCCCATACTATGACCTATTAAAT  
410401 GACGTTATTTAGTTTTTTTTGAACAATAAAATCACAAACCAAATCAACAA  
410451 AGTGGTTTAGTTTTAATTGATCTGTATCTGTTGATTCAATTGTCTCCATGA  
25 410501 CCGGGAATTTAAAGTAAAGAAAGGCCACTTTTTCTTTTAAACAAGCT  
410551 AAAAAACGACTAAAACTGGCATATTCGCTTCCAAATCCATGTAAAAAA  
410601 TAAAAACGTTTTTCTTTTTTTAGGTTTAAAGGCAAATATTGAGTTAAAA  
410651 AGAGTATTTTTATTACTCGTTAGCATTGATTTTAGCTAAACGTTCTGCAT  
30 410701 ATGCTTGGATGCGTTCTTTCTTAGAAAGTTTAGCGAGTTTATCATCCTTA  
410751 TTTTGGATAACAAAATCACGTTTTTTAATTCGTGGTTTTTTTTATTTC AAC  
410801 TGGTTTATCTTCATCACTAGCTTCTTTGATCTCTTCAGTTTGATTAGCAC  
35 410851 TAATGTCATTGAAATATTGCAACTGATTTTGAGTGCTTGGTTTTCTAAA  
410901 AAAAGTTGTTCTTTTTCAATTTTAAATGTTTCTAGTTCATCAAGATGTTT  
410951 ATCACTGGTAACTGGAGTAAATTGAAGTTCTTTTTTAGCATTTTCAAGTG  
411001 AATTTATTTGTTGTTTTAACTGATTATTTTCACTATCAGATGCACTTAAA  
40 411051 CTTTGCTTGGCTTTCTCCAATTCAGTGTGTTTCTTCAAAAGCAGAGAG  
411101 TAAATCTTGGTATTGTTTCATTAGCATCATTCAATTTATTCTTTTTAAGCT  
411151 TTTCAAAATCAGTTTTTAATTTGCCATAGCTTTCTTGTAAGATTTTCATGA  
45 411201 TCAGCTTGGAGCTTTGCTAATAAGTTATTGCTATTCTCAGAGCCTGATAA  
411251 TTCATCTTCTAAATCATTATTTTTTTCATTAAGTGCTAAATTAACCTCTT  
411301 CAAGCGTGGCTAATTTATCTTGAGCAACATTAAAAAGATTTTGAGAGTCT  
411351 TTGAGTTGCTGTTGGAGATTTACTAACTGATTGGTATTTAAATTACTCTT  
50 411401 CTCTTCATTCCATTCTTCTAACTCTGCAATTTTGTCTTGAGTTGTTGAT  
411451 TTTGAATTGTTAAACCATTAAGTTTTTCATCGAGTGCTTTTTTCTGTTCT

411501 TCAAATGAATTTTGTAGTGTATTGAAGTCATTATCTTTAGACCTTGTTCA  
411551 CTCAATTTTCATCTAATAAAACATCATTTTCATGTTTAAGTGCTGAAATTG  
5 411601 TTTTTTGATAATCTAAGTTTAGCGCTTGTTGTTTCACTTGCAATTTATCA  
411651 AATTTTGTTCATTCTCATCAAAAAGTAGTTCATACTGATTTAAAAGATC  
411701 ATCATATTTTTCATTCTCATCATTAGATGTGTGTCATGGAGTTTTTTTCA  
10 411751 GTTCATTTTTCAAAAAATCATTTTCTTGTTCAACTAGATCCAATCTTTGG  
411801 TTTGCTTCTCTTGCTGTTAGTAACTGGTTTTGAAGTTCGTTTATTTGGTT  
411851 GTTTAAACTGGTAATAAAGCTAATTGTTGTTGAACATTACTGCTCTTAT  
411901 TTTTCAATGCATCTAATTGATCTGAAAGCAAAGCTTTTTCTTGTTTTAAA  
15 411951 TTCTCCAACCTCTCATTAACTTCATCACTTAAAGGATTAATAGCAACTGG  
412001 TTTATTTTGCAGTTGCTCATATAAATCCCTATTTTCTTGCAAAAGATCAT  
412051 CCTGTAATTTCTTGGTATGTAAGTGCTTACTTTTTCTCAGATAACCTC  
20 412101 CTTTTAAGATCATCGATTTTCTGTTCTAAATCAAATATTTGATCATTATT  
412151 ATTCTCTTTAAGATCATCGATTTGTTTTTTTAAATCAGCATTTTCCAATA  
412201 AAAGCTCTTTGTATTATAGTCATCCAATTCACTTCTTTTGTGGA  
412251 TGTGCTCTTTTAAAGATCCTTTTAAACAACAAAGGTTGATCATCATTCTG  
25 412301 ATCATATTGGATCGTTTTATGAACTGGATTGATAGCTTTGGTTAAATTTT  
412351 CAATGGAATAGAAATCATCAAATTGTTTCAAGTTCTTTAACCTTATCAGTT  
412401 GAAAATATTTGAACTTCTGGTTTTTTTGTTCATTAATCTCTTCACTAGG  
412451 TTGGTTAAACAACCTCTTCAAAAGATACTTGTTTAGTAGCTTCTGGTTTTA  
30 412501 TCTCATCCTTATCATCTTCAGCAGTAATCACTGATGGTTTTAGTTCCTGA  
412551 AAACCAGTTTTAATTTCTTGGTTAAACTGATTGATCATCAACTTCTTG  
412601 AAAAGCCATAGTTTGATCAACTGTCTGTTGCTCTTCTCTAGTTTTAA  
35 412651 GTTGATTTGCATAATGATTTAAACATTCTTATCCCATTTTTTATCTAAA  
412701 ACCTTTAAATCTATCATCCAATTAAAAAAGAACTATTGACTTTTCTTT  
412751 CTCAGCTTCATCAACAGTACCAAAAAATGTTTTCTCCAATAAATTTCTTT  
40 412801 CAAAGGGAATAGCAGTAATTTTAGATGGTGAAAAAGGATATTATTAGTT  
412851 CTTTGTAATAATCTTTTAAAGTGTTTTTTCATCAAGCTCATTATCAAA  
412901 ATCACTAATTTCAAGTTCCTTATCTACTGCCATGGATTATGTTGGAATAT  
412951 TAGATAAATAAGTATATTATCTTAACTTCTGGCTTTGTTCTTATCCGTG  
45 413001 CGTTTTTTGATTTAAAGTAAAGGCTAATAGGTACAGAATTTAAACCAAAG  
413051 TTTTCTCTAATCTTATTCTCTAAAAACGTGCATAAGAAAAATGAAGATA  
413101 CTTAGGGTCATTGCAAAATAAAACAAAATGGGGAATTTGACTTTTGGTTT  
413151 GTACTGCGTAAGTtATCTGCAAACGCTTGCTTTTAAAAAGTGAGGTTGA  
50 413201 TTGTAAAGTTGTGCTTGCTGAATAACATCATTTTAAAGTGGTGTGCAAC  
413251 CTTAGTTTCAAGTTGGCTTTGAATAATTTTAAAGTTGTTCAAAAATAGTAT

413301 TTAAGCGCTGATTTTTTCAAAACACTAATAAACAAAACAGGCGCAAAATCG  
413351 AGGTGTTTAAAATGCAATTTTCAGCATTTTTTTATATGCATTTGTGGTGTT  
5 413401 ATTGTTTTTTAAAACTAGATCCCATTTATTACACAAGAATAATAACAGGGA  
413451 TAAGTGAGCTTGTGCCAATCCACCAATCACTTCATCTTGTTCACTAATA  
413501 GGTTTTGATCCATCTACCATCAAAAGGATAACGTTACTACGGGCAATAGC  
10 413551 TAGCTTTGTTTTGATGTAAGATGCGGTTTCAATTCCCATGTTAATTTTGC  
413601 CTTTTCTTTTAATACCAGCAGTATCAATCAAAAGAAATTTTTACCATTAA  
413651 ACTTTTAAAGGAACATCAATAGCATCTCTAGTTGTACCACTCTCATTTGA  
15 413701 AACTAAAACACGATTTTGTTTTACAAGTTGATTAATAAGTGAGCTTTTAC  
413751 CAACATTTGGTTTGCCAAATTACACAAAACCTTATTTTTGCTAAATCATCA  
413801 TTATTTTCATTAGGGAGTAATTGATTTTGTTTAACTAAGAGATCCATTAA  
413851 ATCACCAATTCCAATTCATGAGCAGCACTAATAACAACGGTCTTCCAA  
20 413901 ACCCTAAGCTGTAATAATCTTTTAATGTTTCTTCAGCAGTTTtagggTTA  
413951 AAATTTTCAGCTTTATTTTACCAGTATTACTGGTTTATCCTTATTTTTT  
414001 TTTAAGAACCTTAGCTACATAAAAATCATCGCTATTTAGTTGTTCTTGTA  
414051 GTGACACTAAAAAATAATAGCTTTGGCTTGACTAAGTGCTGCTGTACT  
25 414101 TGTAATGCAATTAGTTGTTGCAAGGGAGTTGTTTTGCAATTAATCCACC  
414151 TGTGTCAATAAAAGCTATCTTTCTTTTAACCATTACCAATTCCAAAGA  
414201 TCCTATCTCTTGTCGTGTTAGGAGTATCTGAAACAATAGCCATTGGCTTT  
414251 TGAATTAAGCGATTAAATAAAAGTTGATTTACCAACGTTTGTACGACCTAT  
30 414301 TATTGCAACAGTAAACACAAATTAAAGTTTAAAAACCTTCTTTGCTTCTT  
414351 TGAGGGTTTGTTTTACTACTGCATCAAAACTTAGTTTCAAGAGTGTCAAGA  
414401 TAAATAGCGTCCTGGGCTTTTTTTAATGGGTCTGCAGTTCTAGAACTATC  
35 414451 AATTTGATCACGTTGCTTTAATTCTTGAATTAGTTCCCTTAGTTTTTTTTT  
414501 CATTTGATAGAGAAATTCCTATATCTTGTAATCTTCGCTGCGCTCTAATT  
414551 TCAACTTTAGCATCTAAAAAAACTTCAATTGAGCATTTTTTAAAACTAC  
40 414601 TGTTCCTATGTCTCTACCATCCATCACTATGTTTTTATTTTCTGCTAGTT  
414651 TCTGTTGTTTAATAACTGCAATTTTTCTAATGTTAGGATCAACAGCTATT  
414701 TTACTAGCAATGTTAGCAACTGATTGGGTTGTAATAACTGTTGTAATATC  
414751 AGCATTGTTATAATACACAGCATCTTTCTCAAAGCGTCAGTTAATTTGAT  
45 414801 TAATGATTTTTTAAAAAAGATCAATATTTAATCTATTCATTGCAATTACA  
414851 TAGGCAAAGGCACGATACATTTTTTCCACTAGAAAAATAAAAAAATCAAG  
414901 TTCTTCAGCTATTTTTTTAGCAACACTGGACTTTCCAGAACTACTTGGAC  
50 414951 CATCAATTGCTATTTGTCAATTCATAACTAAATTTAAACAAATGAAACAA  
415001 AACTAACAATCAAAAAAATAAGAAAAAACAAATGCTAAACAGCATGAAA  
415051 CTTATTAAAGTTATCACTAAGTTCTTAAAAATAGCCTTATTAGCATTA

415101 CAAATTAGGTTTCGATGTTATCAATGCTTTTTTTAAAAGCAAAACTtTCAG  
415151 TTGAAAAAACTGTTAGTATCTTGTTGTATCTTTTTAAATCACTAGTTAAA  
5 415201 TTGCTTGTTTTTTtTTAATCATTGTTTCTCATTAGCTTCATAAAATTTACT  
415251 TAAGTGGTTAATCTTTTCTATTCCCTTATCATCACTAATTCAGCTTTTCAT  
415301 AACCGCTAGAAGTTTGGTTATATGCTGCGTTTAACCACATCCTATCAACT  
10 415351 TTTTCTTCTAATAATTTAAAGTCAGTATTTTTTAAATCAACTATTAATTC  
415401 CTGAAGTGTTTTTAAACAGTTTATTTGGTTCAGTGTGATGTTTAACTGGAT  
415451 TTTTATTAAATTCATAAAAGGATGGTAATTAATCAAGATTTTCTGATTA  
415501 ATTTTATTAAGCTGTTTTTTTTCAGCTTTTCAGTGTCTTCTGAGCGTTAAT  
15 415551 TAAAGCTTTTTTAACTATCTTATTGTTATCAAACTTTGTCTATAAAAGC  
415601 GAAATTTTTCTACTCTTCCCATGGGTGGCATTATGAACAACAACTGAA  
415651 TGTATCATCTTTCCTCACAAGCATTGAGAAAACGTGATAATAAAGTTTGC  
20 415701 TGATTCTATCTAAATCAACAGTTAAAAGAGGTACCAATTTAATTTCACT  
415751 ATCTACTATTGAAAAATTGTTTTTTTTCAACAGCTCCTTTGCATGAAAAT  
415801 AACTATTTGAATGCAAGCTAATTTCAAACACTCTTCATCATAATCAACA  
415851 TCAATTAAGTTAATATTGTCCAAAATTAATAATTCAATTAGATCATCTTT  
25 415901 CAAATAGTTATTTTTTATTAACAAAGATAATCCCTTCTTCTTGAAAATTAA  
415951 TCTTGACGCTATTTGGCTTGGCTAATTGTCCTTTTAGTTTAGCTAAATAA  
416001 CCGTTTAACTACTGAGTAAACGGTTAGGATTATCAGTTAGTCCAAACAC  
30 416051 AATAATTCACACCATTTGGTCCAAAAATCTCATAACAAAACCTCGCTAA  
416101 TTTTAGTTGTATCTTTTTCACTACCATGGATATTTCTTTAATTGAATCC  
416151 ATGCTTAGACCCTTAGCTAAAGCAAGATCAACTGCAACTTTTAGATGTGG  
416201 ATTTGACTGGATATTAGTTCCACCTTTTTTAACAGCTGAAGCTATTCTTT  
35 416251 TTGCTAGTTTTTGAAGTTGTTTTGCACTTGTTTGTTGTTTTATTAGTT  
416301 TGATTAGCAATTAGATGCTTACGTGGCATGTAAGATTAAAAATTATTAGC  
416351 AACTTGGTCAACTTTGTGTGCAACAGATCAACTACCTCTTGCTTGTTTT  
416401 TATCTTTGTAAAGAATTTTAGTGTCATCAATTAACACTCTCAAAATGT  
40 416451 GTAACACCTGCAAAACCAACAAGCCCTTTAAATTACTAACATGATCAGC  
416501 TCAAGGGTATCATCCTAATGGTGCACCTTGTGACGCTAAAACAACCTACCT  
416551 TAAGATTAGTAAGTAATCCCTTAGAAGCACCTTTAGTAACATATTTGTCT  
45 416601 TGAAAGGTTTTATTAGCTACAAAGACATGATCAATAAAGTTTTTTAACT  
416651 AGCAGGATAATTAAAGTTGGTCATTGGTGCAAGGATAACAATTCATAAG  
416701 CTGTTTTTAGGAGCATCAATATAATAATCACTATTTCAAACTAAAAAA  
416751 ATTACTAGCGTTTTTGGGTATTATAAGATATCTTACCTACTGGTAATTCAT  
50 416801 TTAAATTTCAATCAATAAATTCAACACTACTATTTTGTTTTTTATAAGTT  
416851 TGAAGGAAACGATCTAATAAAAGGTGGGTGTAAGAACCAGAAGGGGTAC

416901 AGAAGCATCAACAATAATAACTTTCTTCATAGCTAATAATTAAAAAGTCTA  
416951 ATTTTTATTGTTAATTCTAATGAGCTTTAGTTAATTTAGCAATTAATTGG  
417001 TTGGTTTCAGTAAGTTTTTTTTGATATTCTTCCAATTTTAAAAATTCAC  
417051 TTTTACCTTTTCTTTGGGTGCTTTTTCTAGAAAGCTTTTATTTTAAACAA  
417101 TAGCTTGGCTACGTTTACTTCACTTTCAAAAAAGCTTGTGCTTCTGT  
417151 AGAGATTTAAGTCTTTGGGTGTATCATCAACAATTTGGTATTTAAACT  
417201 AACTTTTTTATTAGTTTCAATTTTCAGTTCAATTCAACTAAAGTTAAAGT  
417251 ATTGTTTAAACATCAACAGCATTTTTTACCAGATAAGATAACAACACTAGTTTT  
417301 TGTGTGAATTAAGCATGTACTGTTTTCTGTAATTGCGTAAGTCATTAAT  
417351 AGCAGCTAAAACAAGATCAAAAAGTTTGGGAATTTTAATTTTAGTTGCAA  
417401 GAGGTCATGTTGCTTGCATAACACTTTTATTGTTAAATTGCTGTATAATA  
417451 CGCTCAGATAAAAAAGGAACAGTGATACTAAGCAAAATAGCAATATTAGA  
417501 TAAAACTGATTTAGCAGTATAAAAAAGCTGTGGTTTTAGTTGATTTGGTT  
417551 CTTTTTTAATTGCTTCAATGAAAGTATTGCAAAAATCATCCCAAAACAAAT  
417601 TTAACAAGAATTTGGTTTGCTAATGCTAACTGGAATTTATCTAGTAGCTT  
417651 AGTTATTTTTTTGAATTACTTTATCTAATTTAGCTAAGATTCAAGTTTCAC  
417701 TTAATGAAAGTTTGTCCAAGTCATAACTAATTTCTTGATCATTTTCTAGT  
417751 TGGATAACAACTTAGTAACATTCCACAATTTATTTAAAAAATTTTCATGC  
417801 ACTTTTTATTTTTTGTTCGCTGAAAATTAGATCATCTCCTGGAGTGTGAT  
417851 TTGAACACAAAAATAAGCGCACTGCATCCGCTCCATAATTTCTAATAAGA  
417901 TCAACAGGATCAATGCCATTATTTCAGTGATTTTGACATCTTACGATTTTG  
417951 TTCATCGCGTACTAAACCGTGGATTAAACAGTTTTTAATGGCAGTtTTt  
418001 TAGTTTCAAAAAAGGAGTTAAATAACATTCTTAAAACTCAGAAAAATAGA  
418051 ATATCATAACCTGTAACTAAAAGCTCAGTTTCATGAAAAGAGTCATCCTG  
418101 TTCTCAATTCAAACAAATTAAAGGTCAAAGCGAAGAAGAAAATCAAGTAT  
418151 CAAGTACATCTTTTGATCTAGTGTAGTTTTGTAAATTTTTTGAAGGTTTT  
418201 TCACCAACAACATTTTACCTGTATTGTTTTCAAATCAAACAGGAATTTT  
418251 ATGACCCCAAATTAACGTCTTGAAATACCCATGGTTTGAGTTTATTCA  
418301 ACCAATTTGACACTTGCTTATTAAAGCGTTTGGGAATAAAATCAGGATAT  
418351 TTTTTTAAATATAAGTGATCTTTTAACTTTGGTAAATCAACAAATCACTG  
418401 TTTTGAAAGCATGGGTTCTACAACAGTGCCACTGCGTTCAGAAAAACCAA  
418451 CATTACTAGTTAATGGTATTGATTTAACAAGTAATTTATTTTTTTCTAAT  
418501 CATTTAACAATTTTATTTCTTGCTTGTAACAACTAAGGCCTTGAAATTT  
418551 ACTTGCATTTTGATTGAGAATACCGTTACTGTCAATGCAGCTTAGAAAAT  
418601 CAAATTTATATTTAGTGTGATTTTCATAGTCATTAAAGTCGTGTGCAGGA  
418651 GTACATTTCAATATTCCTGTACCAAATTTAATGTCAACATAGCTATCTGT

418701 TACAACAGGAATTTGTTTTCTGTAAAGGGTAACTACTAATTTATTTTC  
418751 AGAAATTAGTATAGCGCTTATCTTTTGGGTTTACCAATAGACAAACATCA  
5 418801 GCAAAGATAGTTTCTGGTCTTGTTGTTGCAACTATTAGTTCTTGTTTACT  
418851 ATCATTCGCTAGTTTATAAACAACATAATGAAGATGTTGATTAACAGGTT  
418901 TATTGATAACTTCAATATTTGATATAGCAGTATTCAATTTTGTATCTCAA  
10 418951 TTAACAAGCGTGATGCTTGATAAATAAAACCGTTTTTCATAAAGGTTTTT  
419001 AAAACAATTGTTAACAATTTTATTAGCTTGTTCTGAAAGCGTGAATTTAG  
419051 TTTGAGATCAATTTAAGCAAACCTCTAACTCTTTAGTTGATTTTTTAATT  
419101 ATTTTCGCTTTGATTTAATGCCCAATTCATGATCATTTTCAAGTTTTTATC  
15 419151 ATCATCTGCATCAAAATATTTTGATTTTCTTTAATGCTATTTTTTCAT  
419201 ATTTGTTTGAGTAGCAATGCCAGCATGATCAAAGCCAGGAATTCAGTTA  
419251 ATACTAAATCCCTGCATCTTTTTAAAACGCATGATTTGATCAGTAATACT  
20 419301 AACCTCAAAGCATGACCAATATGAAGAGTACCTGTTAGATTTGGAGGGG  
419351 GAAGAATTGCTGTAAAAGAATTGTTTTTATCTTTAGGTTTAAAAAACCA  
419401 GCATTATTTCAAATTTTATAAAGCCCATCACTAACTAAGTTGAAATCATA  
419451 GTTTTTTTGAAAATAAATTTATCTTTTCACTTTCAACGAATAATTCGAAA  
25 419501 ATTTTTTTGTGAACTAAAGCAAGATTATGATGTGTTTTGTACTTGCAA  
419551 AACACATTATCAAAATTAACTTTTAAAAAATTTGCAATATTCTTAAGCG  
419601 AAAAATATCTTTCACTTTGATTTAGTTTGTCAAATTTATTAGCAACAATC  
30 419651 AAAAAGTTCAATCCTGTTTGCAAAATAATTTAACCCTTCTGATCTTG  
419701 AACAGTAACAACTCCACTATCTACTATCAAAACAACACCACTAGATTAC  
419751 TACGAAAATTTAAAAATTGGGTAAGTAAATTAGTAATAAAATCTTTCTTA  
419801 TTTTTGTTTATTTTAGCAAAGCCATAACCTGGTAAATCAACAAATCTTTT  
35 419851 GTCTTTATATTCAAAGTAATTTAGTAATTGTGTTTCGACCTGGTGTGCTG  
419901 AAGTTTTAGCCAGTTTCTTTTTAAAAAAGCATTAATCAAACCTTGATTTA  
419951 CCAACATTACTTCTTCCCATGAAACAAATCTCTGGGATATTATCTTGAGG  
40 420001 ACAATCTTTTAAATCACTTGCACTCTTCAAAAAATGTGCATCCATGTGTA  
420051 TTTTATTTTTGGTTTTTAATGGAGCGCATTATCTCTTTTACCTGGGTTTC  
420101 AGATAATTTTCTACCCATTTTGCATACATTGCTTTAATTTGATTTTCAG  
420151 TAATAGGTGGATTGTACGCATCTGTTTTTTAAAGATTTTTATAGAAATA  
45 420201 AAATAACCAAGAATCATTCCCACCAAAAGCGAAAGAGGGATACCTAAACC  
420251 TAATGCAAGTGCTAGATCATTATAGCTATATATTAATAATTAAACATTT  
420301 TAAAAGTCTTATAAAATTAAATAATCGAATTAATGGATAAACTTGTAGT  
50 420351 ATATTAGTTCCTTGTTACAAATCAAACCTTTTTTAAAACGTTTTTTTAA  
420401 TTCACTTTTAAGCAAGATCTTAATCAAGCTAAAATTATTTTTTTCAATG  
420451 ACAATGTTGCTGATGAAACCTATGAAGTTTTGCAAAAATTCAAAAAGAA

420501 CACAATAACTTAGCAATTGAAGTCTATTGTGACAAACAGAATGAAGGTAT  
420551 TGGAAAAGTGCGTGATAAGCTAGTGAATCTAGTAACAACACCTTATTTTTT  
5 420601 ATTTTATCGATCCTGATGATTGTTTTTAACAACAAAAATGTCATAAAAGAG  
420651 ATTGTTGAATCAATTAAAAAGAAGATTTTGATCTTGGTGTATTAAAAAG  
420701 TATGGTCTATTTATGCTTCTTAAAACATGATTTTCATTATTAAATTTTTGC  
10 420751 CTTTAAAAGGTATTTTTTCaAGGCAGAGTAAAATTAATTAATAATAACaAT  
420801 GTTAATAAATTAAATTACATCaAAAAATAATGATCaATATATTTGAAATAT  
420851 TGTATATAACACAGATTTTTTTAGGAAGCTAAATTTAACTTTtGAATCAA  
420901 GGTtATTTGAAGATATACCAATCTGATATCCGATGTTTTTTTCATCACAA  
15 420951 AAAATTGTTTTTTATTGATGTGATAGGAACaAATTATTTTTATTCGTAATGA  
421001 TAGTTTATCAACTACTATTAGTGCTCCACGCTACTTAAATTTAATCCAAT  
421051 GTTATGAAAAGCTATATGTAAATCTCAGCCAAAATGGTTCTCTTGCAAGT  
421101 TTTATTGATCCAAATCATAAGATTGAAGCTAGGTTTTGAAGAAGGCAAAT  
20 421151 GTTTGTTTGATTTGCACTTTTCAGCTTTGAATACTTTAAGAAAAATTTTT  
421201 CTGAATCAAAAAAAATCTTGAAAACTATTTGTTTTTTTGAAAAAAAT  
421251 GGAGTTTATGAACGTGTTTTTCAAACAAAAAATCAAGGTATTTACTATAT  
25 421301 TTGGGTACAGCGACTAAAATATTTTAAACATGTTTTGGAATCTAAATCAG  
421351 ATAECTAATTAAGTTCTCTTTAAAAAATCAATGAGATTAAAGTTATTTAA  
421401 AGCTTATTGTTTAAATTTACTTAAATTAAGAATCTTTATCTTGTTAAATTA  
421451 ATACTTAACTGGTTTAAATGTCTGCAATTAAATTTAATCCTAGTTCATTCA  
30 421501 GAAAAAACTTTAAATGGTTTGAAAATAACAAAAATTGGATTAATTTTGAT  
421551 AATGCTGCTACTTCCATTGCACTTGATGTTGTGGCTGAAGCAAGCAAAGA  
421601 ATATTACCAGTATTTTTGTGTCAATCCTCATAACAAAAATCCTGAAATTA  
35 421651 ACCAAAACTTATTGCTATTATTGAAGAAACAAGAGATTATTAGCAAAA  
421701 TTTTCAATGCTAAAAAAATGAAATAATTTTTTACAAGTTCTGCAACTGA  
421751 ATCGCTTAACTTATTCGCCTTTGGATTAAGCTCTTTAGTAAAAAGTAATG  
421801 ATGAAATCATTCTCAAAGAAGATGAACATGCTGCTAATGTTTTTCCCTGA  
40 421851 GTAAATCTAGCAAAAGAAAATAAAGCCAAACTAAAAATAATTAAAAAAC  
421901 ACCAAATAAATCTTGAACTGATGCTTTTTTAAAAGCTTGTACACCATCAA  
421951 CAAAACTATTAGTTATAACTGCAACATCTAATCTTTTTTGGAATAGTATT  
45 422001 GACTATGAAAAAATTTCTAAACACTTAAAAAAATATCACCAAATAGCTT  
422051 TATTGTTGTAGATGCAAGTGTACCACACCATAAAATCGATATTA  
422101 CAAGTGCTAATATTGATTTTTTTAACTTTTTCTACACATAAAATTTTATGGA  
422151 CCTACTGGTCTTGGCATTGCCTTTATCAAAAGCGAATTACAATCACGACT  
50 422201 AAAACCTTTTAAATTAGGTGGTGATATTTTTTAAATCATTGGATAATAACT  
422251 TTAAGATAATTTTTTAAAGAAGGTCCTTCCAAATTTGAAGCTGGAACGCTA

422301 AATATTATGGCTATTTATGCTTTGAATAAACAGTTAAAAATTCATGCAAAA  
422351 AGAATTTAATTTTCAGTGAAATGGTGTTTTACAGCAAACAATTAAAAAATT  
5 422401 TAGCTTATCAACTGCTAAGTCAAAATCCTAATATCGTTTTAGCTAATCAT  
422451 GATCAAGATGTTCTATCTTTGCTTTTAAGCATAAATATATTAATTCTGC  
422501 AGATCTAGCAACTTTTTTAAACATTAAAAAATAATTGTTAGACAAGGAT  
10 422551 CCATCTGTGTTGGTAAATTTAAAAATAAAGAGAGTTTTTTACGTGTTTCT  
422601 CTACTCCATTACAACACAAAAGAGGAATTACTTTATTTAGAAAAATTATT  
422651 AAAAAGTAGTAAGAATTCCATTATTAATGAAGTAATATATTAGCTAATGG  
422701 ATATTAGAGCAAGAACAAAAATTATTGATATTTATTCAAATTTAAATAC  
15 422751 AAAAAACCTCTCAAAAGTTTTTCAAAAAATTTTAACAACAAGTGATAGTGA  
422801 TAATTGTGAAGACTTTTTTAATATAGGTTTAAATATTGATAAAAAATAAAA  
422851 TTACTGCAATTGGTTTTGATGGTGATGGTTGTATTATCTCTACAATTGCA  
20 422901 ACTGAATTAAGTATTAAAGCAATTGAAAATAAAACTATTAACCAAGCAAA  
422951 AAAAATATTATCAGATTTAATTGCAACTTATAAAGATAAAAAATTCAGCAA  
423001 ACCAAGTTGTTGAAGAATTAAAGCTTTTAATTGAAATGAATGTAAGTAA  
423051 AAAAGGTTACAGTGTGTGCTTTTAACACCAAGCAACTTATTGCAATGGTT  
25 423101 TAAAAATTTTTAGCATTAAATAGCTAACGTTTGTCTTAGGATATCATATAA  
423151 GCGTTTATCACCAACTAAAAATCTGTTGATGTTCTCTTTGGTGTGCTTTT  
423201 GATTTTCACGAATTAAATCTAAAAATGCCAACTCTTGAGTGCCTTCATCT  
423251 AAAGCTTGTTCAATAAGTAAAGACATAAAGATCTCTTTCTTTAAACCTAA  
30 423301 TGAATTAGCTTTATTATTTTTTCAATTACTAGAAATCTTATTTACATCAT  
423351 CATTTGTTATCTGAATAACATAACTAAGAGTCTGGATACTAGAGTCATTT  
423401 GTTAATGGAAGTGTGTCACAGTTTTATATCCTTCTGTATTGGAACCATC  
35 423451 TGTATTGTCAGCTTTAGATAAACCAACATAACCTTCAAATTTATGAAAAT  
423501 AAAGATCATCTAGTCTATCAACTACATTTAATAAAAACTTTTTTTTATTA  
423551 TCAAACTTATTAAAGGTTACCTCTAGAGTTAAAGCGACTTAAATTATT  
423601 TGTATCAACATTAAGTGAAGGATGTAATAACTCACCAAAAGCATTAAAGTT  
40 423651 CAGCATCAGAACTGGTTTTATTAATCAAGCTTCACAAGGTAACTTATCC  
423701 TTATATTGACTTAAAGCGCTGCTTTATCAGTTGCTGTAATTAAGTGTCC  
423751 GTAATTATTAAAAAGCTGTTGTGTTAAACCAGCACTAGCTGTTGAAATAC  
45 423801 TTTGATTGGAATTAATTGTTAAACCATTAAATCCATAAAAAATTTTTTTA  
423851 TCAGTTGATCCTTGTGATTATTAGATAAAGCTACAGAATTATTAAACGG  
423901 TTCATCAGTAAATCTATAAGTGTGTTTTCACTTCAAGCAATGAATCGGGTT  
423951 GAATTGGTGTGTTTATCATTGAATCAGTTTATTTCAGAACCTTGAGTA  
50 424001 TAGTTAGGATTTTGTAAAAACCTATTAAGGGTTTTTCATTAGCTGATGA  
424051 AGTACTGGATTTTGTGTTTTTGACTAACAGTAGCGCTAGGGTTTTTATCAT



5

10

15

20

25

30

35

40

45

50

55

425901 CTGCAGCAGATAAGTTAACAGTTTTTAAAACAGAGAGAATGTTATTTTTTA  
425951 CTAATTA AAACTTTGCTTGCACTATACTTGTTTTCAAAGTCAAGTAAATC  
426001 ATTTCTGGTATTAGTAGCAGCTGAACTTTGTGATGAACCACTAGAATTAG  
426051 CAGTTTGTAAATTGTTTATCAAACCTCTTCAAATAATTTTGCAGAGTTTGTT  
426101 TGACCACCACTTTCACTAGGATCTTGAAAAGCAGGAAAGTTATAAGAAAG  
426151 ATTTAGATTGGAAGCTCCAATTGCATTTTTCATCATAAATACTGCCAAGTC  
426201 CAGCAATTGGAGATTGGTAATTGAAAGAAGCTTGATTTAATAAAAAATGGG  
426251 TTTTCTTCTATTAATCACTGTGAAAATAAATAAGCTTGAAGATTAGTAA  
426301 AAAATCACCATTTACATCATTTAAATTGCTGTTAATAAACTTAAGTTTAT  
426351 TTTCTGTTTTTTCAATGTTTTCTTTAGTTGTTGCAACGCTTGATCACTT  
426401 GAATTCACATAAACTAACATTTGCACTAATGTTATTGAATATTAAAGATTG  
426451 AAAATCAGTAATTAATCTATCATAGAGTTTAAGTTTTTTTCACTTTCTT  
426501 GATTACCACCGAACTGATCATATTCTTTTTGTACTTCAATAGGTCACTTT  
426551 ACTCTATCAGCACGTTTCTTTTCATCTATCAAGTTATCATGTTTCATCTTC  
426601 AACATTTTCTTCAAATATCTTTAATCGATTAGAGATGTTTCTATCTGCAT  
426651 TTGCTTGGTATCATTTTTTGTAATGCTGATCCAAAACAAACGTAAGATA  
426701 GAATCAACACCACTACCATCATTTAAAGCAGACTTTAAACTACATCTGG  
426751 GTTTATGATATTTTGATCACTAAAACCAATTAGTTTTTGGGATCGATTGA  
426801 GAGTAGGAAAAAGATTAGCAGTGTTTATTGTGGAACAGGCTGTAATTATT  
426851 GCTGTTGCACCCACTCCACTAAATGCTAAAGCAATTAATGATCAGCGCTT  
426901 AAAACGATGAGCCATCTTATACTAGCAGTTTGATAATTATCACATTTAAA  
426951 AATCTAGCTAATATAATTGCAAATCTAGATTATTAAAAAATGTATATTAA  
427001 TTATAAATAAGTTAATTTTTCTAATTTAAGCATTAAAAAAGCTTAAATCT  
427051 CTCTAATTAAAAATGCTTTACCAGAAAATCAAAAAATTAGTTTTTAGCTAG  
427101 CTGTTTGTGAAATGAATTTTTATTAGCCAATTGTTGAACAGTTAGTTCT  
427151 TTTATTTGTTCAAATAATGCTGGCTTTTCTGATAAAACATTTAATAATTT  
427201 TTCTTTACCAACAGCAATGCTTTTCATTGTTAAAAGAATAAGAAATTTCCAG  
427251 CTCTTACAACAACATTAAATTTAAGTGCTAAGTCAATAACTTCATGTTCA  
427301 TGTACAAAACACCGGTTAAACATGATTTCTAATATAGCAACACCAAAAGG  
427351 TTTAGCAATCTTATTTTTAGATACCATTACTTTGTTTTTATGCCAACAT  
427401 AATTGTTGAATTTATCCTTAAGTAATTCAACACGCTTAGCTTCCATTCTT  
427451 AATGAACATAAAATCTTAGAGCTTTTCTCCTGTTGTAACCTCGTTATT  
427501 TCCAAACATCACTCCTGGTTTTTCGCGTAACTGATTAATGAATAAAACAC  
427551 AAGTTTTAGAACTCTGGTAATATCGATTGTATTCTTCGCAAACCTTTTGAC  
427601 ATCATTCTTGCAATGCAAGCCAATAGTTTGTCTTCAATTGTGCCTTCTAA  
427651 CTCTTGTTTAGGAATTAACGCTGCTACAGAGTCAATAACAATTAAAGATA

5

10

15

20

25

30

35

40

45

50

55

427701 TCTTGTTGTTTTAATTAATGATTCGATAAGAGCAAAGCGTTTTACCA  
427751 TGCCTAGGATGAGCAATCAAAAGTTTATTTAGATCAATACCAATTGATTT  
427801 AGCATATGCTAAATCAAGTGCACCTTCAGCATCAATATAACATGCTGTTT  
427851 TACCTGCTTTCTGAAAAGTAGCGACTGCATTTAGTGCAATAGTTGTTTTT  
427901 CCAGATGATTCATTTCCATATAGTTCTACTATCCTACCTAAAGGTAGACC  
427951 ACCAGACCTTAATGCTTCATCTAAATTTAAACTTCAGTTGAAATTGTTT  
428001 CAATTTCACTGTTTTTCTTTGCATCAAAAAAATCAAACTTGTCAAATTA  
428051 TTACTTTCAATAAAACTACTATTTTTTTGAGTATTTTTCTTATTAATTAT  
428101 TTCTTTTGAGCCATCTTTCATTACACCTTATAAATAAGTGCAAAAAAAT  
428151 AAAAAATGACATTTTTTTTATTAGAAATTTGTTTATTTTTTAATTTTCTT  
428201 AAAAAATCTCTTTTTTAGGAGTTTATTTTTTTATATTAGTTAACTTGTTT  
428251 GGTGTTGTTGACATAAACACTCCTAAACTCCTATATATTATTAGTAAATA  
428301 TATAGATTTTTGTTCAAGTCTACTCAGGTGAAGCTTACATACAACAGTTC  
428351 AAGTGGCTCAAATAACCAGATTAGTTTTGATTCAACTAGTCAAGGTGAAA  
428401 AACCATCCTACATCGTTGAGTTTACTAATCCACCAATGTTGGCATCAAG  
428451 TGAACGATGGTGAAAAAGTATCAGTTAGATGTACCGAATGTTCTAGCAA  
428501 CATGAACCAAGTGTGCAAGAATTGATCCTAGAACAACCTTGACTAAAT  
428551 ATACCTTAAACAGTAGTTTGGCCAAACAAAAGGGCAAAGCCAGATAGAG  
428601 GTACATCTTGGTTCAAATCAAATCAGTGACGATCGATGCGCAACTCCAT  
428651 TGGCTTAAACAACAATCCCAGCCCCAATGCTTCAACTGGATTTAAACTCA  
428701 CTACCGGCAATGCATATAGAAAATTAGATCAATCCTGACCAATTTACCAA  
428751 CCAATTGATGGGACCAAGCAGGGCAAAGGGAAGGATAGTAATGGGTGGAG  
428801 TTCAACTGAAGAAAACGAAGCTAAAAATGATGCGCCCCTAAGTACAGGAG  
428851 GGGGAACATCAGACAACGCTTCAAATTCACCAAGTACCTCAACACCAA  
428901 CAAGCATTGGAAGGATCGGTATCTTGTGTTGATGGGGATGGAATGAGGAA  
428951 TGTGGTTACCCAACCTCTATTATGCTTCTACTAGCAAGCTAGCAGTCACCA  
429001 ACAACCACATTGTCGTGATGGGTAACAGCTTTCTACCCAGCATGTGGTAC  
429051 TGGGTGGTGGAGCGGAGTGCAACAACCTGATTCATCATCAAAACCCACCTG  
429101 GTTTGCTAACACCAATTTAGACTGAGGGGAAGACAAACAAAAACAATTTG  
429151 TAGAGAACCAGTTGGGGTATAAGGAACTACCAGTACCAATTCCCACAAC  
429201 TTCCATTCCAAATCTTTCACCCAACCTGCATATCTGATCAGTGGCATTGA  
429251 CAGTGTCATGATCAAATCATCTTCAGTGGCTTTAAAGCGGGGAGTGTGG  
429301 GGTATGATAGTAGTAGTAGTAGTAGTAGTAGTAGTACCAAGACCAAGCA  
429351 CTTGCTTGATCAACAACAACCTAGCTTAGATAGTAAACGGGGTATAAGGA  
429401 TTTGGTGACCAACGACACGGGATTAAATGGTCCAATCAATGGGAGTTTTT  
429451 CAATCCAAGACACCTTCTCATTCGTTGTTCTTATTTCGGGGAATCATAGT

[illegible]

431301 TTAAACGTTCAAAGCCTTGTGCTAAGTTGTTTTTCAGTTGAAACTCCCCC  
431351 AGTATGGAAAGTACGCATTGTCAATTGGGTCCCAGGTTACCAATTGATT  
431401 GAGCAGCAATCACCCCAACAGCAGTTCCCAATTCCACCAACTTACCAGTT  
431451 GACAAGTCAATGCCAAAGCAGTATTGACAGATACCATTTTCCCTTTTACA  
431501 ATAGATAACAGATCTAACTAAAACTTCTTTAATAGATGTTGCACAAATCT  
431551 GTTTAGCTAATTGCGTTGTAATAAGACTGTTAGCTTCTACAATAGTTTTT  
431601 TGTGTTTCAGGATCAACTATAGGAGTAATTGAGTAGCGATTAAACAATCCT  
431651 GTCAAATAATGATTCAATCAAGGATTTGGTTTTGGTTTCAACAATTGCTT  
431701 CAACAACAATTCCTTTTCTGTTCCACAATCATCATGGTTAATAATTAAT  
431751 TCATGAGTAGCATCTACTAGCTTTCTTGTATATAACCAGACTTTGCTGT  
431801 TTTCATTGCAGTATCTGTCATCCCTTTTCTCGCTCCATAAGAAGAGTTGA  
431851 AGTATTCATTAATGGTCAAACCTTCAAAAAAGGAGTGTTAATAGGAACT  
431901 TCTATCGTATCTTTAATGATCTTAGATTGGTTATTTCTTTCATAGTTAAA  
431951 GCTTTTAGACATTAAGCCTCGCATCCCAAATAACTGGGTAAAGTTAGAAA  
432001 TGTTACCTCTAGCACCTGAATCAGCCATTACCACAATGGAATTATCACGG  
432051 TACTGTTCTTGTTTAATTAAGTTTTGGATCTCATCAGATACTTTTTCTTT  
432101 CACATTGTTTCATAACTTCACAACGCGTTTATAACGTTTCATCATCGGTTA  
432151 ACAAACCCTTGTTATAAACTGTTTGTATTTAGCACCTGTTGATCAGCA  
432201 CTATCAAAGTAATTTTGTATTATTGGTGTACTTAGGGATATCAAATACCTGA  
432251 AACAGTAGTTGAAGAAAAAGTAGAGTACTTAAAGCCAAGTGCTTTGATAT  
432301 TATCAAGTGTTTTAGGAAGGTCTTTAAATTCCAATAAAAGATAGAGTAGA  
432351 TCGATTAACTTGGAATAACCTTTTTTGAAAATGCAGGGATAATTTGATG  
432401 CTTTAAAATTGATTGTCTTACATCTTCTCCCTGTTTCACAATGAACTTT  
432451 CGGGACATGCATTTTCATCAAATTCCCCGTCATTAATATAAGGAACATTA  
432501 TTGCCTAAAACATCATTAAGATAATCTTACCAACTGTTGTTATTAAAGT  
432551 TCCTTGGCATGCAAACCTTCTTGTGGGAAATGCTTTAGTACTTATCCCTA  
432601 CAATAGCATGTAAATGAACCTTTTGACTTTTCATAAGCAGCAGTGCTTCA  
432651 TAAACTGTGCTGAAGATAATCCCCTCTCCCAACTGTCTTTTCTCTCTGT  
432701 GGTTAGATAATAGTTACCTAAAACCATGTCTTGAGTAGGAGTTACAATAG  
432751 GTCTTCCATCTTTCAAACCTAAGATATGTTTTGATGCAAGCAGAACAGCT  
432801 CTTGCTTCATTAAGTGCATTCTCACTTAAAGGAACATGAACTGCCATCTG  
432851 ATCACCATCAAAATCAGCATTAAATGCAGTAGTTACTAATGGGTGTAATC  
432901 TAATTGCTTTACCATCAACAATTCTTGGTTCAAATGCTTGGATCCCTAAC  
432951 CTATGTAGGGTTGGAGCACGATTTAGTAAAACGGGACGATCTTTGATAAC  
433001 ATCATAACTATTTCCCCAGATAAGATCATCTGGTTTTTAATCATATCTT  
433051 CAGCTTGTCTGATGGAAGCGGCAATTGGTCTAATCTCATTACCATTTTCA

433101 TCAAACCTATTGATCAATCCATGGATAATAAAGGGTTTAAACAGCTTTAA  
433151 GATCATTAGTGCTGGGATCCCAACTTCATACATCTTCAATTCAGGGCCAA  
5 433201 CCACAATTACACTTCTACCTGAATAATCAACTCTTTTACCAAGTAAGTTG  
433251 TGTCTAAATAAACCTTGTTTTCTTTTAAACGATCTGTTAAAGATTTCAA  
433301 TGACCGTTTGTCTTTGGAAAGTGATGGTTTATGACGTGAAGAGTTATCAA  
10 433351 ATAAAGCATCAACAGACTCTTGTAAGTCTTTTTTCATTGTTAACAACA  
433401 ATAGAAGGTACAGTACCATCTTCCAAAATCCTTCTTAATCGGTCATTTCT  
433451 AATGATTACCCTGCGGTAAAAATTGTTGATGTCACTGGTGGTAAACTTAG  
433501 CACCATCAAGTTGGATAATAGGTCTGATATCAGGGGGGATAACTGGAACA  
15 433551 GTATGTAAGATCATGTTTTTAGGATGAAGCTTAGAATTTCTAAACCAACT  
433601 AATAGTTTCCAGTTGTCTTAAGATCTTCTTAACCTTAGCATCTTCAACAC  
433651 TATCTTTCTTGGCTTTTCTTAAAGCATCATTTAACCTGCTAAATTCGAAG  
20 433701 TTAAGATCGATTTTATTAAGCAATTCCAAAATGCTTCAGCCCCCTATTCC  
433751 AACCCTAAAACAGTGTAATCTTAAATGTAATTAAGCATCATTTAGAG  
433801 AAAAGGGGAGAGAGCTGTTTTTAAACTTTTATAAAAGATTTTCCCTTA  
433851 CGGTAATCTTCACTACTCTTACTTTTAAATGAGATTTCTGAAGATATAACC  
25 433901 TATCACACGACGCATTTTTTGTGCGTTGAAAGTGAACCCTTACCAGTTA  
433951 AGTCCAAAACCTCTTTGAACTTAAAGGCATGATTTTATCATCTTTGATC  
434001 TTACCTGTATCAAGTACTATGTAGTTAACAAAGTACAAAACCTGTTCAAC  
30 434051 CTCTTTGTAAGAGATGTTTTAAACTAATGATATTTTGAAGGAGATGGTA  
434101 ATTCTTTTGACATCCAAATGTGAGCTACAGGACTCACAAGTGCAATATGT  
434151 CCCATCCTTTCTCTACGTACAATAGATTAGTAACCTCACACCCACAGCG  
434201 ATCACACCTCACACCACGGTATTTAATCTTTTGAACCTGCCACAAGCAC  
35 434251 ATTCATAGTCCTTAACAGGTCCAAAGATTGCTTCATCAAACAAGCCTCCA  
434301 GGTTCTGGTTTAAATGATTTATAGTTAATGGTTTCAGCTTTTGTAACCTC  
434351 CCCTTCAGATCAGTTCAAATGGTGTGATTGGAAGCGATGGAAAGTTTAA  
40 434401 TTGCTTTAATGTTTTTATAAAGCTTGTTATTTCTTTTATTACGTCTTGTT  
434451 GTTGTCAATTGTTAATTTCTAATAACCCTCAGTGTCAAATTCAAAATCATT  
434501 GAAAAATTATCTTGTTCCCATCACTTTGCAAGATGGAAACATTATTGG  
434551 AGTCTTGTTGGGTGTTGTCATCATAGATAAATGAAACAGATAAAGCCAAG  
45 434601 CCCTGTAATCTTTTGTCAATAATTTAAATGATTAGGGATACCAGGCTC  
434651 TGGGAAAGCTGCACCTTTAACAATAGCAGCATAAGCCCTATTTCTTCCTT  
434701 GTACATCATCAGATTTAATGGTTAAAGTTCTTGCAAGTTATAAGCAGCT  
434751 CCATAAGCTTCTAATGCTCACACTTCCATCTCACCACCGCTGTCCACC  
50 434801 ATTTTGCGATTTACCACCTAATGGTTGTTGAGTGATCTTAGAATAAGGGC  
434851 CAACAGCACGAGCATGGATCTTATCATCAACCATGTGATTAGCTTCATC

434901 ATGTACATAATTCCAAGTGAAATAGGTCTTTCAAATGGCATTCCACTCCT  
434951 ACCATCAATGAGTTTAAACTTACCCTGATTTTTTTGGGGATCTAATCCTG  
435001 CTTCTTGCATAACATCTTGGAGATCTAAGAAGTTCACCTCCTTGGAAAATA  
435051 GGGGTTGCAATTTTGTAAATAAGATCATCAAAGACATCCCTATCTCTTT  
435101 CAAACTAAACTAATGTCACCTGTTATCGAGTTTTTCAAGTGCTTCTTTTT  
435151 CACTTTTAATATTGCGATCATTGATTTGGTTTTTTAAACCTTTAATTAAT  
435201 CTTTCAACCCTTGCTTGAGGTTGATTGATTTCAATGGCAAACCTCCTTAGC  
435251 TTTATTTTGATCAAAACAACACTACTAATTAAAGAACGAACCTGCTAGCTTGT  
435301 GTGCTGCATAACCCAAGTGGGTTTCAAAAATTTGTCTATGTTTCATCCGA  
435351 CTAGGAACACCAAGGGGGTTGAGCAGAATATCAACTGGGGTTCCATCTTC  
435401 TAAATGGGGCATATCTTCAATAGGCACCACCTTTAGAAAATAACTCCTTTAT  
435451 TTCCGTGTCTACCAGCTAATTTATCACCATTGAATCTTACGTTTTTGA  
435501 ACCACATAAACCTTGATCATTTCAATCACACCATCATTAAAGTTTCATCACC  
435551 ATTAGCAATTGAAAAACGTTTTACAGCTGAAACAATACCATCCCCACCAT  
435601 GGGAACTTTAAGTGAAGAGTCTCTCACGTTTTGAACACTTTTCAAGGAAG  
435651 ATGGCTTTAAATAGCTTTTCTTCAGGAGAGACTTCGACTTGACCTTTAGG  
435701 GGAACTTTACCAACCAAAACATCCCCTTCTTTAACTTCAGCACCCACCA  
435751 TAATGATGCCATTCTCATCAAGATAGCGTTTGTGTTGCATCACTAACATTA  
435801 GGGATATCACGGGTAATTTGTTTCATCACCATTTTAGTAGACAAACATTG  
435851 AGCAACATACTCATTAAATGGTTAATGAAGTGAGAATATCTTCCTTAACTA  
435901 ATCGTTCTGAAATGACAAATGCATCTTCATAGTTATAACCATTTCAGTT  
435951 GTAAAAGCAACTAAAACATTCTGTCTAATGCCAACTCACTCTTATTAAC  
436001 AGCAGGGCCATCAACAATGATTTTCATCCTTATTAACCCTTTGGCCTATTT  
436051 CAACAATTGGTTTGTGGTTATAACAAGTATTTTGGTTGGAACGTTCAAAT  
436101 TTAAGTAGGTTAACTGTCTCTTTTTTAGAACTATCACTTGTAATAATAAT  
436151 CTTACTGTTATCAACATAACTAACAACACCTGAGCAAGGAGAGGACATTG  
436201 TTAAACCTGAATCACTAGCAATTTTGTGTTCTTGACCAGTACCTACTGCA  
436251 GGAGCATATGGCTTTATTAAGGATAGGCCTGACGTTGCATGTTGGTTCC  
436301 CATTAATGCTCTAGCTGAATCATCTTTTCCAAAAGGGGATTAAAGAAG  
436351 AACCAATGGAAACAACCTGGTGTGGTGCTACATCAATGTAATCAATCTTT  
436401 AAAGGATCATAAAGTCTTGCATAGATCGATACCTACCAATAATTTCTTT  
436451 ATCTAAGATCTTGTATCGTTACTAATATTGACAAGTGAAGAGATCTCAG  
436501 CAATAATATGTTTCATCTTCTCTAAGCGCAGTTAAATATTCCACCTCATCA  
436551 GTAATTACCCCAGCTTTGATTTTGCATAAGGTGCCATTAAAAATCCGTT  
436601 TTCATCAATCTTAGCAAAGCTAGCTAAAGACATGATCAACCCCTATGTTCA  
436651 TCCCTTCAGGTGTTTCAATAGGGCAAATTCTACCGTACTGAGAATAATGC

436701 ACATCACGGATATCTAAATTAGGGTCCTCTCTTGATATCCCCCAGGTCC  
436751 CATTGCTGAAATCCTTCTTTTATTACTCAATTCTGATAAAGGGTTTTGGT  
5 436801 GGTCTAAAAAATTGGGTTAATTGGTGGGTATTGAAGAAGTCTTTAATCACA  
436851 ATTTGAATTGGTTTTGAGTTGATTAAAGATTTAATAGTTAATTCCTTTTT  
436901 TTCACCTTGTTCAATAACCTGACCCCTCTTCATTAATTTGCTGGCCACGGT  
10 436951 TAACTCCATCAGCAATAGTTAACTTTTCTTTTAAAAAGCGCTCCATTCTA  
437001 GTGAAGCCGCTTTCTAATTTAGCAGTAATTAATTCATTAATTAACCTTAAC  
437051 CCGCTTATTACCAAGGTGATCAATATCATCATATTTACCAATTCCATAAG  
437101 GTAAATTAATCACATAACTAATTGAAGCGATGAAATCACTGAGAGTCATT  
15 437151 GCTTTGTTTCAGATCATTTTTCGTTATGGATCCCTATAACTGGTACTGAAAC  
437201 ACTAAGATTATCATTAGTGATATATACATCTATCGTTTCATAAAAGAGTG  
437251 ATTCTTTTGCTAAATCAACAGCCTTACCATCAGTTGTAAGTTGCATTTTA  
437301 TTAACAAAATAATTTTCATTGTTCTTAGCAGCTTGTTTGATTTTGTCAT  
20 437351 CTCTTCTTTTAAAAGTAAAGTACCTTTTTTTAAAAGTAGCTTGCCATCTT  
437401 TTAAGAACAAATCACATGCCAGAGTTTTTTGATAAATACGTTCTGTAA  
437451 CGTAACCTTTCTAGATACTTTGTATCTCCCTGCATTAGAGAGGTTGTACCT  
25 437501 CTTGTTTCTAAAAAACGCGCACATAAAAGTGCATGGAACTCACTTCAT  
437551 GACACTCTTCAGTGTTTTCAATATCACGCAGTGAAATAGAAAGTTCATTG  
437601 ACAATGTGTTTAGCAGCTCTTTCAGTAATAACACTATCCATTTTGTTTTC  
437651 CATTTCCAGTTCAAGTGCAAGTTAACTAGAATCATTTGGACTTGTTTGT  
30 437701 TTAGCGCATTATATTGTTTCTCAAGCGTTACATATTCATTAACAAGTGAT  
437751 CTTAATTTCTGATCAGAAGCGATCCCTTTTCTTCTTAAATCAGTTTTACC  
437801 ATCTCTAAATCTTTTAAAAGGTTTTTGATTTCAAGGATCAACATTGCTTA  
35 437851 AAAAATCCTTAGCATTGTAAATTTCCGCTTCCAATGAACGTTTGATAAAT  
437901 TCATTGTTTTTAAAGATTTTAAGGATCTCACGATTATTTAAACCAACGC  
437951 TTTTAAAAGTGTTGTAATAGGGAAAATCTTAGCACCTTCTCTTACCGCAT  
438001 CTCTTAAAAGAATTTGTACAAAAGCATCTTCAATCTTTTTTTTATTGGAG  
40 438051 ATGTATATAAGCATCACTGAACCATTAGCAGGTAAAACCTCACAAACATA  
438101 ACCTTCCTGTACTCTTTTACGGGAGTTGGATAGTTTTAGTTGGGATTTTG  
438151 TTAGCATGTATATCCCTGGGAGAACGGGTATTGTTGGGAAATAACAACTTT  
45 438201 TCTATCCCATTGATAATAAAAAACCCATCATGGGTATTAAAGGCATGCT  
438251 AGCTAAAAATACACCATTTGTATTGCTAGCAATATTTTCTTTGATTTCC  
438301 GTGCTTTTTTAACTGTTTCTTTATCATTATCAACTAATTCAAGATCAGCA  
438351 TAAATACCAACTTCATAAGTTTTAGATTGAGCACGTGATTGTGCTTCATC  
50 438401 ACGTTCGGTTTCAGTTCTGTGTAATCCCCTAAAATTGATAGTGTAGCGAT  
438451 CATTAGGGGATTTGATTGGAAAATATGAGGCAATTAATTTTTCAAGATCA



438501 TGATCTAAGAATTTTTGGTAGCTTTTAATCTGAATATCAGCTAAATTTGG  
438551 TTGGATAAAAATTGGTCTCAATTTTGCCATAATACCTTCTGGTAGCTGTAG  
5 438601 GGGAAATAACGTTTTTGAAGAAATTAGATTTTGTGACATTTGTGGGGTG  
438651 AAAAGCGGATCAAAACATTAAAAAGCCACTAACAGCGTTATAAAACGCAT  
438701 GCTAATGGACTTAATCACAGTTCGCTAAATTATATTAATTTTAACTTG  
10 438751 TTCAATAAAAAGGCTTAAATCAAAGTTCTCATGATAACCGTTGACTAAAA  
438801 CTGTTCCTTTAACATTAAGACCGCTAAAACTTAAAAATTTATCTAGTAAT  
438851 TCTAGAACAGTTTTACCCCCACCCGCAGTTGCTGGAGTTACACAACAAAT  
438901 AACTCCATTAAGACCTTTTAAAAATTGATTCTACCATACTGCTCATCAC  
15 438951 GAGTCATCCAGTCAATGATGTTTTTAGCAAAAGCAGGGATAAAACCGTTG  
439001 TGTTCAAGGGTAACAAAAATTAAATTGCTATGTTCTTTGATTTTTCTAAC  
439051 TAAAGTTTTAATTTTGTGAGAAAGTTAGTTGCTTCTAAATCAACAGAAT  
20 439101 AAAAAACAACCTTGATAGTCTTTAACTCAATCAATTCACAACCTTAAAGAA  
439151 TGTTTTAATTCATTAGCAAATTTCTGTTAATGGAATGTTGCGAATTGGA  
439201 GAGCATTAAAAATTAATGACTTTTGATCTTTTGACATAAATTAACACTTAA  
439251 ATTTTAAATAAAAAGTATTTAAAAACAATTTAATAGAAGCGTATAGCTAT  
25 439301 TTTTTCAATGTTGTTAATTATTGAGAAAAATAGCAACCTTGATAAGTCTT  
439351 AATATCAGCAACCTTAGTATCTAAACTAACGGTTGGTAAATTGGGGTTTT  
439401 GTTCTTTATTTCTTCAAGTAAACAGATACAATTCTCATCAAAATTAAAA  
30 439451 CCTTTCATTATTTCAACAATTAAGTGGAATCCAAATCAAAATCAAAGC  
439501 ATCAACTTTTAATTTAGTAGGAGAATTTGAAAATACTTGTAATTTGGAAT  
439551 AATGCAGTAAAACTGCTGATTAAATCTTTAACAGTTTGTTGTCAAATT  
439601 AAGTTCTTTTGCTCAAAGTTAGGATGCTTAATGTTTTCTAAATTTTTTAA  
35 439651 CAAGTATTTATGAGGCAAGATAAAATGGCTGGTGATTTTTAACTTTTTTT  
439701 CAATTGTGAATCTGTCTTGAAAAGTAGTGAACTAAAATCAATGTACTT  
439751 TTTTCAAAGTTAGTTTCATAACCAACACACCGTTTAGTTCAACAAACAT  
40 439801 TACGTTATTTTTAGACTTGCTTTTTTTCTAATTTTCTAACTAACTTAA  
439851 AAACTTATTTTGAAATGATCTTAAAGAATAAACTTCATGTTTTATTTTT  
439901 TGTTTTTAAATTTCTTTAATTAGCGAATCAGAAAGCTTAATAGTTGTTTT  
439951 TTCTTCTGGTGAATTAATTAATAAAAAAACTATTTTCAAACCCCTTAAAG  
45 440001 TTTTCAGTATTTTTTAAAACTTATTAATTTCTGTATCTGTATTTTTGGTT  
440051 TTTTCAACAAAAGCAAATACAGTATCGTTTTGACTTTTATTTCTTAATGC  
440101 TAAACCAAATGCACCTTACAAGTTATTATCAAAACCTAAAAAGGGAAGT  
50 440151 TATCAAAATAAATCTTTTGATATATTGGAAGACTTACTTTGTTAACAAGC  
440201 AGATAATTTACTTTTTTAGATCTAACTAAAAAATTAACAAAATCTAGATA  
440251 TTGTAATGTTGATAAAAGTCCAACCTTATTGCTATTTTGAAAAAATCAT

440301 AAGCTAATAGGCGTTGCTCATTAAACGAGGGTTTGATCATTAAATTTTATGA  
440351 GACATTGTTTAAATAAATTTTACTTAGTTTATTATGATTCAGGATATCATC  
440401 CATTGCTTTACAAAAGCTTTCATATTTACTATTAAACATTTGGTGTTCCAC  
440451 TGTTTAAAGATAACAGATGATTGCAAATTATGTTCCTTAATTAGGTATTTA  
440501 TTGAAATAGCTTAATGTTAATTTTGTGGCATAAAATAATCATTTTGAGC  
440551 TAAACCAAAAAACACTGGTAACTTTAAATTTTATAAGTCTTATTTAAAA  
440601 CTGGTAGTTCTTTCAAATATTATTAGAAAGCTTTTAGCCATTTTACTG  
440651 TGTTTTGACAGCTCATTTTCTCAGCTGTTTTCATCAGTTAAATTACTAA  
440701 TTTAGTTTGAAACATTGCTTTAAATTTAGCCATTCTTCTGCCTTATCTT  
440751 TTTTAAAGAAGCTTTTAATTTTGAAATATCTCAATAAGTTACAGTATGAA  
440801 AGAGGTGCTAAAAGTATGAGTTTTTCAACAGTTTAGCATTTAATAAATT  
440851 CATGGCATAACTACAAACAGCAGCACCATACTGTGTCCTATTAGAACGA  
440901 TGTTTTCCAGATCCTTATTTTCTATAAAAGCAGCTAATAGTTCTCCATAA  
440951 TGGATTGGAGATAATTCCTTATAATCAAACCATTTACATTATGACCAGG  
441001 TCAAAGTGGAGCGTAATAGTCATAATCAGTAAGGGTTTTATAAAAACTTT  
441051 GAAAGTAGCTATGAAAAACAGAAAATCCATGTGCAAAAACAACCGTTTGT  
441101 TTTTTTGTTTTTTTTGCTGGCTGAAAGAAAACCTCAAGCTTAGAAATATC  
441151 AATCTGATTAAGATCTGAAAACCTTTTCACAATTATTTTTTTAACACACT  
441201 TTAAAACAACGTGAGCACAAATTATGATCTAATTTTTTGCTTAATGATTGT  
441251 TTGAAAATTCAGCATCTTTCACACATTGTTTTTTTAGTTTTTTTAACTT  
441301 TAATTTTCATTTTCATTATTTGTAAATTAACACTGTTTACATTAAGTCAA  
441351 AGTGCGAGATTATCCTTTAATTTTTTGGGTATTTTTTTATTAATTCCAAC  
441401 GGTAAATCAATTTGATTATTTTAGAAATCAACCCCTCTTTTCTTAGCT  
441451 TTTCAATTTCTTTGAAAGCAGCATTTTTAATACTAGTAAAAGTTTTATAG  
441501 ATATTTCTTAAATTCTTAGAGTTAGCAACTTTAAAAACAGTCGGTTTTGT  
441551 AAAGAGGTTACACTTATTGGTTTTTTATTGAATGAATAGTTTTTTCAAG  
441601 CATCTTCTGCAGTGTGGGGAATAAAGATATTTAAAAAACTGATTAGTTGT  
441651 GTAAAAATATAGTTTAAAACAGCTTGTTTAGCTAAACGATTAGGATTATT  
441701 TTTAGCATCACAATATAAGGTGTCTTTAATTATTTCAAAGTATCAGCTTG  
441751 ATAGTCATAAAACAAACTTATTAATCACTTTTAGGCAACCTAAAAAATTA  
441801 TATTTCTCTAAAAATTTCTCAATTTGTTCTACTAGTGAATTAGTTTTATG  
441851 GATAACTATTTTGTCTTCTAGTGAAAACCTTATAATCATCCATTGATGTAA  
441901 AGTTAAATCCATTAATATTACCCAAAATAAAACGTAGTAACTATTTCTA  
441951 ATTCTGCGGTATTGTTTCAGCAACTTGTTTAAGAATATTAACACCTATTTT  
442001 GTTATCAATTTGTCAATCAGTATTAGCAACTCACAACCTTAATATATCCG  
442051 CTCCATATTGATCACAAATTTTTAAAGGATCAACTATGTTTCCTAATGAC

442101 TTTGACATTTTATTGCCATTTTCATCAAGTGTAACCATGTGAAACAAG  
442151 TGATTTAAAAGGGATTAAATCATTTTGAATAATCCGCAATTTGAAGAAG  
442201 AGTTGAACCAACCCCGATATTGATCAGAACCTTCAATATAAAGATCAGCT  
442251 ATTGAACCATATTTATTTATTTCCAAAACATTATAGGAAGAACCTGAGTC  
442301 AAATCAAACATCTAATGTATCAATCTCCTTGTGATACTTAACTCATTTTT  
442351 TGGTTTTATCAGGTTTTAAAAACAAGTTACATCTTTTTCAAATCAACTA  
442401 TCAATACCATGCCTTTTCAATTGTTTAATTGTGTATTGAATTGTTGAAAA  
442451 ATCTAACAATGGTTTGTATTGTCATAACAATTGGTATAGGCAAGCCCC  
442501 ATACTCTTTGACGTGAGATACATCATTATCACGTTGTAAAAGCATCTCT  
442551 TTTAATCTCAATTGATTTTTTGAATTTAAAAAATTAACCTGATTAATTTG  
442601 TTTTTTTAACTGCTTTTTTATTGATTTAGTTTTAATGAATAATTGTTTGG  
442651 AAGCACGGTATATAACTGGAGTTTTTGAGCGTCAATCATGTGGTTCGCGG  
442701 TGGGAAATAACTTCAGAAAAAATAAAGCTATTGTTTTGTTTTAAACGATT  
442751 AATAATTAGATCATTTGCTTTAAGATAAAAAACAATTCTCAAGTTCTTTAT  
442801 CATTAAGTAAGTTATTAAATACACCTTTCTCATCAATAGAAATCAAACT  
442851 TCTTTAATCTTGTTTTTTGACAAAGATAAAAAATCATCAATCCAAATGC  
442901 AGGGGAGCTGTGAACAATACCTGTTCCCTCATTATCAACAACATGTATTC  
442951 CCATTAGAACTGGTAAAACCTTGTTATAAAAAACAATGAGAATAGCTTGAA  
443001 TTTTTTAAATTTGAACCCCTGAATTTTTTTAGTTTAATTGCATTTGTTCA  
443051 ATTTAACTTATTTGTAAAAACTTCAAATAATTTTTCCAAGATAACAAATT  
443101 TTTGTTGGTTATATTCAAAAAGAAGATAATCAAATCAGGATGAATGGCA  
443151 ATtGCTTGATTAGTTGGTAGTGTTCAAGGAGTTGTTGTTCAAACATAATA  
443201 ATTAGCATTTTCATCTAAAAAATCACTTTTAGAACTTTAAAAGTTAAAT  
443251 AAAGTGCAATTGAATTAACTTCTTTATATTCAATTTCCGCTTCAGCAAGT  
443301 GAAGTTCTTGAAATGGTGATCAATAAGTTGGTTTTAAATCTTGAAAAAT  
443351 GAGCCCTTTTTTAAATTGCTTGTAATAATAGTTCAAGTTCCTTAAATTGAA  
443401 AACTCTCATCTATTGTGTAATAACAGTTTTGAAAATCATTAAAAAGTCCC  
443451 AGTCTTTGAAATTGTTCTTTTTGAACTGCAATTTGTGAAAGTGCAAACCTG  
443501 ATGACATAATTTtCTTTTTTCAACAGTTGAAAGATTGCTATAACTACTAG  
443551 GGTTTTTCTTACTAACTGCATGTTCTATTGGTAGTCCATGACAATCCCAA  
443601 CCAGGAATAAAAAACAACATCATATCCtTCATATAACCAACTACGTAAAAT  
443651 GAAGTCTTTTAAAACTTGTTAAGAGCATGTCCACATGAATACTACCAT  
443701 TTGCATAAGGTGGTCCATCATGCAGTATTTTTATCTGTTTTCTTTATTC  
443751 TGTTTTTTTTAATTTTGAAGACTTTTTTATCTTTTCAAAAATCATGAAA  
443801 ATTCTTTTCACTAGTAGATAAATTTGCCTGCATCGCAAAGGATGTTTTAG  
443851 GCATTAACAATGTCTTTTTTAAGTCCATTAAATCAGAGTAATTTTATTAA

443901 TATTTATCTAACTTACATCTGATGTATAAATCAGTAATAAACATAGTTTT  
443951 ATTTTGTCCAGAAATTCCTAATAACACTGGCAACATCGTACGTAGTTGCA  
5 444001 CTGCTTTTAAAGCTAATCTACACTTAATTAAACCTTATGGCTTTTTCTTA  
444051 AATGATAAAAGGATGGTTAGAGCTGGTTTAAATTGTTGAGATAAAATTCA  
444101 ATTATTTGAACACAAATCATGAGAACATTTCTTACAAGCAACCACTGAAA  
10 444151 ATAAACTATTTGGCTTTTAACTAAAAGTGGTGATAAACTCCTGATCAA  
444201 ATTTGCATGACAAATAAATTACCAAACGAACCTTACTTTGTTTTTGGTCA  
444251 GGAAACAAAGGATTACCTAAAACAATCATGGATAACTTTAAACAAAACC  
444301 AAATTAGAATTCCTATTTGAAATAGTGTTAGAAGTATTAATCTTGCTAAT  
15 444351 GCAGTTGTCTGTATTTTGTATGAATATTCAAAGCAAAATCAATACTCTAA  
444401 TTTAGATAAACAGTGGCTTAAGAAAAGTTAAAAACGCTCTTTTAAAAAT  
444451 TAATCAAAGTCCTTATTTTTATTCAAAGATAAGTTTGCTAAGTTTACTA  
20 444501 AAAAACAATTAGTGCTGGAATTGGGTTGTGGTAAGGGTACTTTTTTAATC  
444551 AAAGAAGCACAAAAAATAACAATTTTCTTTTATAGGAATTGAACGTGA  
444601 ACCTACAATTGTTTTAAAAGCAATTAACAAAATTAACAAGTTGGATTTTA  
444651 ATTTGGAAAATATCTTATTGTTGTGTACAGATGCAAAACAACCTTGATGAT  
25 444701 TATTTTCAAGCTGAATCTGTTCAAAAAATCTTTATTAATTTCCCTGATCC  
444751 TTGACCTAAAAAGCGTCATATACAAAGACGCTAACAAGTCCAGATTTTT  
444801 TGAAACTTTTTTGAAATTTACTAGTAAAAAATGGCTTAATTGAGTTTAAG  
30 444851 ACTGATAATGATAAGTTATTTGAATATACTTTAACAACATTGCAAGAAAA  
444901 TAGTCAAATTTTTGAAATTATCCATCAAATAACTGATCTTAACAATTCTG  
444951 AATTCAGTTTTCAAATAGTATCACTGAATATGAACAGCGCTTTATGGAA  
445001 TTAGAAATTCCAATTAAAAACTAGTGATTAAGAAAATAATTTAATTAAA  
35 445051 GTTATTAGAATAATTATTAGCTTGATGGCGATTGTGGCGAAGTGGTTAAC  
445101 GCACCTGATTGTGGATCAGGCATTTCGTGGGTTCAATTTCCATCAGTCGCC  
445151 CCATTAAAGATTCAAAGAGCAGCAGTTAGCTGCTTTTTTTTATTAGCTAG  
445201 TTTAGTGGAGTATAAACACTATCCAAGAAATTTAAAAAATCAACACTAAC  
40 445251 TCTTACTGCGTGTGTTTAAATCCATAAGATTTTTGTGATCTTTGAACTG  
445301 CTGGTTGAGAAGATTGTGGTGAAGTAGGAGTAGTATTTGTCCATTACCA  
445351 CTACTTGAGTCACCACCTGAACTGCCATCACTACCGCCCCCTTCACCACT  
45 445401 TGAAGCTGGTGGGGTTGAATCACCCTGACCTGATCCAGGTGCATTAGGAT  
445451 TTGTAGAGTTATCCAAACCATAAAAAATTAGCTCTTATCTTATTAAGGTTA  
445501 TCTTTTCTAAAAGCAATCACAATTGCTTTAGTTACATCATTACCAACTGT  
445551 TTGAGCATGCACATTTGATTGATTGATTAAGTTAGCTACATTACCACCAT  
50 445601 AAGTACGTTGAATAAAATCAACTATTTCTCTATAGCGAACTGCAGAAGCA  
445651 TCTGATCTTCTAACTTATTGGAATTGTCTTTATCTTCTTGACTTGCAAG

445701 TTCGTTTTTCTATCCACAACAGGAAAACGTGCATATGGGTTTCACTTTA  
445751 CTGAACCAGGAGCAATATCATTCCAAATTA AAAATTTAACTCCGTTTGGA  
445801 TAAGTAGAATAACGGTTTTGACCTGTCTGATGGTGGTACCCAAGGTACC  
445851 TCCTCAACTAAGAGAACTTGTACCTTGATTAGTAGAACCGTTTAGAAAAAT  
445901 TAATTTGGGAACTATCTGTTTCGGTTGCAATAACAACCACATAATTACCA  
445951 TCGTTATATGATCTGGTTCCAAAACTAAGTTTCTAAATGTTGTACTGTT  
446001 AACAGGCAATTGGTTGTAAGCTGTATTTTTTTCCACACTTTCAACAGAAA  
446051 GTTCACGAAAAAAGACTGATCGATGTTACTACAAGAACTTAAAAATCATT  
446101 CCTGTTCTAGTAATAAACTAACCATGCTTTTTTATGTTTTAGATTTCA  
446151 AAAAAAGACGCTTCATTTCTAAATTGACTGGTGTGCGAGACCAGACTTGAA  
446201 CTGGCACAGTCTTTAACGACCACAAGCACCTCAAGCTTGCGTGTCTACCA  
446251 TTCCACCACTCCGACTATTTGCTTGTAGTTAATATTGTTTATATTAATAA  
446301 AAATTTTAATACAAGAGTTAACAAGGCTATTAGCTTGTACTAGCTTAAAC  
446351 TAGGAATATAAAGGTGTTATTTCAAGCTAAATCCCGCTTTTTTCTCCTT  
446401 AAATTCAACTTTTTTTATCCGATTATTGGTAAATAAATCAGTTTAAAAAG  
446451 TTATTAACAAAATGTTTATAAGTCTCAAAAAAGGGTTGTTTTAGACTGTT  
446501 TTTAATGTCAATAAGTTGTAAATAAATGGCAGAAAAATCTTTTTTTAGCC  
446551 TTTAATGCAAAGTAATTTCAATAAATGGAGGATAGCGTCTTATACTCTT  
446601 TTTACTTTTGAACGTATATGCAACCCAACTATTACCGTGTGATCAAAAAA  
446651 GCAACATCATTTTTCTGGATTAGAAATGATCTCTCATGCTTATGGTCAAAT  
446701 TGCGGGAGTGGAAGTTGTTGGGTTTTATTTATGACTAATAACAGAAGCTA  
446751 ATATTCAGGCGTTCAACAGTGAAATTAGAACCCCATTTCCAGGATTACAA  
446801 AATGCCTTTAATCCTTTTGAAATTAAAAAAAACCAAGTCTCTGAATGGAT  
446851 TTATAAACTATTAGCAAATTAGAGAGTCTTGGTTTAGTGAGAACTTTTTT  
446901 TTTCAACAAAACGCTCTGAAATAACTTTTGTATTATTGATCCTTTAGAT  
446951 TGGAAAGAATTTAAGCAAAACAAACAATTAAAGAAAAACTAGTTGAGGC  
447001 AATGGGAAAAGTTGAATATGACCGAAACTGCTTAGCTTTTGATCAAATCG  
447051 ACAATCTTCAATTTGATAATGCGCTTGAAATCTCTGCTAACTTTGAAGTT  
447101 AATTTCACTGCAAACCAAAGCGATGTTTGATTTAGCTTTAACTTCGAGGA  
447151 ACTACATAAAGAACTTGTA AAAAACAACTTTTAATTTCTTTAGATGAAA  
447201 AAGCTAAGACTTTAATTAATGGTTATTTTGAAAAATACAAGCTTTCATTG  
447251 CAACAAATTACTGATTGCATCATCAACAGTAGTACTCAAGAGAATGAGCT  
447301 TGATTTTCAAAGTTAGAAATGATGTTTTTTCAAATAGTAAAAAATGATA  
447351 CAGCTCCCATTTTAGAAAACAGTTTCAAACAACAAAGACTTTTTTTATAAG  
447401 AATGAAATTTTAGATGAATCAACAAAAAAGCAATAACAGACTGTCATGT  
447451 AAACCTCAATTCTGAAAAATACCTTTTTCTTCTATATGGAAAGATAGATG

447501 AATCGCAATTGCAATTAGTTAGACAATTGAGAAGTGATTATCAACTATTA  
447551 GATAAAGTAATTAATTTAGTATTAGACTTTTCCTTTTGAAAAATAACGG  
5 447601 AATGTGAAGAGAAAAATACATTCTAAAAATTGCCCAATCCATCAAAATTA  
447651 ATAACAGTCAAAACAGTTATGAAAAACCCTTAATAATTTTATTAGAGCA  
447701 CTAACTTTAAATAAAAAAGCATTCTTTAAATAATATAAAACCAGTTGAAAA  
10 447751 AACAAATTCCTTTACTGAGTATTTTGAATTTATTAAATAATGAAAATTC  
447801 ACCAGATCAAAAAGATAAAAAGTCATTATTTAAAAACATTTTGCTTATT  
447851 TGAAATTAAC TGAAAAAGAACTTAATGATCCTAAGATACAAACACTTTTA  
447901 GAAGTTGCGTGGAATCATTTTGATCAGTG TAGAAAAATTAAAGAAAGAAG  
15 447951 ATGTAGTAATAAAGGTGATATCCATCTTCAAGCTGTTAGAGAGTGGTTAC  
448001 CTTGAGAATTTAACGCTAATCAACTTAAAAAAAATAGTACAAAAGAAACA  
448051 ACGCAAGTTAGTGAAAATGAATTTATGGGTAATGTTATGCTCATGCAAAC  
448101 TATTTGTCCTAAATTAGTTAATAAAGCAAAC TGATTTGATTTAAC TTATG  
20 448151 AGCGTTTTATTGTTACAAAACCAAAC TGATTTAAATACATGGATTTGATT  
448201 CCAATGATCCAAAATTTACCAGTAACTCCAAGTGATAAAAAATAGTTTTGG  
448251 TTATGCATACAAAAGATATCTAATCTTTTTGAACTGAAAAGAAAACAA  
25 448301 AGAAAAGGATATTTTTTTTCAATTTACAAAAGAATAACATTAACAATATG  
448351 GCAGCTTGATGTAACTTGTAAGTAGCTAAGAAAAATATAAAAGTTGC  
448401 TTTAATTTATTGTGAAGAATTTGTTAGCAGATATGACAAAAGTTATTGAA  
448451 AGGTAGATGATGATTTAAATTTACTTGATGAGGCAAAAGTAATCATATTC  
30 448501 ATTGGTTTAGGTCAGGAAAGTTTTCATAACAAAAC TATATCTTGTTTAT  
448551 GACAAGGCTTTTTATAAATTGTTTTTTGAAAAGAAAAGATGTTTTCTTTT  
448601 TTAGCACTACTTATAGTGATGGTAATGGATTAATTCAAACATTTAAAAAC  
35 448651 CAAATTATTAGTAGTGCAATTGAGTAAAACACTTTTTTGAACA ACTTAA  
448701 TGATTTATTAATGATTAATATTTAAAAATTACATTCCTTCACCAATAAAT  
448751 AGCTAAGTTTATGTAAATTTATCTTGATTACCTGGAGTGGCGGAATGG  
448801 TAGACGCGGTGGACTCAAAACCCACTAGGAAACTGTAGGAGTTCAAGTCT  
40 448851 CCTCTCCAGGACCATAATTAAATACTTAAATTTACACTACGAAATTACAA  
448901 GCTCAGTTTAAAGCTGAGCTTGTTTTATTTTTTATAGTGATTTCTATTTAG  
448951 CTAATGCTCTTTTTCAATAAAACTTTTGAAAGGAACGCATAATTGGCACT  
45 449001 CCAAAACA ACTAACAAGTCCAAATTTACCAAATTA AAAAACGAATATAA  
449051 ACAGAAAATCCCAGCCAATAGTTATTAATTCCAAAGAAAAGAAATGAA  
449101 AATCAGTGTCTTGTTATATTGTTTCAGCAACTATTAAAAAGTTAGGTGTT  
449151 TGAACATAACCAAAGTAGTATCAAAACAAAGGTGTTATCAAATACCGTT  
50 449201 AAGCGTTGTTAGTAATAAAGCATTGGATAAGGTTGTAAATAAAAACACAA  
449251 AGATTCAACAAAATCTTCTTTTTGAAAATAAACAAAAATAAGCCTTGTA  
55

449301 AATAAGATAGTCGATAAGTTAGCTAAAGTTACAGTTAGAACACCAATAAC  
449351 ATTATTAGTATTTCAAAAAAACTAGTTAAAGCAGAAGCTAATGTAATTG  
449401 TTAAGCTTCAACCTAGTGACACAAAAAAGCACATGCAACTAAAAAACA  
449451 ACGGAAATATCAAAAGTTAGTTTTAGTTGTGAGAAAAAAGGAATACTAAT  
449501 AAATTCACTAATTAATGATGTAATGATGGCCAAAGCAAGCATCATTGCAC  
449551 TAAAAGTAATATTAAATAACTGATGGTATGATTTTTTTGGCAAAAAAAC  
449601 AGTTTATTACCATTTCATTATTTAAAAGACTCTTGAATTATTAGTTAATAA  
449651 TAATATTTATTGATATGGACAAATTTTAAATTGATGTTATTGTAGAAATC  
449701 CCTAAAAACAGCAAAATAAAGTATGAGTATGATCGTCAAACTGGTCAAAT  
449751 TCGCGTTGATAGAATCCTATTTGGAAGTGAATCATATCCACAAAACACG  
449801 GTTTTATTAAAAATACATTAGATTGAGATGGGGATGAACCTGATGTTTT  
449851 ATCTTTCAGATCAACCATTTTGCCTGCAACAGTTGTGCCTACAAGAAT  
449901 TG TAGGAGCACTTGAGATGATTGATGATGGGGAAATTGATACTAAGTTAT  
449951 TAGGAGTTATTGATTGTGACCCTAGATATAAAGAAATTAATCAAATTAGT  
450001 GATTTACCTAAACATAGAATAGAAGAAATCTTATCTTTTTAAAACTTA  
450051 TAAATTACTTCAAAAAAAGACTGTAATTATTAAGGGTTTAAAAGATGTTT  
450101 GTTGAGCTAAAAAAGAATATGAAATTTGTTTGCAATTAATGAAAGATTAT  
450151 GGTCATTTATCAAAAGATCAATTTATCCAAAAATGCAAATCTTCATCC  
450201 AGAACATTACCAAAAGTAAATATGATAAATGCCAATCGCGGAATGCTTTT  
450251 AGAGACAATTGTTAATCAAACAATTGCTAGGTTAAAGGATCATCCAGATA  
450301 TTTGACTGGAAAAGCGGTTCTTACCTATTAAGCCTATAGCTTTTCGTCAT  
450351 GCTCATGTATCTGGCAACGTATCACAAAAATCAAAAAGTATTATTATGG  
450401 AATTTACAAGGGAATGTATTTTGATTTTGAAGCAAAACAAACAAATAAAA  
450451 GTAATTTTCCAATTGCTCAAATAGCAGAACCAATTAATCATTTGAAA  
450501 AGAATTGACCAAAATTGGAGGAGTTAGCTTCTTGCTAATTTACTTTCAAAC  
450551 TAAAGATCAAATTTTTGCATTTCACTAAGGATCTTCTAGAAACAATAA  
450601 AAAATCAAGAAAGCAAAACAATTAAGGGAATTGATAGAACAAAAATCT  
450651 CAGAAAGTTCCACTATTGTATCCTGGTATTATTGATTTAATTTCAATAAT  
450701 TCAAAGCTTTAAAAATTATTAGTCTGCGTACTTTCAACGCACTTTAGCTG  
450751 CAGTTTCTTTGATCGTTTTGCTTGGACTGTAGCGCACTAATGGTTTTGGT  
450801 GGGATATGTCTAATCTCACCTGTTTGCATATCCTTCTGATAACGTGCATT  
450851 TCTAATAGTAATCCTTAATTTACCTAAATTTTCAAGTAATATACAAACAC  
450901 TTCTACTTACCAATTCATTTAGTAACAATGTGTTAAGGTATTTAAAGATT  
450951 TCCTTAATTTTTTTTTCTTTTATACCAGTAGCAACTGCAATTATTTTATT  
451001 GATTTCACTACGAGAAAGTGGCTTACTTGTATTTGATGTTTTTTCCATAT  
451051 AATTATTTTTTAAACTTTATTAGCTCTGTTATTGCTAAAAACAAAAGAG

451101 AAACAATTTAACGCATTCTATTTTATTATTGATTCAACAATTAAATTAAA  
451151 ACACCTTATAAAGTAAATTTTTAGACAATTATTTCTATTCTTAAGACATGG  
5 451201 AACAAAACAATATTAAAGAACAACCTTATTTCTTTCTTAATCAAGCATGT  
451251 TCTACCCACCAAGAAAGACTTGATTTTATCTGTTCTACAAGAGAAAGTGA  
451301 TACTTTTTCTAGTGTTGATGTACCACCTGAACCCATTAAAAATATTATTG  
10 451351 AAATAACTAAAGATGAAAATCAACAAATTGAAATTACAAAAATAGCTGTT  
451401 AATAACATTA AACATTATCTTCTGTTGGTGCAACCGGTCAGTATATGGC  
451451 ATCTTTCTTTCAACGAATAGTGAGCCAGCTATAATATTTGCGTCATTT  
451501 ATTTTTTATATCACTTTGGTTTTTTAAAAGATAACAATAAAAAACAAATA  
15 451551 ATAAAAAAGGCTTATGAACTATTGCTGATAACATTGCTGACTATTTAAA  
451601 TGAAAATTAGGTTTAAAGACTTATTATTTTGTGTAATGGTAATATTGTCTT  
451651 TAACAACCTGCAATGTTGTATCCAACACCTTTTTTTATCTTTCCCTGAAGG  
20 451701 ATATATTTAGCTATTAAAGTTGCAACACTATGATCAATAAAGCGCTTAAT  
451751 TGGTCTTGACCAAACCTGTTGATCAAACTACTTTTATAGATAAACTCTG  
451801 TTAGATTTGAAACAAAATTAAAAATAAATTTTGTATTATTCAAGCGTTTT  
451851 GAAAGTTGTGCCAACAAGCTGTTGATTATCGATAAACTGTATCTTTCTC  
25 451901 AAGAACATTGAAAAATACTATCTCATCAATACGATTTATAAATTCAGGAC  
451951 GGAAATGTTTCTTTAGACTTTGAATGGCCAAATCTTTTTTTCCTTCTAAA  
452001 AGAAAATTTGAACCTAGGTTAGAAGTCATAATTATCAAAGTATTTTGA  
452051 ATTAACAACCTTTCCTTGTGAATCTTTTAAAGTACCATCATCTAAACCTT  
30 452101 GTAATAAAACATTAGTTACATCAGGATGTGCCTTTTCAATTTTCATCAAAT  
452151 AACAAGACGCTATAAGGTTTTCTTCTAACCGCTTCAGTTAGCAAACCTGA  
452201 TTGTTTCATAACCTATGTACCCTGGGGGTGCACCAATTAATTTAGCTACTG  
35 452251 AATGTTTTTCCATATATTCACTCATATCAAACGAATCAGAGCTTTTTCA  
452301 TTGTCAAAAAGAACTTCTGCTAATGATTTGGCAAGTTCAGTTTTACCAAC  
452351 ACCAGTAGAACCTAAAAAGATGAAAGAACCAATAGGTTTGTGTTGGGTCAT  
452401 TTATATTTACTCTACCTCTAATTACAGTGTTAACAACAGCATCGATGGCT  
40 452451 TCATCTTGTCCTTTAACTCTTTTTTTGATTTTCATCACCTAAGTGCAAAAG  
452501 TTTATCCTTTTCACTTTCTAATAGTTTTTTAAGTGGAATTCCTGTTGTTT  
452551 GTGAAATAACTTCAGCAATTTTCATTTTCAGAACTTCAGTTTTAAATAAA  
45 452601 TCGTGCTTAGAAGTTGCATATTTTGTGTTGTCACCTTCAGTTCTTTTTT  
452651 AAGTCTTGGGATATCAGAGTACAGAATTTTAGATGCACTTTCATAATTC  
452701 CTTCACTTTGGTATGTCTCTAGTTTGGTTTGAATTCCTCAATCTCTTTT  
452751 TTGAGCTTATTAATGTTTTTCAAAATCAGCCTTTTCTTTTTTTCATTCAAT  
50 452801 TATAAGTGAATCACGCTTTTGTGTTAAGAGCATCTAATTGTTTTTTTAGTT  
452851 TCTCTAAATATTCTTTCTTTGATTGTTGTTATCATTTTCCTTATCTGT



452901 TTAAGAGCTGCATACTCTGTCTCAAGATTGATTATTTACGTTTAAGACT  
452951 ATCTATTGCAACTGGTTCAGATGACATTTCTGTTTTGATCTTAGCAGCAG  
5 453001 CCTCATCAATAAGATCAATGGCTTTATCAGGTAAATTACGTTCAATTAATA  
453051 TAACGAGTTGACATTTCAACAGCAGCTACTAAAGCACTATCAAAAATAGT  
453101 GATGTTATGAAAGAGTTTCTCAACGTGTTTTTAAACCACGCATAATTGTTA  
10 453151 GTGCCTCTTGACTACTAGGCTCGTTAATAAGAATTTTTTGAAATCTACGT  
453201 TCTAAAGCGCCATCTTTTTCAATGTATTCCCGGTATTCTTTTAGAGTAGT  
453251 AGCGCCAATTACTTTTTATTTCTCCTCGAGCTAGCATCGGCTTTAATATAT  
453301 TGGCAATATCCATTGCACCACTGCTAGAATTACGTCCTAATCCAACATTT  
15 453351 TGGTGAATTTTCATCAATAAAAAGaATAATCCTGCCATTTGATCTTTTTAC  
453401 TTGCTTAAGAATGGTATTAATTCTTTTTTCAAATTCACCTTGGAATTTAG  
453451 TGCCAGCAATTAATCCAGAAAGAGATAGTTCATAAATTTCTACATCCCTT  
20 453501 AAATTTAAAGGTACATCATTACTAACAACCTCTTCTAACAAAACCTTCTAC  
453551 TATTGCGGTTTTTACCAACTCCAGGTTCAACCAATTAAACAGGATTGTTTT  
453601 TGCTTTTACGACTTAATATCTCAATTAAACGACGAATTTGTTATCTCTT  
453651 CCAATAATAGGATCGACCTTATTTTTTAATACTTCATCGTTAATATTACG  
25 453701 ACCAATTTCTTGCAAAAAATTACGATTTTACCAGCAGGTGTGAAATTAA  
453751 TATTCATTTTAATTGCTCACTCCTTTTAATGCAAAAATTATATAAAATTA  
453801 GCACTCAAGGCATTGAGTGCTAATTAAAACTAGGTTTTTTGTTTTATCT  
453851 CTAATTTATCTAATCAGAGTTGATATTTTTGTCAAAATAATTAGAAACCT  
30 453901 AAAATAACTATTAACATATTTTTTTGTGCTTGTTTTCAAATTGAGGGAAAT  
453951 AATGCTTTTAAAAAGTATTCTAATCGTTTTTCAACTCATTTTCGATAGTT  
454001 TAAAATTGCTTCTGTTTGGGGCATAATCTCAGTTCATTGAAAAGCAAATA  
35 454051 ATAAACATAAATAACTGTTTCAAAAACAAGCTTACGCTTAAGTCCACCA  
454101 TAAATATCAATAAGTTTATTTGCTGTTTCTATGGTTAGTTCTTCACGAAT  
454151 AATATTAGCTATTTTCATAATAAGGATTATCAACACAAGATCATTCAAAT  
454201 CAATAAGGATTACTTGCTTTTTTAGGTGTTCAACCAAATTATCAAAAGTA  
40 454251 GCATCATGATGACAGAGAGTTTTTGGTATGTCAATATGCTTCTTAGTTAA  
454301 ATTAAGATATAACCGTTTATAAAAAGCGGAAAGCTTAGTTTTTTCAAAT  
454351 AAACCAAAGGATCAAATATTAAAAGTTCATTAGCAAATGGTTTTTCAGTCA  
45 454401 ACTGAATGAACCTTTTTTTAAAGATTCAACCAATCTGCATAAAAATAGATC  
454451 AGTTGCTCTTTTAGGTTGAGTGCCTTCTATCCACCTTTTTATAGCATTAC  
454501 CTGTTGTTACATCAAAATAAACAAATGGGTTTGAAAAAAAGGTTCTACT  
454551 AGTTGCAAAATAATTTGTTCAATTTCTTCTGTCTAAAATAACATCTTTTCT  
50 454601 TGAAAGTCTTATTTGAAATTTACTATGATCTTTCAATTCACAAAAAAAG  
454651 AAAAATTAGTAAACCAGAATGAATTTGCTCTATCTTGAAATATCTGTT

5

10

15

20

25

30

35

40

45

50

55

454701 TCTACAACCTGAAGTTTTTCACAAAGAAAAGCAACCGCTTTTTTTAAATC  
454751 CATTAATTTTGTATGATTATTTTTTAATGTTTGTACTTACTCTCAAAGCAT  
454801 CTTCTACAATCATCAATTCCTCATTGTACGAACCTAAAAATTTGATAC  
454851 TTGCTTTCATTGTGTGAAATTAGAGAACTATCTTGATAATTTCCAAATAA  
454901 ATTACTGTAGTTTAAAACCAAGTGAAGCAACTTTTCAATTATTAATT  
454951 GCACACAATAACTAGCATTTCACCAACTCCCCAGTAAATACCAAGCTA  
455001 TCAATTTTACCTGAAAGTTGATTTAGGTATTTAGCAATATAGTCAGCAAC  
455051 ACGATTAACATACATTTTTATAGCAATATCATTAAATTTCTGGTTTATCAA  
455101 AAATATCACGCATGTCAGAACTACCTGTTATAGCAAACATTCCACTCTTT  
455151 TTATTTAATTCAATTACAACATCATTACATGAAAGCTTTTGCTGTTCAGC  
455201 AATGTAATAACAATGGCAGGATCAATATCACCACTACGTGTTCCCATTA  
455251 TTAATCCTTCAAGGGGAGTGAATCCCATCGATGTGTTTAGTGATTTGCCT  
455301 TGTTTAAATCGCACAAAACACTTGCAACATTACCAAGATGACAAACAATTAA  
455351 ATTAAGTGGTTTTTTATTAACTTTTTTTCTAAAACTCGTTAATGTATT  
455401 TATAAGAAGTTCCATGAAAACCATATCTTCTTACTAAGTTATTTTCTCT  
455451 CAATTTTTCAGGAACTGCATAAAGATAATTTTCCCTTGAATAGTAGTGTG  
455501 AAAAGTGGTATCAAATACAGCAACATTCTTAGCAGTTTTTATCTCTTTTA  
455551 GAAAAATTTCAATAACATCTGCTTCTGGTTTATTATGAAGCGGTGCTAAC  
455601 TTAATGAATTCTTTATTTTTGCTAGTGAATGTGTATCAACAAGAACTGC  
455651 ATCTGTAAAATAATTTGCTCCTTGTAATACTCTATGCCCTATTAGCCCAA  
455701 TTTCTGAAAGTTCAGTAATAATTTtGTTTTTTTTAAGCGCATTAAAAAA  
455751 TGCTTAACAGCAAGATTATGATCATTAAATTGAACCTTTTCTTCTATCTT  
455801 TTTTGTATTAATTCAGCTTAAAAAAACCATCAATGAAAATACGTTTAC  
455851 AAAGTCCTTTAGCTAGTACTTGTTTTTTATCATTAAAAAGTTGAAATTTA  
455901 ATTGAACGTCTACCTGCATTAAACAACCAAGATTTGTGACTTTGCATTTA  
455951 ACCGAAGAATATTTACCTTATTTATTAATAAATAATACTAAATTAATATA  
456001 GTGTGGAATAATTAAATGTTTTAACTAAAAAGAAATATTATTAAATCTTA  
456051 AACAATGAAAATAAAAAATGCTATATTATCGCTGTTATTTTACGCTTTTA  
456101 TTGGTTTTCTTTTTACTTTTTATCTTCACTTATAGGGATAACAGATGTT  
456151 AATAATGCAAAAACAGTAGCAACTGTATTTTTTGTATTAGCAACATTAAT  
456201 AGTTGTTAATGCTATTGTCTTCTGGATTCTTTATCTATTCAAAAAAAGA  
456251 ACGTAGTTAAGTAAATTTATTTGTCACTAATAGTTTTTTAGCACATTAAT  
456301 TTGATAGAAAACAAATTGAATGTAATATGGAACTATCAGAGAAACACTT  
456351 TCTTCTATACAAAGAAGCAATTTTTTATTAAATGAAAGCGCACAAATTCT  
456401 CAATACGTGTGTAAACAAGAACACATTGCTTGACGATAAGCTGCGCAATT  
456451 CGATTAATTTTGCACTTAGCATCATTAAAGCTAGCAGACTTTTGTCTAAAG

456501 GATGATACTGAAAAAATTAATCAATTCTTAGGTAAAACATATGATTTACC  
456551 ATGAGAGTTTCAATTTAACCAAAAAGACAAGCATATAGAATGCACTGTCA  
5 456601 AAGACAATTTTGGTCGTGAGAACTAATAAATTTGATTTTTCAAATTGGT  
456651 GATGCTATTGAACTTATCATACTACTTTAATAAGATTCAAAATTCCCAA  
456701 GCATTGTTTGAATGCAAGGGATCAAATCAAAAAAATAATGGAGGGCAAAT  
10 456751 AAAATGATTACATCTATCTTTGGAAAAGTTACTTTTGTAGGCAAAAGAA  
456801 AAATAATTGTTGAGCACAACCTGGATTTTCATATTGATTTAATACAAAAGAA  
456851 AACCATAAATTTGAAAAAATTTGGAAAAAATAAGCAAATTTTTGTCA  
456901 TATTATTAATAAATTTGTCGCTAACCAAATTATAGAAGAGGCTTTTGCCT  
15 456951 TTAATACTCTAGAAGAAAAAGAGTGGTCTGTAGATTAATAGAACTCAAT  
457001 GGTATTGGTAGTAAACTGCACTTAATTTGCTCAATAATGACCTTGAGGA  
457051 AATTAAACAATACATTCTGGAAAATAACTACAGTGCATTATGTGGTATTA  
20 457101 ACGGTGTAAATAACAAAATAGCTCGTGCACTTTTATCACTTGAAATATTT  
457151 GAAAAATCTGAAAATAATAAAAATATTAAAGGAGTTCAAGTTGCTGATGG  
457201 TTATGATGAATTGTTTGAAACACTAAAGTCACTTGGTTACAAACAACAAG  
457251 AAATTCAGGATGCACTAAAAATGATAGAAGTAAACCTGATTTTGATATA  
25 457301 AGTCAGTTAGTTGCAGAAGTAATTAATAATGTCTTTTAAGAATAATGA  
457351 AATTACAAATAAAACCGCCTAATACCTTTGATGAATTTGTAGGAAAACAA  
457401 GAAATAATTAGTCAAATTCATTAAGTATTAAAGCATCTAAATTAATAA  
30 457451 AACACAACCTAGATCATATCTTGTTATATGGCCACCTGGTGTGGGTAAAA  
457501 CTACTTTAGCCAGATTAATAGCAAATGAATTGAAAACAAAGTTGCAAATT  
457551 ATTCAAGGTGGACATTTACAAAACCAAGCGATTTCTTAAACGCAATTTTC  
457601 ACTCATTAAAAAAGGTGATGTTCTTTTATAGATGAGATCCATGCCGTAG  
35 457651 CACCTAATGTCAATGGAACCTAATGTATCCAGTTATGGATGTGTTCAAATA  
457701 CAAGTATTAATTGGCAAGGATTTTAATTCCAAGATAGTTGAAATGAAGGT  
457751 AAATCCTTTTACTCTAATTGGTGCAACTACACAACCTGGTAAAAATCATCA  
40 457801 ATCCTTTAGAAAGATAGATTTGGCGTTATCTTAAACATTAACATTATTCA  
457851 AATGCTGAAATTGAAAAGATGGTAAGTATCTATGAAAGCAAATGAAGTT  
457901 AGAGCTAAATTCAAATGAAATTTGAGCTATCACTGAACATAGTAAACAA  
457951 CACCAAGAATTGCAATTAGAATAGTTAGAAGAATATTTGAACAAAAAATT  
45 458001 GTTAATAAAAAAATAGACCTTGAGGGTTTGTTTAAGAATTTAATGATTTA  
458051 TAAAAATGGTCTGCAAAGTATTGATGTCCAATATCTTGAGGTTTTAAATC  
458101 GCCAAATGAACCACAAGGAATTAAGTCAATTAGTTCCATGTTAGGTATA  
458151 GACAGACACACTATAGAAAATAAAATTGAACCTTTTTTGTGCGTGAAAA  
50 458201 TATGATTCAAAAAACCAAAAAGGCAGGATTATTACAAATAGCGGAAGAG  
458251 AATATTTAGTTAACTTTTAAGCTTATTAGCTCTTTTAATAATTTCAAAAC

458301 CAAAACCTTTCATTAATATCAAAAATTAATTTATCAAGTGAAGATTCTTCG  
458351 CTTAATTTGCTAATTGATTTTGGTATGAATTGATAAAATAAGATTTTTT  
5 458401 CTGTCCTTCATCTGTATCTATCTTTTTTAAATCAAAAAAACTAATACCTA  
458451 TTAATCGAACGTTCTTTTCAGTATTAATTAATAGTCTGTTGAATAATCGT  
458501 TTTGTTATTGACAGTAGTTTTCTATAATCGTTTGAATATTTTTTCATTT  
10 458551 ATTTGAATGAGAATTAACAATAAAATCATTGCTTTTCAATTGCACAACCTA  
458601 TCCCTTTACACACTTGTGAAGAGAGTTGTAATCTTATAAAGAGCTGATCA  
458651 AATATTTGCGTTAACTTTTTATTTAACTGATTGTTTGAATAATTTAAATC  
15 458701 TTCTAACGTTTCACTGACTGCAAAAGAGCGAGACTTAACCTGATTGTTAT  
458751 TATCTGTATATCATTTGCCTAGTGAAACTGCTTTTAAAGATTCTCAAAAA  
458801 TTACCAAATACTTTTTTTAAAGCGAAGCATCTTCACAAACTGCTAGATC  
458851 ATTTATTTTGTA AAAATTATTTTTAAAACTAAATCAATATGTTTTCTC  
20 458901 CTATCCCTGGAATTTTCAGTAATTGGTAGTGGTCAAAGTTTTTTTTTAATA  
458951 TCCTTAACTGAACAACCTTTTAATTCCAAATGGTTTGTCTTGATTGAAAA  
459001 AATCTTAGCAATTAAAAAATGATCTGAGATGCCAATTGAAATTTTGATTC  
459051 TCAAGTTTGA AAAACAAAATTTTTATTTTTTTTCGCTATTAAAAATGCC  
25 459101 TTTTTAAATGAAATGTTTTGAAAACAAGCAACCCCTTCATCAACAGAAAG  
459151 AACATCAATTTTAAATGAAAAGTGCTTTCAATAACTGAAAAATACGTT  
459201 TAGAATGTTTTCTGTAATTACGAAAATTAGAATGTGCAAAAATAGCATT  
30 459251 GGACATAGTTCTAATGCTTTTAAAAATAGACATTCAGATCTAATCCATA  
459301 ACTACGAGCAACATAGTTACAAGTTGAAACTACACTTCTTGAAAAGCGAT  
459351 TACCAACTATTAAGGGTTGATTAACTAATTCTGGATTTTCTAATCTTCA  
459401 ACAGATGCAAAAAAAGCATCAAAATCAAAATAAGAAAAATTAAATTTTT  
35 459451 ATCAATTAAATATTCTGGTTCAAAATATGTAAAGGTGTTAATCATATTTA  
459501 TCAAGTTATGTTATTATTTACTTGCAATAAAACCAAAGAAAATAACGAGT  
459551 TTTTAACTTTAATAAAGTTATCGAGGATTTATCATCGTTTGTGCTATTGC  
459601 GAATATTGTAGTTAATGGTAGATAGTAAGAAAAATAAAAAACAGCAGGTT  
40 459651 ACGGATTTTTCTAATTTACTCTCTCAAAGTAAAGGATTTGTTATTTTTGA  
459701 CTATTTCAGGAATGTCTGCTGTTGATGCAACTTTAATGAGAAAAAAGTTGT  
459751 TTAATAAGGGTAGTAAGATAAAAAATTGTTAAAAACAATATCTTAAGACGT  
45 459801 GCTTTAAAACTAGTAATTTTGAAGGTGTTGATGAATCGGTCAACAAAGG  
459851 AAAAATTGCAGTTGCTGTTGGTATTAACGAGATCTTAGAAACCTTAAAAAG  
459901 TTGTTGATAGTGTAGTTAAAGAAAAAGAGTTAATGAAATTTGTTTGTGGT  
459951 CATTTTGATAACCGTATTTTTAATAGTGATGACTTACAAAAAATAGCAAA  
50 460001 ACTCCCTGGTAGAAATGAACTTTATGGAATGTTTCTTTCAGTTCTACAAG  
460051 CACCATTACGAAAATTTCTCTATGCTCTTCAGGCAGTAAGGAATGCTAAG

460101 TAAATTAAATAAATAGaAAAAATATTATGGGAAAAC TAGATAAAAAACAAT  
460151 TAATTGAATCTCTAAAAGAGATGACTATAGTTGAAATTGATGAAATAATC  
5 460201 AAGGCTGTTGAAGAAGCATTTGGTGTAAC TGCAACTCCAATAGTAGCTGC  
460251 TGGCGCAGCTGGTGCTACACAAGAAGCTGCTAGCGAAGTTAGTGTAAGG  
460301 TAACAGGATATGCTGATAATGCTAAGTTAGCTGTTTTAAACTTTATCGT  
10 460351 GAAATTACTGGAGTTGGTTTAATGGAAGCTAAAAC TGCAAGTTGAAAAATT  
460401 ACCTTGCGTTGTAAAACAAGATATTAAACCAGAAGAAGCAGAAGaCTTA  
460451 AAAAGCGTTTTTGTGTAAGTTGGTGCAACTGTTGAAGTTAAATAAAGATGG  
460501 CAGTACAACAACGGCGTTCTAGTAAACACCGTCGTGATAAAAAGACGTTCT  
15 460551 CACGATGCACCTACTCTACAACTTTAAGTGTTTGTAAGAAATGTGGTAA  
460601 GAAGAAGTTATCACATCGTGTGTGCTCTGTGGTATGTACGGTGAAC TAA  
460651 GAGTTAAAAAGCTCACTAATTCACAGATAAATATTATTGTTTTTTTGCA  
20 460701 GTTGAATTTGTATTACTTTTATGCAAAATAACAGCATTTTTGTATTTTAA  
460751 ACGCTTAGCTCTGTTTAAAGAAATAATCCCTTTTCTGGCTAAACGATCTG  
460801 CTTGAGAATAAACAGAACTGAGATTATCTAAATTAATCTCTTTATTAAAT  
460851 TTTTAAACATTAGTTTTTTAGTTTAGTTTTTGTCCTTATTATTTAAATT  
25 460901 TCTCTTAATGTCTTGACGTAATCGTTTTTCGTTAGATTTAATATTAGCCA  
460951 TTTAGGTTATTAAATTAGTTTTAGAGTATATTATTATCTTGATTATATTGT  
461001 AACTAGAACCATATATGGATGGTGGACAACAAGGGAGTTTTTTTGGGCTT  
30 461051 TTAGTAATTGTTATTCCAATAATTTTGTTAATTGTTTTTTTTCCAAGAA  
461101 AAAAGGGGCACAAAAAAATGATTTTAGTGGTGAAGGAGGTAATCGATCAT  
461151 CAAGAAAAGATGAAGTGTGAAAAACAATTAAACAGTTTTTGCAAGAAAAG  
461201 AATGAACGTGGTAAAGAAATTATTAAAACTTTTGTAGCTAAAAAACCAAA  
35 461251 CCCTTTACATTCAAAAAAAGACCGCAAGCTTTTCAATCAAGAGATACAGG  
461301 CATATATTACTAGTAATAACTTAGGAAAAAGCGAAGCAAAACGTTATAAA  
461351 AATGAGCAAACTCGCTTAATGCAAAGAGAACTTTATTGTATTTATTTGT  
40 461401 TACAAAAGATGCTAAATCAACTGAAGTTGATGATGCTAGGATTATAGAAG  
461451 CTGAGGTTTATCAAAAACCTACAAAAACCAAAGTACTCCAGAGCGGCTA  
461501 ATTCGTATACTTGGTTTTAAAAAATTTTGAAACTGAAATGCAATGAATTCA  
461551 ACCATTAATGGTTCGTGAAGAAAAGAGAAAAGAAAAAGAAGAACAGAAAA  
45 461601 AACTTAAATTAGCTGCAAGAGAACTAAAAAAGAAGAAAAAGAAGAAAATA  
461651 AAAAAACCAAAAGAAATCAGAAATCAGAAAAATGTTTAAATTTGTTTTCT  
461701 TTGGTACTTCAACGCTTTCAAAAAATGTTTAGAACAACTTTTTTACGAT  
50 461751 AATGATTTTGAAATTTGTGCTGTTGTAAC TACGCCAGACAAAATTAATCA  
461801 TCGTAACAATAAAATAGTACCTTCTGATGTTAAGTCTTTTTGTTTGAAAA  
461851 AAAACATAACTTTTTTTCAACCAAAACAAAGCATAAGCATAAAAGCTGAT

461901 CTAGAAAAATTAAAAGCTGATATTGGTATTTGCGTTTCATTGGTCAGTA  
461951 TCTTCATCAAGATATTATTGATCTTTTTCCAAATAAAGTAATTAACCTTAC  
5 462001 ATCCTTCTAAGTTACCACTACTTCGTGGTGGTGCACCATTACATTGAACC  
462051 ATTATTAATGGTTTTAAAAAATCTGCATTGAGTGTAATTCAATTGGTTAA  
462101 AAAAATGGATGCAGGTCCGATTTGAAAACAACAAGATTTTTTAGTTAATA  
10 462151 ATGACTGAAATACTGGTGATTTATCCATATATGTAGAAGAACATTCACCC  
462201 TCTTTTTTAATTGAATGTACTAAAGAAATTCTCAATAAAAAAGGGAAATG  
462251 ATTTGAACAAATAGGTGAACCTACTTTTGGATTAAACATAAGAAAAGAAC  
462301 AAGAACATCTTGATCTTAATCAGATTTACAAGAGTTTTTTAACTGAGTA  
15 462351 AAAGGTTTAGCTCCCAAACCTGGTGGTTGGTTAAGCTTTGAAGGAAAAAA  
462401 CATCAAAATTTTCAAAGCTAAATATGTTAGTAAAAGTAATTACAAACATC  
462451 AATTAGGAGAGATAGTTAaTATATCTCGAAAAGGAATTAATATTGCTTTA  
20 462501 AAAAGCAATGAAATTATTTCAATTGAAAAAATTCAAATACCTGGAAAAAG  
462551 GGTGATGGAAGTAAGTGAAATAATAAACGGAAAAACATCCTTTTGTGTGTG  
462601 GTAAATGTTTCAAATAGAAATGATTACAAAGAGTTTTTTCCTTAAAAATTT  
462651 TGATCGCTCTAAAGAATTAATTCCTCTTTCATATAACGATGTTTTTAGCG  
25 462701 CTGTTAATCAGTTTCTGAAAAGCTATACTGACGTTAATGATATTGATATT  
462751 ATTGAAGAAAATTTGATTGAAGATCCAGTTTTTGAACCTGATGTTTTAGA  
462801 ACTTTTAAACGAGGATCCAATGCTATTATTGGACAGTAAAAATCCCCGTG  
30 462851 TTCAAGAAGCTAAAATTATTGCTAATAAAGCAAAAAAATATTAAAGAT  
462901 TATTTTAACTCTCCCATTTTTTTTGATACAGATAGTTTAGATAAAAAATGT  
462951 TTCTGTTTATCAAAAAGCTGAGCTTACTGAAAAGAAAATTCAGAAATAA  
463001 TAACATCAAAAAAATCAGCTATTATTTTTAAACCTATTTTTGAAATAGAA  
35 463051 GATTGCTTAATTCAACCAGATGCTATTATTGTTTCATGAAAAGGACTTTG  
463101 TGAATTTGTTGTTATAAAAGCTACAACCAATACAAAAGAAAATATTTTT  
463151 TGGAAATAATTTATGACTTTGTGTTATTTAAAAAATAGGTAAGTATAAA  
40 463201 CTTTTAACTATTATTTTTGTACTGTTAAATACGAATTACAAAATAAAAA  
463251 TAATGTTTCTTCTTTTTAAATACTGAAATAAAAAACATCAAAAAACAGTT  
463301 TTAGTTTAAAGTTCAAAGAAAAAGATTATTTTAAGAATAAACCTTTTAAT  
463351 CACCCTGAAAAAATTGCTTACATACACAAAAAAGAGCAATGGAGTTAA  
45 463401 TGGTTTTTTGATTGTAAAACCTATTGATAACCTTATTA AAAACAAATATAG  
463451 TTGATTTAAACAAAATAAGTGATTTTGTACTAAAGAAATTGACAGTAAA  
463501 AGTGTTTCGTAATATTCAACCACTTATTA AAAATGCGGCTAAAATACAAAT  
50 463551 TAATTTTTGAGATCAAATACAAGATATAAAAAAATATCAAGAACTCAAAA  
463601 TAAATCAAATTGTTTTTAATTACAGTGAAAATTTTGATTCTTTTTGGAGT  
463651 AACTATTTATTAAGAAATTTAATTAAATTAGTTTTTGCTCATAAATACAA

463701 TGAAATTTTAAATTATCTGGTAAATTAGCTAATTGAAGTCaATTAACAT  
463751 ATGCATATAAAGAAAAATAAATCAATaACTATAAATCAACTGCTTCACGAA  
5 463801 TTAATCAGAAAAAAGCAAGGCTAATTTTAATAACTCAACTAATAAAAT  
463851 AAGTTTTTTCTTGAAGCGTGAAATAGTGAAAAAGGTTTTGCAATTGGCA  
463901 ATAAATTTAAAAATACTTGAAATAAACTTAAAAAAGAAAGTTTATTTT  
10 463951 GATTTTGAAACAATTAGTTCATCAATCAGAATCATAAATAATTCATTACC  
464001 ATTTAGTCAAATTGTTACCCAATGCTCATTAATAGTTGATAAAAAATGAAA  
464051 TAGATGATAAAAGAAAACTTAATTGTGAAAATCTAATTTTGTATCCCTTA  
464101 TTTATTAGCGTTAATGACTTTAAAAAAGTAATTGATTCACTCTATCAAAA  
15 464151 CAATTGCAGTGATTATAGTTTTGTGTTTTTAATAAATCTTTTGAAAAAA  
464201 ACAGATTATTGGAAATGGCTACATTGATTAATGAACAAATATATAAAGAA  
464251 AAAGTAAAAGCTATTGTTGACAATCTTTTGTACTTAGCTGATATTTTAC  
464301 TATTGAAAATAACTGTTTGGCTTTCAAACAGCTAAACGGTTTTTCCTCTA  
20 464351 TCAAAAAGGTTTTAACTATTATAGATGAAAGCTTTTTAAAGGCAAGTAAA  
464401 TCAATTGGTTATCAAAATTTAAAAATCCAAAAGGTGATGTAGCACAAGA  
464451 AGTTGCTTTATCGCGTTTTCTAAATGCTTAAATAAAAAATGAATGAAATC  
25 464501 AAGTAGCTTTTGAATTAAAAAATATTGTGAAAATGATGTCAGAGCGATG  
464551 ATTTCAATTGTTTTATTTATCCAAGATTTAATCAAAAAAATGATCTATT  
464601 TACTTTTTATTAGAAAAATTAGAACCTGCTTTTCTACTATTTACCTAAT  
30 464651 TTTTTTTAGGTTTAATAGCTAGTTTCTTACACATCTTTTGATTTTCTATC  
464701 TTCTCTTTTAAATCACTAAAAAATGGCTTCCTTTACTACTTTTTAAAAA  
464751 ACTTGTAAGAAGCCATTGCGTTGTGCTCTAAAACACTTTTATCATCGT  
464801 AATTTTTGTTATTGTTGGGATAGCTTGTGATCAAATAATATCACCATCAAGT  
35 464851 TCAATTATACTAAGTACCAAATTATTGAAGTTAAGCTTACCCTAATCT  
464901 TGGTTCAGGTAATTTTTGCTCTTGAAAAAGTGAAAAGAAATCGTATTTTA  
464951 AAATCTCAGAAAAAGTTCTTTCAAAAATATATTTTTCAACAAATTCAGTT  
40 465001 GCTTTTTTCATCCCCATATCTTCATAAATGGCGCCAACCAAAGCTTCAAG  
465051 TACATCACCACAGTGTTTTTCAGTTAGTTCAGCACCATTGCTTAACTTAA  
465101 CAAAATCACCTAATTTTAGCTCCATACCAATACGATTAAGATTTTCACCC  
465151 TTAACAATTTCAATCTTAGTTCCTTGTTAAAAGACCTTCGTTATATTTAGG  
45 465201 ATAAAGTTCAAATAGTTTTTTAGCAACAACAAAGTCAATTAAAGCATCAC  
465251 CTAAAACTCTAAGCGATCGTAACTTTCACTAACATCTTCATGTTCAATG  
465301 ATGTAAGAAGCGTGAATAAAAGCTTTTTCAAAAAATCTCAATTATTAGG  
50 465351 AAAAAATATCTAAATCTTTAAAAAAGTTGCTAGTTTTTTATCAAAAATCT  
465401 TATTATTTTTTAGTTTTCAAACTTTATTCTTCATAGTTATTCAAAGAAGT  
465451 TTTAATTGCATTAATAAGATCAGATTTTAAGCTTAGATGTGCTAATCTAA

465501 TCGTGCTTAAAAATTGTTGTTTATCAGCAGAACCGTGAGTTTTTAAAGCT  
465551 AATTTATTTAAACCCATTACAACAGCTCCAGCGTTATTTTGTAAATCAAA  
5 465601 TTTTTGGCTACACTTTTGATAATACCTAAGCTAAATAAGCCAGCAAGAG  
465651 GATTTCTTTTATAACCCCTCTTAAGAATCCGTGCTATCGTTTTAAAGTA  
465701 CCTTCCATTGCTTTTAAAACTAAATTGCCGCTATATCCATCAGCTATCAA  
10 465751 AATATCACATATTCATCCAGTAAAAACCTTGATTCCACAAATCCTAAAA  
465801 AGTTAAGATTTTTATCAGCTTTTAAAGCTTAAATGCTTCTTGATGATAA  
465851 TCAAAACCTTTATTTTCTTCTGTTCCTATATTCAATAGTCCAATTTTAGG  
465901 AGTTTTTTTTGTAGTTGTTTTTTTAAACAAAATATCAGCCATTAAACCTA  
15 465951 AAAAAATAAGTTCTTTTCTGTGAAATATTTATTAGCTCCAACATCCAAA  
466001 AAATAAAACCAATTATTGTTATCTGTCCGTACATAAGACATAAAAGCACT  
466051 CTTAGTATTTTTATTAATTTTGCCAAAAGCATCATTTGTTAAAGAAGCAT  
20 466101 AAAGTCTGAAGAGCCTGCTGAAATTACAACATCAGCATTACCTTCACGA  
466151 ACTAAGTTTATGGCTATTTGCATTGAACTGTTAACTTTTCTTCTTGCACT  
466201 TAGTGAGTGTCCGTCATTTCAATGAAAGAATTAGCAAGTTTTTTTGTA  
466251 TATTTTTTGAAGTATATCAAGACCATCAAAAGCCTTTTCATCACCGATC  
25 466301 AGAATGAAATTTAAGTCCTGATGAAAACCTCCAATATTTCAATACTGCTTC  
466351 AATTGCTTCACTAGGTTTGTTCCTTCAAAACCTAAACAATCAACTGCAAATC  
466401 TAAAGGCCATTACTGTATGCCTATTATGTAAGAGAACACTTTTTGTTCTC  
466451 CAGGTGAAAATTCACAAAACAATTTATATTTTTTTCAACTAAAGCTTGC  
30 466501 ATTTTTTTCGCATCTTGTTTCAGTGATGTCTTTGCCATAATAAGCCAAAAG  
466551 GAACTCAGGTTTTTTCACCTTTTTTTGAAAGGATATCAATTGTTTTAAAAA  
466601 AACAGTCTGTAAGTTGAGATTCACTAGCAATAATACTTTTATTTGTAACA  
35 466651 GCAATAAAATCATTTTTATTACCATTACTTTGTTTTCTTTATATGACTT  
466701 TGAAGCTTGTGTTATCGTAGCGGAAGCAAACCTTTTAATAAAGCGCTTCA  
466751 TTGCTTTTACATTAGTGTGAATAGAAAGATCACTGTTAAATACAGTTAAA  
466801 GCAGCAATTGACTCCACAGGATTTGCTGTAATAACATAATCTGCATTAAT  
40 466851 CTTTTGGTGTTTTAACTGTTTAATTGTTTCATTGGCAGATAGAAAATAGT  
466901 TTTTATCATGTAACAAAAAGATTACATTACTAGAATTGGTTAACTTAACA  
466951 GCCTCAAGTAAAGAAAAAACAGAAGGAGCCCCAGTATCATCAGTACATAA  
45 467001 TATGGCGTTAATATCATGATCTTCACGAATTCCTTCAGCAAATGCTTCTG  
467051 TAGGTACAGTAGCTACTATAGCAGGTTTTAAACTCTTTTTGTTGGTGAG  
467101 TTATTCTTGTTATTAACCTGTAAATTCATGTTATCAATTTGACAAATTC  
467151 AAATTCACCATAATTAAGACCCATTTCTAATAAAAGATGTGGTTTTAAAG  
50 467201 TATGAGCATGAACCTTAACAAAACCATGTCTTTATCACTAGCAATTACT  
467251 ACAGAATTGGCAATTCTATTTACTTTACTTTCAAACCTTTTTTGATGAAA



467301 TTTTGTCTTTTCAACTGTCTGATTTATTTTAAACCTAGTCTTAAACAT  
467351 ATTCTGTACAATAACCAAATTCATCTTCATTAGCATGTTGTTCTTTAAAC  
5 467401 TTGTTAAATTTAATTTCTATAGTTGATAAAGTATTGTCATCTAAATTAGA  
467451 TTCGCCCCCATAATATGACAACATTCCTTCAAGAAAACAAGCAAAACCAT  
467501 AAGCACCTGAATCAACCACACCTGATGCTTTTAATACAGGTAAACATTTGG  
10 467551 GGAGTTTTTTTCACTGCTTGTCAAGCTACTTTAACAGCTTGTTCAAAAAG  
467601 TTTTCAAGTGTTTTAGGACGATTTTTTTGACTCTTAAACTCATTGCTTA  
467651 TTAAACGAGCAACTGTTAGCATAGTTCCTTCTACTGGTTTTGATACGTTT  
467701 TTATAAGCCACTTCTTGAGCAACAATGAATGCATTTGCAACATCTTCTAT  
15 467751 ACTCAACTCTGAATTATTGCTTGTTTTATTTACGATTATGTTACTGAAAA  
467801 ATCCTTTCATTATTTGTGAAAAGATAACCCCTGAATTGCCACGTGAAAAAC  
467851 AAAAGTAAATCTCTAGTAAAGTTTTTACCAAGTTCACTAAAGCTTTTTAT  
467901 ATGACTTTTTTTCATTTCTAGTTTCTTGATGGCTTCTGTTATTGTTACTT  
20 467951 TCATGTTTGTTCAGTGTCAACCATCAGGAACAGGAAAAACATTCAACTGG  
468001 TTTATGTATTTCATAATTTTATAGCGATGTTATTACAGCCAAGGCGTAACAT  
468051 ATCGATAAAAGAAGATAAATTTACTGATGACATCTAAAGTAAACCCCTAG  
25 468101 CTTATAAGGGATAAAAAAGAAGTTTATAACCACAATAATTTTAAATTTTA  
468151 ACTATTGAATTAAATATTCAAACCAAGGTACTATTTTACTCTTGAATTGC  
468201 ATTAATGAATAATTTGTTAAATGGGAAACTTGCTCGTTTCTAGTTTAGG  
468251 AAAAATAAATTCATAAGCGTGAAGTGCTTGATGCTTATATTATTATTAC  
30 468301 GATTTTAAATTTGAATCAAGCTGTATTTTTTATCACCAACTAGTTGATTT  
468351 GAAAAATAAATTTAAACACGCACGAATTTGGTGAGTCTACCACTAATTAA  
468401 TCTAATTGTTATTAAAGACATATCTTTTTGAGCTATGTATGAAGAATTTT  
35 468451 CAAAAAAGTGCTTATCTTTTTTGCTTCTGGAAAAGGTTTTCATTTTACT  
468501 GTTACAATGCCATTATTGTTATCTTTTTTCAATAAGCAGTTTGTAAGCC  
468551 AAGATGGTTAAATTGACCAAAAACTAAGCCTTTATATCTTTTGGTTAAAT  
468601 GGTTATTTTTTAAAAACTTTGTTCAATCTTTTAAAGCTTTGTTTGTTTTA  
40 468651 GCACCAATAACAATTCCAGAAGTATTACGATCAATACGATGTGCAAACTG  
468701 GGGATAAAAGTTAAGTTTATTACTGTCAAATTGTCTATATCCACAGTGTT  
468751 TTAAAGCATATTTGATAAATTAATAATGCTATGTTTTTTATCAGGTTGG  
45 468801 CAACTATTCCAGTTGGTTTGTCAACTACAATAATATTTTCATCCTCAA  
468851 TATAATTTTAGCTTATCTTTTACCAAATCTAGAGATAAATAGTCATTAT  
468901 TAGTTTGTAATAGGGATTTATATCAAAAAGAAAAGCTATCTCATCTTTA  
468951 GTTTTAAATCTTGTTGACCTGTGGTTTGTGTTTTATTTAACAAAACCTT  
50 469001 TCCTAAGCGTAAATACTTAAAAAAGTCACTTCTTTTAATTAAGGGAAGGA  
469051 TTTTAAACAAAATTGGTCAATTCGTTGGTTTTCACTTCTTTAGGAACT

469101 AAAAATTTATTAGCTATTCTCATTTTGTGGCAAGAAATCATCCATTA  
469151 TCTGTACTAATTTCATAAATTGATTTTTTTCATCCAAAACAAAAGCAGCT  
5 469201 GCATATTTATGTCCACCACCATTGAACATTGTGCAAAGTTATTAATTGG  
469251 AATATTACGTGAGCGAATGGAACCAATTCATTTTTTAATGGACTCGTTAA  
469301 AGTAAACAGTAGTCCATATTTTTACTCCTTTTATGTTATTCAAAGCATGA  
10 469351 ACCATTGGTAAAGGAGAGACAACACCAAATGTTTATATGCTCCTTTTTT  
469401 AATCAATGCATAAGCTAACCCATTTTTAGTTATTTTGGCTTTGCTAAGTA  
469451 CATAGCTAAAGTACTTATGTTCTAGTAATGGCTTTAAATAAACTGCATCA  
469501 TGAACCTTATTGCGGTTAAAACAGTTTCCATCAATTTTGTGTTAGGGC  
15 469551 AAATGTTTGGGGTGTAGTAGTTGGACCTCAGAATCGCTGTGTATCAGTAA  
469601 TTATTCCTGCATAAAGATATGATGCAATCTCATCTTAATTTGTAACCC  
469651 ATCTGCAAAATTAAATAACCAATCATCTCAGCAGTTGCTGAAAAAGAAGA  
20 469701 ATCAATTCATTCCATATCAGCAAATTTTTCAGTTCTAGGATGGTGATCTA  
469751 TCCTAACTGTCTCTTTTGCCAACTTATGTTTTTGAGTTAAAACCTTTTCT  
469801 TGGTTGGAAGTATCAAAAATAATAGCTAAAGATTCTTTTACAAAATCATC  
469851 ATTTATGTCAGTTTGTCTAAAAGGAAAAAGTTCTCTACCGTCTGCATTAA  
25 469901 TATTGTATGAACCCATAACATAAGCTTTTTTTTCACTGAAAAAAGTATTT  
469951 AGGAAAGTTTTGAAAGCAAAAGCAGATCCAAATGCATCAAAGTCTGGGTT  
470001 TACATGTACAAATAAACTGAACTTATCAAACCTGTTTAACTTTTTTGAAA  
30 470051 AATTCTTAATGAATTGTGGATCGATACTAATCATTGCTTAATTCACCTAC  
470101 TCCCTTTTCAATTAAATCATTTAAAAAATAAGCTCACTTTCAAGCTTTT  
470151 CAACATTTATCAATTTAGCTTTTCGTTGTAGGATTTTTGGGAGAAAACCTCA  
470201 CTACAAGTATCTAAATGTTGTTCAATAGAAATATCAAAGTATTAAAAAA  
35 470251 TTTAGCTAATTCAATAATTTTATCTTTACTAAAGCCAATTAAGGGGCGAA  
470301 CTATAAATGTATCTGGTGTGCTGATTGAATAACTTTTAAATTTTCAATG  
470351 GTTTGGGATGCAACTTGTCCCAAACCTCACCTGTAAGTACATAATCATA  
470401 CTAAACATACTAGCAGCTTTATAAAAAACACGACGATTAAACGATAC  
40 470451 GATAAGATTCACTACTAATATGAATTAACCTTTTTGAATTGCAGTGAAA  
470501 TCAAAAACTAATAATTTACCACTACAAATCGTTTTATTAAAAGAAATTAA  
470551 ATTTGCTAACCTTGTGATTTTTTCAATTGTTTTTGAATCTTATTTGGTT  
45 470601 CATTAATAAAGGTGATAAAATCAATGTTAAACACGTTGCATTACAAGT  
470651 GAAGCTGCAACTGGGCTATCAATTCCTCCTGAAAGTAAGACTAAAGCTTT  
470701 ACCACTACTATAAACAGGTAATCCACCTTTACCTTTAAACGTTCTGTAA  
470751 AAACAAGAAAATGCTCCTTCAAATCTCTATATTAGCTATTATTTAGGG  
50 470801 TTATTAATTACTCCTTTTAATTGGTATTTTTCAAATAGTTTAACTGCTAA  
470851 ATACTTCTTAAATTAATTTGAATTTTCAGCAAAATTTTATCACGTCTCT

470901 TAACTTCTAATTTAAAGGAATTAAAATCTTTAAATAAATTAAAAAGAAGA  
470951 TCTAATAGTTTGTCTTCTCCCTTACTATCTGTGATGCAAAAAAGAACAA  
471001 ACTAATTCCAGGCAAAAACTGAATAATTCTTGGAGAATCGCTCTTTGTT  
471051 CTTTTTAATATCAAAGACAACAATTCTATCAAATTCATAACAATACTA  
471101 TTGTTAATTTCCAGTTTTTTTAAAGCTTTTTTGATGTAAATTTTAATTG  
471151 TTTTGTGAAATAAGAACGGTTTTTTCCTTTTAAAACCAATTCACCATAAC  
471201 GCGCAACTAATACATCTTCACTATTCAATTCATTTTCCTTTAATCATTG  
471251 AATATCACTTTCTGTTAGTTTAGGACTTTTACCAGTTAATATGTAATTTT  
471301 CATATCAAATCTCGCCTTATCAACTAAAACACTAAATCCCTTATGATCT  
471351 ATCTTGATAGGAATTAACCTAATTTCTCTATTGCTAGCATTAAATTGTTT  
471401 TGGTAAGACATAATCTTCTGGTTTCAAAAAGGCAATTGCAAAAAGTCCTT  
471451 TATTTACATTGCGCAAATATAGATAAAGACCAATTTGACAATAATATAAA  
471501 GTA CTGATAATAATTTTCCATTACTGTCAAATCAACTATCTTTTTTGCC  
471551 ATCTTCTTTTTTAAACAATAGGCATACCATTTTCATCAAGAATCATCTTGA  
471601 GATTTCCATTGATTTTTTTATAAATAAGACTATCGCAAGAAGTTGTTTTA  
471651 ATCTTAACATAGGAAGATCATTTTGTATAAGCTAATTCACCATTTTCATC  
471701 AAGAGGTTACCATCAGGTATCCCACCAAAAACACTATCATCCTTAAATA  
471751 AATCAAATTGAACTTTTTTTAGGATCATAAGAATGAAAATTTAAACCAGTT  
471801 TTTAAATTGACATAATCACGTATTTTAGGTTCTATTATGTTTCCAGCTTT  
471851 TGCCAGTGTTTCATCAAATTCATCTTCATAAATTTTGACCATATTAGCTC  
471901 AAGTTTTAAATGATGACTCATATTTCAGATAAACCTAAAACCTTGCCAAAG  
471951 CGAGTACCGGTTATTTTTTTTAAATAGAGCTTTATTTCTTAAAAAATACTG  
472001 TTCTGATAGAACAATTTGATTATCAACTATATCAAATCAGTTTTATATT  
472051 GCTTTATAAATCCCATTTATTTTCATCAACTGTTCAAAATTCCTTTTAAA  
472101 ACAATTGATATTTTCAGGATTATTAAATTCCTCATCATTATCTGGTTGTTT  
472151 TTTGCTTAAAAATACAACACTTGCTAATTGATTAATGTTATTAATTGGAA  
472201 CTTCTGTCACATTTAAATAATGAACATCTTTTAAAGAGCAATTCCTGCTT  
472251 TTAACATATGTTTCTAAAGCACTAACTTGAATTTTTTGCTAGTAAA  
472301 TAAAAAATTTTCGTTATAAAAAATTGCTGTAATGAACTTAGGCTGACCAC  
472351 TAGAAATATGTTCCATAAGTTGAAAGTCTAAATGATACTGAGGACTAAAT  
472401 ACATAAATAGAACTAACATCCATTTCACTGAGATTTTTTAAGAAATTTTG  
472451 GTACTTTAATGTTTGGTCAAATTCGTTAATCAAATTAATTTGAATTGCT  
472501 TATATTTTTCTAATGAAATAAAGTAATTAATTGTTGTATTAGGTTCTCA  
472551 CTAATCTTGCTTTTTCCAATTGCAAAAACACCAGAATTAGTAATAATAGC  
472601 ATGGTGTAATAGTGTCTATACTAACAGAATCTAAAAAAGATTGATAGA  
472651 TAAATTCATTGGTTTTGCTAATTCATATAATCGCGCTGATTCTGCAATT

472701 ATATCAACATCATCTAACGAGAGTAAATCAAGTAAATAAAGCACTGCTTG  
472751 TTGTCAACAACTTGACATAAAAAACAAGTTGATGGTTATTTCGCTGAATGA  
5 472801 AATTAAAAAGTTTTTTCATACTTCTAAATCCTTTGTAGTGTTAAAAAA  
472851 TTTGCTGTATTAATATCTAAAACAACATTTTTTCTATCCATCTCTTCTAA  
472901 CTCTTTTAACAAAATTATTAAAGCTAATTCTGGTGATTTTTTTCACCTTTA  
10 472951 AAACCACGGCATGTCAACTTCTCTAAATTCTCTATTTCTTTATCTCCAAC  
473001 AATAAGTTGTAAAGGAATTTTTTCAATGATTGCTTGTCTAACTTTTTTAG  
473051 CTAAGCGATCTTGATTATCATCTAAATTTACACGGATGTTTTCTTTTAGC  
473101 AATTTGTTATAAAGTTTTTTTGCTGCCTTTAAATGCTTTTGGATATTAAC  
15 473151 AGGAATAATTACGGCTTGAACAGGTGCTAACCATAAAGGAAAATTACCAC  
473201 TTGTTTTTTCAAGTAAAGCAGCAATAAACCTTTCATAAGTTCCAATAATT  
473251 CCAACATGGATAATAACTGGTTTTTTTTAGTGATTTTTTTTTATCTATATA  
473301 AGTTAGATCAAATTTTTCTGGTAGTAAAAATCTAGTTGAATGGTGGCAA  
20 473351 TAGTAATCATTTTTTTAAAGATTGTTTTGAACTGAAAATCAATTTTTGGT  
473401 CCATAAAAAGCAGCAGCTCCTATCTCTTTTTGATATTGGATATTAAATC  
473451 TTTTAAAACATTCTCCATTTGGCTTTCAGATTCTTTCATAAACCAGGAT  
25 473501 TATCAATAAATTTTGATTGATTTTTAGGATCATGTAGAGAAAGATCTATC  
473551 CTATCAAATATAAATCCAAATTTTTTATTAACTTTTTGAATTAAATTAAA  
473601 TCGGTTTTTAATCTCACTTTTAATTTGATCTGCACGACAAAAATGTGAT  
473651 TATCAAGTAAAGTCATGCACCTCACTCTTTCTAATCCTATTAAATCCTCCA  
30 473701 GAGGCTTCAAACGATGCAAAATAGAATCTTCTGAAAAGCGCTGTGGCAT  
473751 TTTTTTATATGAATATCGTTTTTGTTTGAAAATCAGACAGTGATGAGGAC  
473801 ATGTCATAGGACGAAGCATCATTGCTTGACTATCAAGTTTAATAGCAGGA  
35 473851 AACATATCTTCCTTATAGTGCTGATAGTGGCCGTAATTTTAAAAAGCTC  
473901 TATGTTAGCTAATACAGGAGAACAAACAGTATTAAAAACCAACAATAGTT  
473951 GCTGGTGATGCACAAAATTACCGATTATATTCCTTAGTGTTGTACCCTTT  
474001 GCTAATCAAATAGGAAGACCTGCACCGATCAGTGGGTCAAAGCTAAATAA  
40 474051 CTCTAATTGTTTACCTAAAGATCTGTGATCCTTCTTCAAGCGTTCTTCAT  
474101 TTTCTTTTATTAATTGTTCTAATTCTTTTTTTGATTGAGCAAAAATGCCA  
474151 TTAATCCTCTGAAGTTGTAATTGTGAAGGATCTCCCAAAAATAATTTAC  
474201 GCTTACATTTAATAGCTTAATAAAAACTTTTTTTAATAAAAGTTAAAGTTA  
45 474251 AATCTTCTATTCAAAAATGTTTATTTTCAAAAAGGTGATTTTAAATTTG  
474301 TTTAAGTTGCTTTTTTTTAATAAGTTTTTTGTAACTGATCATTTTCAAA  
474351 AAAACTTAATGCTTCATCTAAAGAAACAAATTTTTGAGAAATCCCTTCTA  
50 474401 GTTACTAGAAAGAGAGTTTAAATCAGATTCTATTTTTGCAAAGTGT  
474451 GTAGAAAAATTCTCATTTATATAAAAAATCTAAATAAAATTCATCTCCATT

474501 AAAACCATGTTACCAAACCTGAACATTAGCATATTTGCATTTTAACCATA  
474551 TTTGTAATAAAAGAACTCCTGCAAGCATTAAAGATTCTTGATAATCAATCA  
474601 TTACTTTTGAATTTGGTTTCATAATTTTGACAACCTTCGATTGTTGTTTTT  
474651 CAAATTCCACTGCGTTTTTCTAGGTAAGTGCGCAGAATACCTTCGATGCT  
474701 AATTGTTTTAAATTTTTGAGTATATGCTTCAAGTTCAAATGCTAATTGAC  
474751 CATTTGCATAAAAAACAAAAAATCAGTAAACCTTCGTTACCAAACAAA  
474801 CGTTTCTGCTTAATAGTTACTAAAAATCCTGTCTTTTTGTGGCTTCACTT  
474851 TGTGCTTTCTATTTACCTTCCAAAAAACGCAATTTAACATGCTTTTTTA  
474901 GCTAGGTAATTGACCTGTTAAGTTGAAATGAAATTTAAAGTGGTTAATTG  
474951 TTTCTAAAACCATTCTTTCTTCTATTAATGCAGTTCTAATACCTTCAAAC  
475001 TTTTGTATCATCAAGATATTCTCTAACATTCTGATTAGTTTTTTCATA  
475051 ATACAAGCTAATAACTCTTTTAACAATATCATCACTAACTTCAACCTTTC  
475101 ATTCCTTTTGTAAAGAAATTAAATACTAAAGCTTTTTTAATGATTTTTTCA  
475151 GCTATTGATTGAATTGTTTTTTCATCAGCATCTTTAACAACATCTCTTTT  
475201 CAAGCCTTCAACAACATTTTTTAACTCTTCAGGGTTAATTGAAATTCAA  
475251 AATAACTAACAATTTTCATTTCATTGCTGCTGAAAACAAATTATCTTTAATA  
475301 ACAATATGAGTTAGTTCGTGGTAAAGAGCACTTTCCTTAGCATCTTTAAA  
475351 AGAAGCTAAAATCTTTGCCGATGTTGCTCAATAAAAGCAGGATCTGCAA  
475401 AAATACGATCAACTTCAATTACCTTATCATACTGAATAGGTTTTTGCAAC  
475451 TTTGCAATAGATTAAAGATTAGTAGCCATATTTTGAAGAACTTATTAAAT  
475501 TTTAATTCCTATATGCGTGAAGAATTTACATTTGTTGTGGTGTTGAAATC  
475551 TTCAAAACATCAAGGATTTGTTTAACTATAAATTGTAATGATCTCAATAA  
475601 AGCAAGTCTTTGTGCTGATAAAAGTGAATTTTTATCATCATTATTTTGC  
475651 AAACCTTTATACCAGGAATGAAATAAACTAGCAGTTTCATATAAAAAGTTA  
475701 GTTAATAAGTGAATTCGCCTGTTTCCATAGCTTTTGTGCAACATAAAAGG  
475751 ATAATAGACAAGTTGATTTAAAAGTGATATCTCTTTTTCATTAATCAAAA  
475801 GACTGCAATCAGTAATTTCTTTTAATTGATCAGAATTTGCAATTCTAAGA  
475851 ATACTATTCATTCTTGCAAACGCATATTGAACATAATAAACTGGATTAGC  
475901 AGAGTTTTGCAAATTAGCTATATCTAAATCAATTTTGATAATTGTGCCAT  
475951 TATTTTGAGATAACATAAATCATCTAGCAGCATCTTCACTAATCATTGAA  
476001 AGCATTGTTTCAATTGTGATTACATTTCCAGCACGTTTTGACAAACGTAC  
476051 TAGCTCTTTATTTTATAGAGAGTAACCAGTTGTAATGCAAAAATTTTAA  
476101 AAGAAGTTTTAGTGGTATTTTTTAAAGCATCAAATGCACAATACATCCTT  
476151 TTAATATGTCCTTCATGATCAGTGCCTCAAACATTAAATAGAATGTCAAA  
476201 GCCACGTTGTAATTTTTCTAAGTGATAAGCAACATCAGTTCCAAAATAAG  
476251 AAGCTCTTTTATCACTTCTAATTAAAACTCTATCCTTATCATCTCCATAA

5

10

15

20

25

30

35

40

45

50

55

476301 AGCGTAGTTTTTAGTCAGAGTGCATTATCTTGATAAAAAATAACTATTTGG  
476351 TTTAAGTTGTCTCTAAAAGATCATTAAAATTTGTTTTTTAACAATTTTCGC  
476401 TTTCAAATTTTCAACTATCAATAAAAAACATGGATTTTATTCAAATCACTT  
476451 TTAATTAAGACAAAACCTTTTTGGGTGCAATTAATAAAAAATGATCTAA  
476501 GAATGATGTTTTACAAAACCTCTTCAAATTTAAATTATCAACTGGAAAAAT  
476551 TTTCAATTTCACTAGCAATTTTATCTATTACTATTCCACTATATCCATCA  
476601 GGATGTTGCTGGATAGCAATATTTTTTTTTAACTGCAAACTTTTGATAAAC  
476651 ACTAAAGCTAAAAACCTCGTGCTTGTGTCCATAATCATTTACCCAATATT  
476701 CACAGACTGTTGTATAACCCAACAGCTTGGCTAAATGTTTAAAACATCA  
476751 CCAAAAAAAGCTATTCTCACATGACCTAAATGGATCCTTCCGGTAGGATT  
476801 TGCTGATACAGATTCAATTAATACTTTTATATTTTTCTTAGTAAAGCAAG  
476851 GTGTTTTTATCAAGTATTCTAAGTACTTTTGATAGCTAATTTGAAAGTTT  
476901 ATAAAATTATTGTTAGCAATAAAAAACATTTTGGTAGTTATCCTTTTTATT  
476951 TTTTAAAATCACTCAACAATACTATCTGCAATTTTTTTATGATTTTCAC  
477001 TTTTTAGTTGGAATAATAGTTGAAGAAAAACCATTAAAACTATTATTT  
477051 TTAAGTAGTTTAAACAAGTTCCTTTTGGTCATCAAATTTAAGCTTTAAAGC  
477101 GCTAATGCATTCTTTTAAATCATTGATGATAAAAAACATTACTTTAAATT  
477151 ATATTTAATGATGCAAAATGTCTTTTATCATAACAGTAATAGGTGCTGGG  
477201 CATGCTGGATTGGAAGCCGCTTTCATTGTAAGCAAATTCACATCAAAGT  
477251 AAACCTTTTAGTTCTTGATATAAATCATTTAGGTTCTTGTCATGTAATC  
477301 CTTCAATTGGTGACCTGCTAAGGGAATTGTTACTAGGGAAATTGATGTT  
477351 TTAGGAGGTATGCAAGCAATTGCTGCTGATAACAATGCCTTACAATATAA  
477401 ATTACTAAATAGTTCAAAAGGACCTGCTGTGCAAGCTATCAGAGCACAAA  
477451 TTGACAAAATAGGTTATAAAAACTGGTTTCAAAGTCAAGTTAAATTAAAT  
477501 AAAAACATTAATCTAATTCAATCTGAAGCAATCAATTTAATTGTTAGAAA  
477551 TGAAAAAATAAAAGGCGTTATTTTAAAAGACGGAAGTGAACTTTTAAGTG  
477601 ATGCGGTTATTATCACTACCGGAACGTACCTAAGATCAAAAACATACTGT  
477651 GGTAATACAGTTAAAAATCAAGGACCTGATCAATCTAAAAATAGTGAAAA  
477701 ATTAAGCACAACTTAATTAACAGAGGTTTTTAAACAATTCGTTTTAAAAA  
477751 CAGGAACCCGCCAAGAATTTTAAAAACTTCACTTGACTATAATCAAATG  
477801 GAATTAGAAATTAATAATAATCAAAACCTTGCTTTTAGTACTACAAATAA  
477851 AAATTTCTTACCACTTGAAAAACAAATACCTTGTTACTTAGTTCATACCA  
477901 ATCAAAAAATTACGATCTAATCCTTAAAAACTTAAAAAAATCTGCAATG  
477951 TTTAATGGTAGTATTTTCAGCACAAAGGACCACTTTATTGTCCAAGCATTGA  
478001 AGACAAAGTTTTTAAGTTCTCTCAAAAACCTCGTCACCAAATTTTTGTAG  
478051 AACCTGAATCATTGAGTCTAGATACTATTTATTTAGCAGGATTATCAACT

478101 TCTTTTACACCAGAAATTCAAAAAGAAATCATCCAGCTTTTACCTGGTTT  
478151 TCAAAATGCAGAAATTAAAAAGTTTGGTTACGCTATTGAATATGATGCTT  
478201 TTCTATCTAATCAACTAAAACCAACACTTGAAACGAAGTTAATAGAAAAC  
478251 TTGTATTTTGTCTGGACAAATTAATGGCACTAGCGGTTATGAAGAAGCTGC  
478301 TGGTCAAGGTTTGTATGGCAGGAATTAATGCTGCTTTAAAAATTATTAAAA  
478351 AACCACCATTTATTTTGCAACGTAATGAGGCTTATATTGGGGTTATGATT  
478401 AATGATTTAGTTACTAAAACAATCAGTGATCCATACCGTTTGTTAACATC  
478451 CAGAGCAGAATATAGACTATGATTGAGAAATGACAATGTTCAAGAACGGC  
478501 TCATTAAAAAAGCTTTGAACTTGGTTTAACAGATAAAAAACATATGAA  
478551 TTGTTCCCTTAAAAAGGAAAAAGAAAAACAGGAATTAATTTCATTTTTAAA  
478601 AAACACTCAAGTAGGCAAGGTTAAAGCATTGAAATTCCTAATAAAAAATA  
478651 CCGCTCAATCACTTTTATGACTTCAACAAACGAAGTGAAATAAATTTAGAT  
478701 AAATTGATCAAAGATCTTCCTGAAAAATACCAATTAGATTCAGAAACACT  
478751 TAAACAAATTGAAATTGAAATTAAATATGAGGGTTACATAAAGAAAAATG  
478801 AAAAGTATTTTAAGGGTTTAGATAAATTAAGCAAAATTAAAAATTCCTCAT  
478851 ACTTTTGATTACCATAAGGTTAAGAATTTAGCTAGTGAAGCTATTTTTAA  
478901 ACTATCTAACTTTAAGCCTAGTAATTTAGCAATTGCAAGTCAAATAGCTG  
478951 GAGTGAACCTTTAATGACATTATAGCCATAAAACATTTTTTAAAAACTTAT  
479001 GAATAATGCTAATTTTGAAAAATATGTTGATTTAGTTTTTGAAGCAAACA  
479051 AAAATTTCAACTTAACAGGATTTAAAAACAAAAGAAGCTATTTATCAGAAT  
479101 TTAGTTATAGAAATATTGACATTATTTAAAGGATATGAAAAATTTTTTAT  
479151 TGACAAAACGTAGCAGACTTGGGAAGTGGAATGGTTCGCCTGGGATAA  
479201 TATTAAAACGTATTTTCAAAAAATAAAAAAGTTAGTTTAAATTGATAGT  
479251 AAACACAAAAAATTAGCTTTTTTAAATAAATTAAGCAACTAAATCT  
479301 GGAGAAAACGTTGCAATTTGTGAACGAATTGAAGTACATAAAAACTACT  
479351 ATGATGTTATCTGTCTCGTGGTCTAAGTACGATTATTAAAGTTAATGAT  
479401 TTAGCATTTTCCTTGCTTAACCTCAAAGGTATTATTTTCATATAAAACA  
479451 AAGCTTAGACCAATACATTGAATTTGAAAAATCAAATCAGAAGAATCAAT  
479501 TTAACCTGTTATTTATAAAGCACTTTACTAGTCAGAATAAAAACTAATT  
479551 TTGATAGCTTTACAAAAAATGATTAAAGTTAGGTTGAGCGTCTTTTAGTA  
479601 ATACAGAATTTGCTCAAGATATCTTTATAAAGTTTGCCAATCAATTCTAT  
479651 AAACAAGATGATGCTGGAACAATTTTATTTGAACTAAAAAAAACATTAGG  
479701 AGTTAATCAACTAGATGAAATTGAAAAAATAAAAAAGTTATTATTGTTA  
479751 ATCAGTTTCAAAATAGCTTAGGCAAATTTTACTTTTAAATAAAGAAAA  
479801 ACTAAAAGAATAAACAGTTTAGCTAATGAACATATAAGTTCTTTTTTAAA  
479851 AAAAAATTTTCAGATTATCTGGATTTAAAGATATGTTGATTGATGTTCAAC

479901 ATCATAAAAAGTTACAAAAATGTTTATTAAGAGAAATTCATCTTTTAGTT  
479951 TGTTTAATTAATAGCAATCAATTTAGTGATGAATTAATGCAAATTATTGA  
5 480001 GTGGTATCAGTATTTAAAAAAACACTCTAGTAACTTTTTGTTATTACTG  
480051 CAAGTAGTGATAAAAAACCAGTAATAGAGCCAACTATAAATGAATATAAA  
480101 GCTATTTTTGGAGAGTATTTATCTTCATTTACCTAGATCTAAAAAATAA  
10 480151 TCAAAGTAATGATTTATTCCAGAAATTACTTGATCAGATCAAAATAAAAG  
480201 CTACCTCAAAAACCTAGTTTGAGATAGCTAAAAATATAAATGGCGCATCGG  
480251 GAGGGATTTGAACCCACGACAACACGCTTAGAAGGCGTGTACTCTATCCA  
480301 CTGAGCTACCGACGCATTTCTTTACTAGAACTATCATATGAATCTTCAA  
15 480351 TAAGACTCTAATAAAAGTTTAGATGATTTTTAACTTTTTTATTGTATTCA  
480401 TGCAATAAAAATTAATTTAAATAAAAGAAATTTATTAAAAAATCCTTAAA  
480451 GCACAAATATCAATAATTTCTTTCTATTGATTCTTAACTATTTTTTAAA  
20 480501 AAAATAGTCAATTTATTTAGTCACAAAAACCTTAGTTAAAAATAAATTTA  
480551 AGTTGCAATTGGATTGAACATATTATTTAACTTTCTTTTAAATTAAGTG  
480601 TTTTAAAAGTTGATTTTTTAATAAATTAATTAACAAAATAAGATAAATAGT  
480651 TAAAACTCAATAATAAACGCTTTAAAAATATTTCACTTTGATGGATGAAA  
25 480701 AAGGGATTTTAGTTGCAATTAGTGGTGGTAGTTGCTCAGGAAAACTACT  
480751 GTTGCTGAAATGATTTATCAACTTTTAAGTAAAAAATTAAGTTGCGAT  
480801 CATCTGTCAAGATAACTATTACAAGTCCTATAAAAAATAAGCCATTATTAA  
30 480851 AAAGAAAAACAATAAACTTTGATCATCCTGATGCTTTTGATTGAAACTT  
480901 TTAAGATCACACATTGAAGATCTTCTAAACGGTAGTATAGTTAATGTTCC  
480951 TTTATATGACTACATTAACTATAACCAGAGCTAAAAAACAGCAAAAATTG  
481001 GTCCAATTGATGTTGTTATTCTAGAGGGTTTAATGCCATGATTTGATGAA  
35 481051 AAATTATCAAGACTTTCTAAGCTAAAAATATTTATAGAAACAAATGGGGA  
481101 AGAACGTTTAATTAGAAGAATAGAAAGAGACTGACAAAGGGGAAGAAATA  
481151 TTGATTCTATTATTAAACAGTGACGCGAAATAGTAGCACCATGTATGAA  
40 481201 ATATTTGTAGAAAAAATGAAGCGAAATGCTGATTTAATTCTGCCTTGAAG  
481251 TCAACGCAGAGAAGTAAGTACAAGTGTATTGGATGTCGCAATTGAACACT  
481301 TATTTACAAAACTGTTGAAAAAAATAATTAGTTCTGGAAATTATAGAGA  
481351 TGTTTAAATTTCAAAGGTGAATTATGTTTATGCTCTGCTTTTGCTTTCAA  
45 481401 ATCTAAAACAATTTTTTGCTTTTCTGAACTAAGTATTAAATCACCTTTTA  
481451 AATATTGATCAAGTTCCTTATAAGTAATGCCATCTCTGTCTCATCAGTT  
481501 TGCCCTTCAAAAAGACTAGCAGTTGGCGCTCTTGTGATTACAATTTCAAG  
50 481551 AATATTAAAAATGCTTAGCTAATTTGTAAACGTCCTCTTTTAAAGCCATG  
481601 CTAAAGGAGCAATATCACAAGCTCCATCTCCTCATTTTGTGAAATAACCA  
481651 AGTGTATACTCTACAAAATTACCAGTACCTAAACTAAGAAGTTGTGTTT



481701 TTGAGCATAAGCATATAAAGTTATCATCCGTAAACGTGCTTTAATGTTAC  
481751 CAGCTGTTAAAAATCTTTTTTTGGATCTATTCCAAGGGTTTTACTAAC  
481801 AGATTGAACTCTCTTCCAGTTCAATGTTAATACTATTAAATTGCATTTT  
481851 TTTAACAAGTTCAGTAGTTGCTTGAAAATCAAGTTTGAATTATTAATAT  
481901 GCATTATTAAAGCTAAATGGTTTTCAAAACCAAAGTTTCTTTAGCAATA  
481951 GCAGCAACAAGTCTGAATCAATTCCTCCAGATAAGCCAAAAATAACACC  
482001 TTTAGCTTTAGATTTTTTTACATAATCAAACAGCCAGTTTTGGAGTTCTT  
482051 TTAAATATTTAATTAAATTAGTCATTAATTACAAATCACAACCATCAAA  
482101 GAAATAATATCACCTTTTTTTAGCACCAACGGATTTAATTGATCTTCAA  
482151 TACCGATTTCTTTAATTTTATTCCTAAGCGACGAATGTTATCAAGCGTA  
482201 GTTTGTGGAATTTTATCAAATCAATATCTTAGACGTTTACAATTAACAAT  
482251 TCATCTGTTTAACTATCTTTTTCAATATTTAAAGGGTCGTTATTATTTT  
482301 CATTGGTATTTTGAAAAACATAATGCTTCTCAAGTTCATTGGCAAACATA  
482351 AACTTATTAGCTCCAAATTGGGAAATTGTTTTATTGTAAAGTTCAAAAAC  
482401 TCTATCAAGTAAATTGCCTAATTCTTTCTTTAAAGCAGAAATTTTAAATA  
482451 CAGAAATAGATTTTTTTTTGAAGAAATTTTCTAATTTTTTAAACCGTTTC  
482501 TCACCTTCATTAACATCAATTTTATTAGCTACAACAAGCATCTTTTTTTT  
482551 AACTAGAAGGGGAGAATATTTTGAAAGTTCATCCATTATTTGTAAATATG  
482601 CTTTGCAAGGATCATCATTATCTACAGGATCAAGTGAAATTAAATGAATT  
482651 AATATTTACACCTCTCTATATGCCGTAAAAAATCATGTCCTAACCCACT  
482701 TCCTTCACTAGCATTTTCAATCAAACCAGGAATATCAGCAAAACATAAC  
482751 TATTATTTTGATATTTAACTACACCAAGTACGGGTATTAAAGTAGTAAAG  
482801 CGATAGTTTGCAATTTTAGGTTTGGCATTGAAAGTTTGGAGATTAGTGT  
482851 TGATTTACCTGAATTTGGAAAACCAACAATTCCTACATTAGCTAAATATT  
482901 TAACTTCCAAACTAACGTTTAAAATCTCTCCTTTATCACCATTTTCATAT  
482951 AGATTAGGAGCACGCATAATTGGGCTTTTAAAAGCAGCATTTCTTTTCC  
483001 GCCTTTTCCGCCAAAACACAAAATAAACTCTGTTTATCATGAACAAAAT  
483051 CCACCAATACACTATTATTTTCTAAGTTTTTAACTGTTGTTCTTATTGGC  
483101 ACTTTAATTAAAAGATCTGAACCATTTTTACCATGTGCTAAATCTGGTTT  
483151 ACCATTTTGTCCATCTTCTGCAAACAGGTGTTTTTTATTCTTCAAGaAAA  
483201 AAAGTGAATCGCAGTTATGATCAGCTTGCAAATAACATTACCACCATTA  
483251 CCACCATTACCACCACCAGGACCACCTTTATCATAATGTGCTTCTCTTTt  
483301 TCATGCTATGATTCCATTACCACCATTTCCAGCAGTAAAGCGACACTCAC  
483351 AATAATCTGTAATAGCCATTATTTTGGTTTCTTTTCTTTATTTTAAAAA  
483401 CGATTTCTGCAGATTTTTTTCTTTCTAGATCACTTTGAATTTGTTGCAAC  
483451 TTTTGTGATTTTTAGTTTTAGATTTACCTGTCTTTAAGAGATTTTCAGC

483501 AATTATTATTGCATATTTTGATCTGATTAAAAAAAAGTTAGTCATTTTAT  
483551 TCAAAAGAAAAAACTTAGCATTAAATGTTATTAGAACTAAAAAAATCGA  
5 483601 AGTAAGATAATTCAACTATTTCAAGCCATTGGTATTATTCCTGATAAAAA  
483651 AAGaACTATTAAAGTAAAAGCAGTAGAATAGCAAAAAGGAATTAATTCCC  
483701 AAATAATGTATTTAGTAAAAGCAAATAAAAAAAGGCTAAAAAAGATAA  
10 483751 ATTAGTAAAGGAACAAATAAAAAATCACAACAAAATAAGTCAAAAATGGG  
483801 CTCTATTTCTTACCCATAAATGTTCTGTTTTGTGCTGCAATTAAAAAAT  
483851 TAAAGCCTAGTAAATTGATTTACCAAAAAGAATTCAAATCAAAAGATAA  
483901 TAAATAAAAATAAAAAGAACTAAAACCTTCCTATTAGTCAATTAGGGGT  
15 483951 TTTAGTTTTTTTATTTGACTTGAAAAAATAATTCAAAACTAATAAATTTG  
484001 TGCAGTAATTTGAAATTTACAAAAGCGATCGTTTTTCATAAATTGATAAC  
484051 GAAGAAGACCCTTGATAACTCAAAGAATAACTGGTAATCCCAGGTTTTGA  
20 484101 ATTTCTTTGCAGTTCTTATGATAAAAACTCTCGTTTGGCACTAAAAAACG  
484151 GCAATATCTCATTAATTCGTCTCTAGAAGCTACTAATAAAGCTTTTTTGT  
484201 TTGCAATTACAAAACCGGTTTTAAAGCCTTTGAAAGTCTCATTTATTAAC  
484251 TTAATGATATGAAAATTACTACTTAACAAAATCATTTTTTCTTTAGCTAA  
25 484301 GACAAAATCTTTGCAAAGCAAATTCAACTGTTCTAATAATGAATTGTTAT  
484351 TTTCTTTATCATCTTTAATATGAATCAGCAAATATTTAAAGGGCTGAATA  
484401 AATTGCGTTAAAACCTTCCTTTAAAGTTTGAATTTGTTGTGAAGTTACCTT  
30 484451 AAGCTTAAATCACTTGCAAGGTTAACCTTTTTAAGATCAACTAAATTAA  
484501 TTTGGTTTAAATCAAGTTTTTATTAGAACTTTAAAGTTTCTTTATGA  
484551 GTTACTACTATTTGTTTATCTTTGGTTAATTGAATATCAATTCAAATACC  
484601 ATCAAAATCAAAAACCTGGGCTGCTTGAAATGCTAATTTGGTGTCTTCTG  
35 484651 GTGCAATAGAACTATAACCGCGATAAGCTATTAAAAACTGTTTTCGCATT  
484701 ACTATTTTTTATCATTACTGCCAAAAACATCCTTAGCATCATCTGCTGAA  
484751 AATTGACTAAGTCATTCATCTGCGTCAATAGAGTCAATATCATAACCTTC  
484801 AAGAGCAGGAATATCCTTAGTTATATCTTCATTTAAATTCTCAGTTTCCT  
40 484851 CAGACTGGAATACTAATCAGTTACCTTCACTATCAAATTCCCCATCATAT  
484901 CAGTTTCATTCAATTGTCTTCATAGTAACCATATTCTTCATTTCCGATTAA  
484951 TTTCTCTCAAAAACCTTAGGTGCCTCGTTAATTCGTGGTTGACGATTCTTTC  
45 485001 ATTGTTTCATCAACAAGAACTCAGTCTCCAGATTCATCATAGAAACCATAT  
485051 CAAATCCACTCACCTTTATTGTTGTACCTACCATAAACTTCATCACCAAT  
485101 AAGTGGTAAATAATCTCTTTCTCTAGCTCATTTAACAGTTGCATCCTTAT  
485151 TTCATTTTTGATCATCACCAAGAATCCTGCTCAAACCTCATTCTCCATCA  
50 485201 GGTTTCATAATGACCATAACTATTGTTACCAACTAATAATTCTCAATCAAG  
485251 TGATTCTTCTCACTAGCTTCTGGTTGAATTTCATCAGCTTGAGGTTCTT

485301 CCAATACTGTTTCAGGTTTTCGTTCTTCAAAGTTAGGTTGAACAACTACT  
485351 TCAGGTTCACTAGAACTTGAGGTTCTTGAATAGTTTCAACTGGTGAATC  
5 485401 AAATTTAGCTTCTTGAGGAGTTTGTTTCAAGTTGAACAGTATCAAAAGTAG  
485451 CTTCTGGTTGAGATTCTACAGGTTGAATTTCTGGTTGAGTTTGAACCTTCT  
485501 TCAAGGAGAGGTTTCAAGTTGTGAATCTTGAACCGATTCAACTGGTGAATC  
10 485551 AAATTTAGCTTCTGCAGATGGTTCAAAAAGTCTTCTCCAGGTTGTGTGTT  
485601 CTACTTGAGGTTCAAATTGTGGCTCTGATGGTTTGTGATTCAATTTCATAA  
485651 TTTGGTTTCATCAAAGTCATAATTAGGTTTCATCTACATCATATTGAGGTTCT  
485701 TGATGGTTGTAGATCTGAATCATAACTAGGTTGATCAAAATCATAGTTAG  
15 485751 GTTCATCAAAGTCATAATTAGGTTTCATCAAAAGTCTTCTGATTCAACA  
485801 TGTGTGTGAGTTGGTTCACTACTAAATTCAGGTTGTTCAACAGTTTCAAC  
485851 TGGTGAATCAAATTTAGCTTCTTGAGGAGTTTGTTCAGGTTGAACAGTAT  
485901 CAAAGGTAGCTTCTGGTTGAGATTCTACAGGTTGAATTTCTGGTTGAGTT  
20 485951 TGAACCTCTTCAAGGACAGGTTCAAGTTGTGAATCTTGAACCGATTCAAC  
486001 TGGTGAATCAAATTTAGCTTCTGCAGATGGTTCAAAAAGTCTTCTCCAG  
486051 GTTGTGTGTCTACTTGAGGTTCAAGAAATACTTTTGTGATTTCATAACA  
25 486101 TCATCAAACCTTAAGTTTCTAGTAGTTTTTTCAGGTTGAACATCAAAAAGTGC  
486151 TTCAGGTTCTCCAACAGTATCAGTAGTTGTTTGTGATCAACTACTTCAGCTT  
486201 CACTAGAACTTGAGGTTCTTCCAATCCCTCAGTTTGTGATTGATTTTTTA  
486251 TCAAAAAGTCTTCATGTTTAAACAGTATCAAAGCTAGCTTCAGTTATTAA  
30 486301 TTGATCAACTGGTTTCAAGTTTCTCTCTAATATTTTTTTCAGTCT  
486351 GTGTTTCTAATTGAGGTTTTTCAAAAAGTCTTCTGATTTCAGCTTCAGAT  
486401 ACATTATCAAAGTAGCTTCAGATTTTAAATCTTCTGTTGATAATGGTTC  
35 486451 AGAGGAGGTTTCTCTGTTGAAGTTCTTTAGTTTCATCAAAGTAATTTTCAG  
486501 CTTCTGTTTCTTTAGGTTGAACCTTCATTATTTTCAACATTATCAAAGTTA  
486551 GCTTCCTCTAGTTTTAAATCTTCTAAGTTAGTTCCATCAAAGATTTGTTC  
486601 AACTTCAGCAGTAACAATTTCTGGATGATTTTGTGATCTAATGCAGGTTTCAG  
40 486651 ATGGTTGATCTTCAGAGCTAGGTTCTAATTGGGTTTCAATTGTTTCTGGT  
486701 TCAAAAGCAGTAAGTTTCTAGGTTGAACAACTGTTTCTTCAGACTGATT  
486751 TTCTAATTGTTGATGATCAAAAAGTCTTCAAGTTTCTTCTAATTTAA  
45 486801 TTTCATCAGAGATTTGTTTCAAGCATGAAATTCAGCTTGCGATGATTCTTGG  
486851 GGAATTTGAGCTGGTGAATCAAATTTAGCTTCTTGAGGAGTTTGTTCAGG  
486901 TTGAACATCTGGTTGAAATGATCATCAAAAAGTCTTCAGTAGTAGCTT  
486951 CAGGCTGTAGTTCTTGAGTTTTAATTTTCATCAAAAAGTCTTCTGGTTGA  
50 487001 ACAGTATCAAAGTAGCTTCAAGTTGTGATGATTCTTGAGGAAGTTCAAC  
487051 AGTTGAATCTAATTTAATTTCTTTGAAAGTAGGTTGGAGTTCTGAATCAG

487101 AACTCTCTTTTCGTCTGGTTTTGAATCAAATAAAGCATTGATTCAATG  
487151 ATTTTCAGTTAAATCAAGCGGTAGAGGAGTGAATAAGTTATTTTCATCTTG  
487201 ATGTTCAAATAAATTTTGTCTTGTTCAACTGTGGGTACATTTGATTGAG  
487251 AAGTCTCAACCTCTTGAGTTTGACTAATGAATTCAAGCGTATCTTTTGT  
487301 TCAGATGAAAATTCATTAGGAGTTTCAGCACTTCAGTGAACTGTCTTC  
487351 AACTATTTGATATGTTGGTAATACGAACTCACTATCAGTTTCTAGTTGTG  
487401 TTGTTGGTTGTTCTTGAACCTCTTTTCAGAAACATCTAAATTAATAAAAT  
487451 TCATTACCAATTTCTTCATGATTTAATTCAACAGATGTAGTTTGTAGTTTC  
487501 TAATGATTTATCAACATCATTTACAGAATCTAATTCAAGTGATAGGTCAG  
487551 GTTGAATGAAAGGTGGTTCACTTCTACAACATATTGTTGTTTTTTCATCA  
487601 AATAATGATTTTGGTTCAGTTTCAAGGAAATCTACTTTATATTCCAATCC  
487651 TTCTTGAGGTTTTGGATCATTATTAATAAAAGTTATTTTCATCAACTAGTT  
487701 CACTTTTGGGAAGTTCACTTGAAACCTTAACCTCTGTTTCTGTTGAAAAA  
487751 GGAGCATTAAACATCAACATATTCATTTGTTAAGAGTACCTCATTAAACAAG  
487801 TTTTTCACTAAATAAAGCAGTTAAATCAGTATTAACACTTTCATCACTGT  
487851 TTGTTTCTTTTATCTTTTTCATCTGAAACAACAGGTTGCTAAATTCTTGT  
487901 TGAAATTCATTAACAGAATAAGTAGGTTCAAATTGTTGTTCTGAACTGT  
487951 TTCATTTATTTGAGAATCAATATTATTAACAACCTTCATCTCTAAAAAGGG  
488001 ATTCATTAATGAAATCATTATTAGCATCTAAAATAATTTTCATCTACTTGT  
488051 GATTTTTCTTCTACACTTTTTTGTGTTTCATCAGTAAAAGAACCGAATTC  
488101 TTTTCAAACCTGAATCAATATCATCAGAAATATTAGATAAATCTGCTTTAG  
488151 CACTATCTTTTATTTCTTTAGAATAATCTTGACTTAAATGTTCAACATGT  
488201 TTAGCAATTTTCATCATGTTGTTGGTTCGTTTAAATAATAGAATCTAAGCC  
488251 TTTAAGATCATCTTCGTAAACAAAAACGGTCTCAACTTCTGGAACATTTTC  
488301 CTGCTTGAGTTTGATTGGAATCTAAGCCCTTAAGATCATCTTCGTAAACA  
488351 AAAACAGTCTCAACTTCTGGAATAGTAGTTTCAGGTTCAACAAGCTGCTTC  
488401 AGGTTCAATTTCAACAGGAGCCTCAACTTCAGATTCAACCTTAACCTTCT  
488451 CTTTAACGATTTCAATTAAGGGATGGTTTCATTAGTTTCTTTAACTGGA  
488501 TTTAAGAATTCAAATTTTTCTTTTCAAATGTAATTTAGTTACTGGATT  
488551 ACGGAAGATAACTTCATTTCTTCTGTTTAACTTCTTCAATTACCGGCT  
488601 GCTCTTCACTTGAATTTTCAAGTAATAGTTTCGTTTCTAGAGAAGAAGCT  
488651 AAGCTCTTGGTATTAAATACTGTAACAACAATGTCATTTTCTGTTCTCA  
488701 GTATGGTTGTTGAGAAATAGTCTTTTCTCTATTTTCATCAACTAAGCTAT  
488751 CAGTATGACCAAGTGCTTCTTCAGTAAAGCGAACAGGATCAGGGATCCAA  
488801 TTTAGTTTCTGTCAAAAAATCCTTTTCAGATCCATGTATTATTTGAAC  
488851 AAAACCATAGTTAGGGTTGCCTACAAGTGGTCTTCAAAAATCAATATCAG

488901 CTGGTCTTTGTTTAAATGAAAGCTGCATGTTCTTGAGGAACTTCAACTGTT  
488951 TCAATTACCTTAAAGTAGTTTCATCTTTGTAATTGGTCAAAATAACCTAG  
489001 TCAAACCTCAAGTATGATTTTTTCAAAAACCATATTTTCTATCACCAACAA  
489051 AGATATATCAGAACGCTTGTGAATCTTCTGGATTTAATTTTTTTCTCTA  
489101 ATAGTTGTTGTAAACTATCTTTTTTGTCTAGAACTTTGGTTTCTGG  
489151 TTGATTGTTTAAATTCACCAACTTATTTTCATTAATGGTTGGATAACTGC  
489201 TTGTTTGATTGGAACGTGATTAACAACAGTTTTTGGATTAAGTTCTCTT  
489251 CTACTTAAGATATCTGTTTCAGGTGGAACAATAAAAACACCGCGCTTGGT  
489301 TTCATCAAAAAATCTATAGGTGATTTGCTCTTTGATTTAACTGTTTCCT  
489351 TTTTCTTACTATTAAAAGACTTTGTTTTCTTGAGAATGTTTTTTTGATT  
489401 TCACCTAAAAAAGGTTGATCAAAAAGATTTTCAACTTTATCTGTCTTTT  
489451 TTTTGGTTTAGTAACACTCTTCTTGTTAGCTGATTCTAAATACTTTTTGG  
489501 TTTTGGATTTAGGGGTGGTGTTTTTGTTTTTATTCTTTGTTGTTTTGGC  
489551 ATTAATAAAAAATACCTAGCACTAGTGACTAAAGTTATCTGACTCACTAAA  
489601 TTGTAATTTTAAATATCAAGATAACAAAAGTTAGCTATATATGCTAAAAA  
489651 ATAAATAGATTTTAAATTAATTTATTTATTTAATTTAGTAGATTTA  
489701 ATAGTGTTCAGCTTCTTTTTGCAAAAGAAAAATAGTTATAAAATCAAAA  
489751 ATTAATCACTTTAATTTCAAAAAAATTTGACAGCTAAAGCTTTACATTTT  
489801 ATTAACAACAGaACAAATAATTTTTAGCTTTTAAAAATTTATTTAGAAAG  
489851 AAAACTATAAACAGGCAATTTTTGTTTTTCTGTTTTTACAAAAATATCAA  
489901 TAAAAATATCACAGTCAAAATGATTTAATAGTTTTTTGCGAGTTGCTATC  
489951 CCAATTGCTTTGATCATTTCTGCATTTTTTCCAATGATAATCTTTTTTTG  
490001 GCTTAATTTTGGAACTAATACTAGGTGAATTTTAAACAAGTTTTTTT  
490051 CTTTATTGAACTCTTTTCAATAATTTCAATTCTTGCTATATGGGGAATT  
490101 TCGTTTTTGCAATAAAAAATTATTTGTTTACGTAATCCTTCAAGAATCTT  
490151 AAAGTCATCGTTGTTTGCATCAATAAAATTGATATCTTTACGAAAGATAT  
490201 TATACCTAAGTTCAACTTGTTTAAAAATTGATCAAAAGAGGTTTTTATCA  
490251 AACTTAAGCAAGTTTATTTCAATTGTTTTTGTGGTTTAACTCTTCTAA  
490301 AATAATTGCTTTATTTAACTTCACTTAACTTTTTTGATGAAATTTATTAA  
490351 TTAAAAAATCTTGTAAATTTTGATAGCGCTTTAATTGTTGTAATTGA  
490401 GTTTTTAAAAATCTATCTTGTTATTCTGATCACTTCTAACAACTAAAAG  
490451 TAATACATCAATCCACTTAATGCTTTGCGAATTTCTTTAGTTATTAATT  
490501 CATAATTTGAATGTTTTTCTCAGTAAAACCAGGGACATCAATAAAAACA  
490551 ATATTTTTATTAGCTTGGTTAATTACCTCAGTGGAATAGAAAAGAAGCGT  
490601 TGTGTTATTTCATGGATGATACCATCAGACTATCATCGTTATGTAAAAAT  
490651 TAATTAGCGTTGATTTTCTGCATTAGTAGGTCCTAAAACACCAACTTTT

490701 AAAACTTTTCATACTGATAAGATCTCTTCATGAATTGCATCTTGAAAAAAC  
490751 ATAGTAACGCTTTCAAATGCTTCACTTTCTTCATGATTAAATTCAAAGAG  
5 490801 GTGTAATAATGCCGTGTATTAAGCATCTAGTTAAAAGAAATCAATTGTTAC  
490851 AACCAATCTCTTTAGCTTTTTTAAAGATGTATTTAGGACACAAAAAATT  
490901 TCGCCGATTGCTAGTGAAAAACCGTTTCAGTTTCGTTATAGCACAAACT  
10 490951 AATTACATCAGTACAACCTCTACGTTTTAAAAACTGTTTGTTCAAGTTTTT  
491001 TCATTTTTGAACAGGAAACAATTAAAAGCGCAAATTCTGGGTCAAACGAT  
491051 AGGTTTAAACTGCTTTTAATAATTTGGAAACAAAGTTCGACTCCTGCTTG  
491101 GTAATTTTTTACCAAAAAAGCGCTTAAAAAGGCGGCTTGAATTAATGCTAA  
15 491151 AAGATGACTTCAAACAAATCTTTTGATGGTAACATGATAGTAATATTATA  
491201 TCAGCCCTGTTCTAGAGTAACACTTAAATCTACCTTTACTAGATTTTTGT  
491251 TCAATTCTGATGAAATTTCTGATGTAGAAATTTTCTTTTGTAAGTCTA  
20 491301 AAAGCTTTTTTGTCTGATTTTTCTGTTGTTTCTGCTTGAAAATTAGTCCA  
491351 TGAAACGTTGTTAAAAAGATTTTCATCTTTTTCATTTTAAACATTAAAA  
491401 AATTTTGTTGTTGCGTAGTTCAAAGATTTACATTAAGATATTGTTTTACC  
491451 TTTACTGAAAACAAGATAGCAACTGTTGTTAAAAGCAAAATAATAAAGC  
25 491501 AATTGTTATTCCTAAAATTTTCTGCTTCATAATTTAACTATTTCTTAAGT  
491551 AATTAGTTAGGTTAATCTTGTTTTGAGCTTCACTTGCAAACTCAGATCA  
491601 TGCTCAACTAAGACTACAAAATTATTTAAAGTAAGTGGTTTTACTAATAG  
30 491651 CTGATAAACACGGTTTTTAATTTCAAGGTGCTATTGCATTCATGCATTTCAT  
491701 CAAGTAAGATCACCTTATTCTTAATGTTGCTAAGTAAGAATAGTTGTAA  
491751 ATTTGTTTTTGTCTGAACCTTAACCTTGTGTTGATTTGAACACCTGCATC  
491801 AAAAAGTAAGTATAGATATGTGGATTCTGATTATTAAATAAAGCCTCAC  
35 491851 TAAAGCCAAAATCATTTGCTTCTGTTTGCAATTAATTTTGACCCTTTAGA  
491901 TAATAAACGTTTTCAAAAAGCTGTTCTTTTGAACATCTTTTAAATCGAC  
491951 GTTATTAAATTTAATATTGCCCGTATATTCAAAACCTCTACCAGTTAATA  
40 492001 TTTTTAAAAAGTAGATTTACCACTACCATTTTGTCCAAAAATAACTGTT  
492051 TCATTTTTGATTTTTTAACTAAGGTTAGCTAAATCAACGTGTTGATTAAG  
492101 TGTAAGTATAAATTTTCTAGACTAATTTTCATCAGGACACTGTCAATTTA  
492151 CTTTAATACCCTCATCCTTTTGGTTTCTATAAACAAGTTAACTAATTTCT  
45 492201 TCACGACAATAGTGATAAATGTTTATTGCAGCACCAAAATTGAACAATTCT  
492251 TGTAGCATAAGTTGAAAAAAGTGATTGGATACCAAAAACATAGAATAAAA  
492301 AGCTCAATTGATAACGCTGTTCAATAATACCAATCACCCCCAAACCTAAT  
492351 ATAGCAAAATCAAACCTTGTGGAAGAAGCTTTTAATGTTTTCTATAGT  
50 492401 TAGACGATTAATTTCTTCTGTTGTTAATGTTTGTATTTGTAAAAGTG  
492451 CTTTACGAAAATTCAACATTAAGAAATTAAAGCGCTTTTTATTTTGTCT

5

10

15

20

25

30

35

40

45

50

55

492501 TCACGCAAATTTTCATCTAGCTGTAACTAATTTTGTTTTGCAATTCAAC  
492551 ATAAGGAATTTCTTCTTTGTAAATTTTTTTAGTAAAAAGAAGTCATAAC  
492601 AAAATAAGCCAGCATTGACTACTATTTGTGCAATGGCAATCAATAAAAAAT  
492651 TCTAATTGATTAATTCCTATTAAAAACCCGATAATTAGTGCAACAACACA  
492701 ACTAATAATTAAaTTGGGAATATAAAAGTTAAAAAAGGAAAGAACTTCTT  
492751 TTAAATAAAATTGTCGTTCTATTAAATTGATTGGTGATTTATTACTAAAG  
492801 TAAACAAAGCTTTTTTTGTGCAAACTTTGAATAATTCAACCCAAATATCC  
492851 ACGGTATTGTTTTTCAAATAAAAAATTCCTAATTAGTTGCAAAATAACTT  
492901 GCAAAAGCAAGTTTAATCCCTTTAGACATGAAAAATAAACTACCAAAACA  
492951 ACTAAATTAAGTGCAGTTCCAAAATCAACAGTATTAGTTATTATGGTACG  
493001 CGATGCTGTTGCTAATAATGTAGAGATACCAATAATAATCAGTTCAATAA  
493051 AAACATAAAAAGTGACTAAATTAAATCAAAAAAGTTACTGAAAAAATTA  
493101 CTTTTATTTACTGGTGGAACTCTCTTTAAATGCTTTTGCAACAGTTGCTGC  
493151 ATAACCCGTTTCAGAGTTTTTCTAGCTTTTCATCAGTTAAAAGGTATTTtC  
493201 CTTTTGCAGGATCATATACCTCTCAACTATTTTCATGTTTGTTTTAACT  
493251 ATGACAAAGTGATCTTTAAATGAAGTATTATGAATTTGCTATCAAGTTC  
493301 TTTTAGTTCCTGAAATGTTAATTGATAACTGTTGATTTCAAGACCAAAT  
493351 TTTTGCCATAACTTTCCATTTCAAATAAGCTTAAGCCATTTGGTGGTAAG  
493401 TTAATTTGTTCTAGTAATTCATCATGAACATACTTTTCATCATGGATTGC  
493451 ATTGGCAAGCATACCAATTACGCAAATTCACACTCATTCTGTTGTTCTT  
493501 GATAAATGATTTTCATCGCCTTTGTTTTGTCTTATTAATAGCAATGAAAA  
493551 GTGAAAAATGACAAATTTGTAAGCTGTTACAAACACTACAACTGTTTTTA  
493601 TTAGTTAAAAATAAAGTTACTTATTATTTATTTGCAAGCTGACTAGCACG  
493651 TTCGTACAAGGTTCTCACTAAAACACCTTGTCCAAGGTTCTCAATGGAAG  
493701 CAGTTGATGCAATATCACAATGGATCAAAGATACACCTTCTCTAAATTCT  
493751 GCAAGGAAACAAGCTGCTCTTGAAGAtCCAGCACCTCTTGCACTAGTAGA  
493801 ATTTTGCAAATCAGCAAGTTTTGTTAGCTGTAAAGGTTTTAAATAATCAG  
493851 GGTGCATAGGTAATCTTCATACAGGTTACCTGCACTACATGCTGCTTTT  
493901 TTAAAAGATTCTCACTGGTGATCACAAGTACTGAAAATACCTGTATAGGT  
493951 AGTACTCAATATGTATGACATTAAACCAGTAAGGGTTGCTACATCAATAA  
494001 TATGTGTAGCAGCTAAATCCCTTAGCAGCATATGTAATAGCATCAGCTAAA  
494051 ACCAATCTTCCTTCAGCATCAGTGTTATCTATTTCAACACTTTTACCATT  
494101 GTATGCTATCTTAATGTCATCAGGACGTTGCGCCTTAGCACCAGGAAGAT  
494151 TTTCAGTAAGAGCTGCTACTGCAACAACATTGGTTTTAACCTTGTTTTTA  
494201 GCTAATGCCAAAACAGTAGAACATACTATAGCCGCACCACTCATGTCATA  
494251 TTTCATGCCACGCATATAATCACCTGTTTTAATGTTTATTCCGCCTGAAT

494301 CATAAGTAATTCCTTTCCCTACAAAAGCAAGTTTTCTTTGGAATTTTAA  
494351 TTAGCTTGATAACTAATAACAAGTAAACGTGCTTCTCTTCAGAGCCTTG  
5 494401 ATTAACCCCTAAAAGTAAACCCATTTTTCTTAATTAGATCTGATTGTT  
494451 TAAGAAGCTTTTATTTTACAGGCAATTTACTTGACGCTTTTCAAATGT  
494501 TTAACAAATACTTCTGAATAAAGTAGATCTGAAGGAGTGTCTTGTAAATC  
10 494551 TCTTGCTAGGTTAACATATTCGCCTACTGTTTCATATTCTTTAACTAAGT  
494601 TGTGATATTCAACAGCACATTGAACAGCAACTTCAACATTTTTTTCAGGT  
494651 TTGGTTTTTCATTGTGAAAGGAGTAGTTTCAAAAAAGTAACACTTGTAAAT  
494701 AACAGTTTTTATCGCAGTATGAAAAACAACCACTATTTTCATTTTTCTTAT  
15 494751 AAAGTTCTATAAGACTGTCAAGATTAATGTTTAAATTTGGTTTTCTTTCTT  
494801 TTAAGAAATTGAACTAAAGCACGGTTGAAAGCAGGAAAATCAGTTGGTAA  
494851 AACAACACCAAATTCACATTAGGATTATGTGCAGCTTCTTCTTTTACAC  
20 494901 CATATGTTTTTGAAGTACAAAAACAAGTGTGTTGCTATCATCACTAAAA  
494951 GGTTTATTTATCTCATTCTATATCTCTATTTATTATTCTGAAAAGGAGT  
495001 TATCTTTTCTCTCTTTAACATCATAACAGCAACATTAGTAGTAATTAAT  
495051 GAACTAGCTACAGAAGCAGCTTTTTCAAGTGCAGTTTTAGTTACTTTGGT  
25 495101 GGGATCAATGATTCCATTTGCAATCATATCAACCTTCTTTTTAGTCTCAG  
495151 CATCAAAGCCAACACCAGTTTTTTTCATTTTTCAATTCACTGAGAAATTTTA  
495201 ACTGGGTCAACTCCTGAGTTTTGAATAATTTGACGCGCTGGTGCTTCTAG  
495251 AGACTTTTGCACAATTTCAAACCAAGTAGGATTCTTTAATGTTTTCAA  
30 495301 CACTAGTTTCATTTTCATATCGTTCTTTTAGTTTACTGTTAGTTAAAAACA  
495351 CAAGAAGCATTTAATAAACCAACACCACCTCCAGCGATAATCCCTTCTTC  
495401 AACTGCAGCTTTGGTGGAATTTAAAGCGTCTTCGATTCTGAGTTTAAAT  
35 495451 CTTTTTGTGCGAGTTCAGTTGCACCACCAACACGGATAACAGCAACACCT  
495501 TGACTTAAATAAGCAATTCTTTCTTTAATTAAATCAGAATCATACTTGTC  
495551 AGTGGTTTGTTTAATCTTCCGTTTAGAAGTTCAACATGCTTTTTGATTT  
495601 TATCCTTATTGCCTTTACCACCAATAACAGTAGTTTTTCTTTAGCTATT  
40 495651 TGAACCTTCTAGCATCACCTAAATTATCAACAGTAACATCTTTAAACCC  
495701 ACTATTAATTTCCGGTATTATATGCTAAGGTTCCACTACTAATTGCTAAAT  
495751 CTTCTAAAGCTGCTTTTTGACGTTCCACATATTCATTACATTTAACAGCA  
45 495801 ACAACATTAATGGTGCCCTGAGTTTATTAAGTCTAAAGTAGTAACAAC  
495851 TTCTTCTGCAAAGTCAGGTGCAACAATTAATAATGGATTACCATTTTCAA  
495901 CACTACCTTCTAAAAGCGGAAGAATTTCTTTAATTGTGTTAATTTTAA  
50 495951 GAGCTTACTAAGATTTTAGGTTGTTCTAAAACAACCTCCATTTTTCTTG  
496001 ATCACTAACCATATAAGGTGATGCATATGTTCCCTTTAAATCAATTCCTT  
496051 CAGTGGTTTCTAATGTTGTATTAATGGTTTTTGCATCATCAGTTGTTATC



496101 ACGCCATTTTTACCAACTAAAGCCATTGCTTGAGCGATCAGTTTACCAAT  
496151 TTCTTTAGAACCTGAAGAGATAGCTGCAACTTGTTCTATCTCTTCGTTAG  
5 496201 TATTAATTTTTTTAGAGTACTTTTCAAGTTCTTTAATAATAAGTAAGCTT  
496251 GCATCTTCAATACCCCTGCGGATGTTAACAGGATTAGCACCTTTATTGAT  
496301 AATTTCAATACCACGGTTTGTCAATTCTTGTGCTAATATGGTAGCTGTTG  
10 496351 TTGTACCATCCCCAGCAATGTCATTAGTTGACACTGCAGCAACTGAAATA  
496401 ACCTTAGCACCAATATTTTCAACTGGATCACTAAGTTCTATTTCTTTTGC  
496451 GATTGTAACCCCATCGTTAGTAATTAATGGGTTTGCAAATTTTCTCTCTA  
496501 AAATAACATTTTGGCCTTTAGGACCTACTGTTACTTTAACAGCATTTGCT  
15 496551 ATCTTATTAATACCCTGCAACAAGCGGGTTCTCGCATCTTTACCAAAGAT  
496601 TAATTCCTTTGCCATAATTGTTTAAATTTTATCTTTTCTTTGCTTACCAC  
496651 TTTCTGGTTTTTCAAAGGCAAGTACATCCTCAAATCCAATAATTTTGTAC  
496701 TTGTTTCCCTCATTCTCAAAAGAGATACCACTATACTCCTTAAAGTAAAT  
20 496751 AATATCACCACACCAAAAGCATATTTTGGTTTTTCTGTTTTGCCATATG  
496801 CAGGACCAGCACCAAGAGCAATTACAATCCCTTTATTAGCATTAGCATCG  
496851 CTTTTATCATTACTTGCCAATGAGGTAATAATCCCTTTTTTTGAGACTTC  
25 496901 TTCTTTGTTTGATTCCACAAGTGAAACCAAGACGTTGTCATGAATTGGCG  
496951 TTATGTTCATAATAAAAAATATTTTAATAATTAAAAACTAATTTAAAAGAA  
497001 AGTAAAGTTATCTTAAATTTATCTGATATTAGCGCTAAACATTAATTA  
497051 TATTTAGTGAGATATTGTTAATTTTAAATACAAATTAATAAGCTAAACC  
30 497101 CTTATAGAGCGGAAAGCGTTTTAAGAGATTTAAACAGCTGTTTTTGTTT  
497151 GACTAATTACCTTTTGATTACCATTACTTTTAATAACCTTATCAATCAAA  
497201 CTGGCAACAAAAATAAAGTCATTAGTTTTTAAACCTCTGGTTGTCATTGC  
35 497251 AGGAGTTCCAAGTCTAATACCTGAAGGACTAAAAGCAGATTTTGTTTCAA  
497301 AAGGGATTGTATTATCATATTCAAAACAATGTTAGCTTTTTGTAAACCACAAC  
497351 GCAACATCTTTACCATTACCAACCACTAATGAAAATAAGTGGGTTTCAGT  
497401 ACCTTTTGACACAACACGATAACCTGCTTTTAAAAATCAATTTGCCATTG  
40 497451 CTAAAGCATTATCTTTAACTTGTTGCATATACTGCTTAAACTTTGGATTCT  
497501 AAAGCTTCTTTAAACAAACATATTTAGCTGCTATCACATGTTGTAAAGG  
497551 TCCACCCTGACATCCAGGAAATACTCCACTATCAAGCTTTTTGATAATTG  
45 497601 CTTGGTTGTTAGACATAATGATACCCCCCTAGGACCACGCAAAGTTTAA  
497651 TGAGTTGTTGAAGTGACAACATCCACAAAAGGCAAAGGGTTTTGGTGCAA  
497701 ACCTGCAGCGATGAAACCAGCAATATGGGCAATATCAGCTAAAAGATACG  
497751 CATTAACTTGTTTTGCAATTGCACTAAATTTTTTAAAGTCAACAGTCCTA  
50 497801 GAATAGTTAGAAAAACCACAAATAATTAACTTTGGTTTGTGTTTCGAGAGC  
497851 AATTTGAAGAATTGCATCATAATCAAGAGTTTCTGTTTCAAATCTAACG

497901 AATAAGTTACTGCTTGATATTGCTTACCTGAAAAATTAACGGGGCTACCA  
497951 TGGGTTAAATGACCACCACAATTAAGATCTAATCCTAAGATAGTATCTCC  
5 498001 TGGTTTTAACAATGCTAAGTAACTGCATAGTTAGCAGATGATCCAGAAT  
498051 GAGGTTGGACATTAGCCCATTGTGCTCCAAATAAAGTTTGGCACTTTCA  
498101 ATGGCTAAGTTTTCAGATTTCATCAACAACCTTCACAGCCTTGATAAAAACG  
10 498151 TTTACTGGGATAGCCTTCTGCATATTTATTTGTTAATACTGAACCAGTTA  
498201 CAGCTAATATGTCTTGGCTAACGTAATTTTCTGAAGCAATTAAACAAATG  
498251 TTTTCTCTTTGACGTTGTAACCTCTTTATTAAGTAAAGCTTACCTTTGA  
498301 AAACATTCAACTTAATTAACGTAATAAAAAACGGTGTTTTTTGATTGTTCT  
15 498351 TATCAACATATTTAAATTCTTCCTTTTCACTACTTTTAATTTGGTCGTAC  
498401 AAGTGGGTATTGTGCTTTTTAGCAAATTGTGCATAGAAAGATTTTGTGTT  
498451 ACTGTCACCAAAAAATTAAATCATAGTGCTGAAATTTATCCCTATTATTAG  
498501 TAGTTCCTGGTTTTATTTTTTTTCACTTTCACGTTTAGAAGTTCTTAAAGT  
20 498551 TGAGACATACCAATGTTATCTTTATGTGTTTTGGAATTCTTATATACCTC  
498601 TAAACACCAAAATAAATACTGTTAATTTTTTGGTTGTTGTTAAATATAG  
498651 CACTTCCAGAAGAACCACCAGGGAGATTGGTATCATCAAGCATTAAACCA  
25 498701 TATCCATACTGTTGGTACTCTTTGTCATGATATTTAAGTTTAAAGTTTTT  
498751 GAAGTTTTGAAATGTAACAATCCCTTTTTTCGTGTTTAATAACTTTATCAA  
498801 CATGACTGTCTTGGGTTTTTTTTGGAAAAATATTTCACTACCTATTTGACCA  
30 498851 TCTTTTCTGGCATTTTTTGTAAATTACAGGGATCTCTTTAGCAGTTGAAAC  
498901 TAAATATGTGTTTTTACTCCATAACTGACTTTTTTGATTAAAGTTATGAG  
498951 TTCTAGCAAACCTCTTCTTTTTGTCTAATAAGCGGTTTTGATCATAACCT  
499001 CTTTCAAGTACAGGATAACCCAAAAGATAGTGGCTATGGTTTCAATGTTG  
35 499051 TTCTAAATCTTTGGTTTCAAATATATTAGTGCTATCACCACAACTTTTAT  
499101 AAGTATTAATTGCTGGCTTAATGAATTCATTGAAGATTTGTCAATCACGA  
499151 AGATTTTCTAAATTAAGTTCCAGTTCTATAACAGCAAAGTCTGCATAAAC  
499201 AGGCTTAATACTGTTAACACCTTTCAAGAAATTAGTTGCGGTATACGCAG  
40 499251 TTTTAGGAATATTTGATGTTTGAATAGAAAGCAGTGAATCATTTACCTTT  
499301 CTTTGTCTAATTTTTCTTCTTGATAGAGTTTTGTAATATCTGTTTTGTT  
499351 AGTGTATTTACCAATTGAAAAATAAACAGTTGATTCATATTCATTAACT  
45 499401 CCCTTTGATCATCTGTTTTGCTGTAAGGTCAATGATCACCGATATTTCTC  
499451 AACCACATCAGCAACATGCAAATTGGTTGCAATGTAAGCGAAAAAGAACC  
499501 TTGCTTTTGGGTTGTGTTTTTCATCACCTTTTCAGTCAATTAATCAACCAG  
499551 TGCCATAAGAGTCATTACTAAAGCTAGTGAAATTTAAAGTAAAGTTAAA  
50 499601 TCATATCCTTTTCTGTATATATCACTTTCTTCTGGGATAAAACTTGTATT  
499651 AAATTTAAAGTTTCTGTTGTAAACCTTCTGTTCTACCTTAGGTTGCTGAT

499701 TTACTTCTGTTCTCTTGATCAGATTGTTTCATCTTTAAAAGGAGTAGCGTTG  
499751 TTATCTGTTGTGCTGTCGTTTTTTCTTCTATAGGAACAGGAACAGGTGA  
499801 AACAGCAGAACAAGAAGCTAAAAGTGCTTGAATGAAATTAGTGAAAAAC  
499851 CTAAACTTTTTAGTTTAAACCACATATCAATCTTTAACATTTTAATACAA  
499901 AAATATTTCAAAACCTTTAATTAATGAAGTTAAGAAGCACCTTGTTAAACT  
499951 TAGGCTTTAGCTTCAAAAATAATTGAGTTCATCTTTTCACTGATAAATTT  
500001 AATTATTTTTATTCTGCTTAGTTTTAGATGCAATTAAGAAAGAGCTA  
500051 ATGAAAAAACTAATGAAAGCAAATGCAACCATCAAAAAAGTTAAAAATGA  
500101 AAATAGAACTACTATTGACTCAGGTAACTAACTAAATTAACCAAAAAA  
500151 AATTAATCCCGTTAGAATTTGCATTGGCTTGATAACTACTATCTAAAGCT  
500201 AGAAAGCCAACTACAAAGCTACCAATTAGAAGAATTAAACCAAAAAATAA  
500251 TCAAAAAACACTATTTCAGTTTCTTTTTCATATCGAATAATCTTATCTATC  
500301 CGTCTTTGGTGTCTACCACCTTCAAATTAGCTTTGAGAAAATCATCCAC  
500351 TATTTTAATGTTTTCACTGTGAGTTACAAAACGACTGGAAAGACATAAAA  
500401 CATTGGCATTATCATGTTGTCTAGCTAAAGCTGCTGTTTTCTCACTAACA  
500451 ACCAAAGCCGCTAATACTCCTTTTACTTTATTTGCTGCCATACAAACCCC  
500501 AACACCAGTACCGCAAATTAGTATCCCAAGATCTTTATCAGAATTTTTCT  
500551 TGACCTTATCAGCTACCAAAAAAGCAAAGTCAGGATAATCATCATTAGCA  
500601 TCAAAATAATTAGGGCCAAGATCAACTACATTAACTGCTTAGTCTTTAG  
500651 GTGTTCACTAATAATTTTTTTAAGAGTTAAACCGGTATGATCAGAAGCAA  
500701 TAAAGATATTAAAACTCATTTAATTGAGTTCCAGATAGTCTTGTTTTGTA  
500751 TTGGTTTTAATTTTAGTTAAAGATTAATTAATCCTTCTAATGTATCAGG  
500801 ATAGTTTTGTCGATTGTATAGTTTTGTAACTGTTCTAATGATCTATCGA  
500851 TATGACTACTCTTTTGACGATATTTATTTGCAAAAAGAAAAGCTTGTTTG  
500901 CACATTAGCCTTAAGTTAACTAACTAACAACATCACAAATAACTTCAGT  
500951 CAATTGAATTTGCAATAAATCTATCTTTTCACTAAACAAATTAAGTAC  
501001 CTAAATAGTTATTATTAGCTTCAGTGAAGATGTTATCAAGTTCTAATTTT  
501051 GATTTATTAATTACTTGCAATGTTTTAGCAGGAACCTTTAAATCTTGATC  
501101 GCTAATTAAATTTTCAATCTGAAAAAATTTAAATCGGAAATCATCTAAAG  
501151 TATAGACAAAAAGCGATAGTCATCAAACTTATTAAGTCTAAATTAAGT  
501201 AAATCAGTTAGTGAATTTTTTCAAGTTTTCTAAAGCTTGATTTGTTTGACT  
501251 CATCAAGTAAACAGTTTTTTCATAATTGATTTGATTCTGAGCTAACTTT  
501301 GATGGTTTAAGTTATTAATATTTTTAGTAATTAGATCGCAGTTCTCATT  
501351 AGCTCAATAATTAAATCATGCACATCTGTTTCATTTTGAACACTAATTC  
501401 AATGGCTTTAATTTGTTGTTTTTAAAGCTCATTTTTCTTTTCATATTGTT  
501451 GAATTTGATTACGAAAATCATCAATATTTTCAACCACTAAATTAATGCTT

501501 TTTTCTTTGGAACTAACTGCTTGAAAAAGTCAACTAATCGCCTCTTGAAC  
501551 TTCATCCATATTCCCTTTCGCATAGCATTAAATTTAAGTTATTAAGAAAAAT  
5 501601 TGGTACAATCCTTTAATTTAATGGTAATGTTATTAATCAATTCATGAAGT  
501651 TTTAAGAGATCTTGACTGTTAATTACTTTATTCTTCATTAATTCCATTTG  
501701 TTTTACCTTTTGAATTAAAAACCTTAAAGTGATGGGTAAATAACTTAACT  
10 501751 TAATATCAAACATATATTGCCTGTTAGCAGTAATAATTGTTTGAAGTGA  
501801 ATGTTATGTAATTTGTTTAAAAAAGCAATTTGCTTTTCTACATCTTTAGC  
501851 TTGAATACAATTTTCTATCTCTTTAAACAAGAGCGAAATCCTGTTAAGAA  
501901 CATTTAAATAGAAAAGCGAATCATATTTTCAATTAAAAAATTATTAATA  
15 501951 AATTGGTTTAAAAACAGAAAGCCTGACGATAAAAAACTAAACAATCATA  
502001 GCTATTGTTGAAATAAAACAATTGCGTTCCTTAGTTAGATTAAATGTATTCTT  
502051 GTTGTTTTGTATATAGATGTTGAAGATTTTATTTAAGAGCTTAATATTT  
20 502101 CTATTAAATCAGATGAAACGATAAAATATTATTTGGTTTACTGTAAACTGT  
502151 TAGTTGCTCAAAAGCTGAATTGATTTTCATTATCAAATTTGATTTGAAACT  
502201 GTTTTAAACTTTAATGGATTGTCTAACGCTTGTTTTTCATTTCTTAGT  
502251 AATTGAAATGGACTAATCACACAATTGAAATTGCTTAATTTCAAGTTATT  
25 502301 ATAGAGTTGTTTGGTTTTTTTTTAAAAGTAAGTTATTTGTCTAACAAAAA  
502351 GACAAACTAATAGATAAGCACCAAAAATTACTAGTAGTAAGAAAGGGAGC  
502401 AAGATTAGAAAAACCAGCATTTTATTTTTCTTACTTGAAAGTTTAAATA  
502451 GTTCAAACATTAAATTTTGTTCATTTTAAACGTTTAGCTTAGCATCCTTG  
30 502501 ATATGGTGAATTTTCTTTCAAGTTCTGTTTTCTTTTTAAGGTTTCATT  
502551 AATATCAACTTCATCAGCAAAAACAAAATTTTCTGTGAAAATCTTAGCTT  
502601 CTGTTTTTTTAAATAAGCATTAAACCAGCACCAATAATTGCTTCTCTTTT  
35 502651 GTTTGATCAGCAAAAATAATTTTGCACAGATGGGATTGAATAGCAGCAAT  
502701 CAAAGGAGCGCGATTAAAATTTAATCCTATGTAACCTTCAGTAGTTTTAA  
502751 CTTGCGCACTAATAATGGTTTTATCTAGTTTTATGCCACTAGGACTAAGT  
502801 ACCAAAAAGCGCAATAACTTCATAAACTATTAGTTTTATCAAACCTCTT  
40 502851 GATTTAATCTTTTGTCTTTTCAACAGCCTCTTGAATGGTTCCAACATAA  
502901 AAGAATGCTTGTTTCAGGCAAAATGATCATGCTTACCTTCCAAAATTTCTTT  
502951 AAAAGATTGAACAGTATCATTTAAAGATACATATTTACCTGCAATACCTG  
45 503001 AAACTTTTCAGCAACAAAAAAGGTTGGGATAAAAAGTTACGTATCCTT  
503051 CTTGCTCTTTCAACAATAATCTTATCTTCATCAGACAATTCATCAATCCC  
503101 TAGTATAGCAATGATATCTTGTAATTCTGCAAAACGCTGCAAGATATTTT  
503151 GCACTCCTAAAGCGACTTTATAATGGTTGATACCAACAACACTAGGATCT  
50 503201 AATAAACGACTTGTTGATTCTAAAGGATTAATTGCTGGAAAAATACCTAG  
503251 TGCTGCAATATTACGATCCAACACTGTTTTAGCATCAAGATGGGTAAATG

503301 TTGTTGCAGGTGCTGGGTCTGTTAGATCATCTGCTGGAACATAGATAGCT  
503351 TGAACAGATGTAATAGAACCTGTTTTGGTAGAAGCAATTCTTTCTTGTA  
503401 CTTACCCATTTCAATAGCTAAAGTTGGTTGATAGCCAACAGCAGATGGCA  
503451 TTCTACCAAGTAATGCTGAAACCTCACTACCTGCTTGAGTAAAACGAAAA  
503501 ATATTGTCAATGAATAACAGCACATTCTGATTATCATGATCACGAAAATA  
503551 TTCTGCCATTGTAAAGCAGTTAAAGCAACTCTCATTCTAGCTCCTGGTG  
503601 GTTCATTCAATTTGGCCAAAACTAAACTGTTTTATCAATCACCCACCT  
503651 TGAATCATTTTCATAGTAAAGATCATTACCTTCTCTTGTCTTTACCAAC  
503701 TCCAGCAAATACACTTAAACCAGAATGTTCTTTGGCAATGTTATGAATTA  
503751 ATTCTTGCACCAAAACAGTTTTCCCAACACCAGCTCCTCCAAATAAACCA  
503801 ATTTTACCCCCCTAACGTAAGGAGTTAAAAGATCAATTACTTTTATTCC  
503851 TGTTTCAAAAATATCAACAGTATTTGGTTGTTTCATCAAAGCAGGTGGGT  
503901 TACGATGGATTGATAGCTTTGGTTTTTTGGTAATGGTTCTTTCCATCA  
503951 ATGGGTTTACCTAAACATTGAACATCCTTCCCAATACATTTTGGCAAC  
504001 AGGTACCTCTATTGGATGGTTATAGTTAGTAACTTTAACATTACGTGCTA  
504051 ATCCTTCTGTAGGACCTAATGCAATGCAACGAACAATGTCATCACCTATT  
504101 AATTGGGTGCTTCTAAAAAAGCTCACTTTTTTTTAGTTGTACTCAA  
504151 ACAATCATAAACTCTAGGTAATTGTTTACTTTCTGAAAAGATAACATCAA  
504201 CTACAGGACCAATGACTTGGTGAACTTTACCATATGTTAGGTTTTCTTTT  
504251 TTTATCAATTTAATTCATACCTCCTATAACTTCAATAATCTTTCTGTAA  
504301 TAGAGTTTTGTCTTAGCTTGTTAAATTGTAAAGTGATTATCAAGTAAA  
504351 TCTTTAGCATTCTTTGTAGCAGCTTCCATTGCATTTTGTCTAGAAGCTGA  
504401 TTCACATAACTTAGTTTCAACAAGGCCACCATACAGAGCCACATCAAAAA  
504451 ACTGTGGAGTAATTAAATTAATTATCGTGGCTTGATCTGGCTCAAAATCA  
504501 AGTTGTTGATCAGTTACAACCGGATTTAAAGTTTTAAAGTTTCAACATC  
504551 GAAAGGAAAACTTGAAAGAGCTGAGATTGTTGGATTAATGAGTTTTTAA  
504601 ATTTAGTGTAACCATACAAATTCGATCAAGTTTAACTCTTTAAATGCA  
504651 TCCATAATCTGATCAAATATCGTTTGACAATAATCAAAATTAATATCACG  
504701 ATCTTGGATATCAATAAATCCAACAGCAGGATTATATTGACTATTTTTAT  
504751 TTCAAAATGATTGGTTTTTTCTACCTAAAAAAGATTTTATCATCAGCT  
504801 TTAAATTAGCTTTTAATAACTTATTCATGTTTGAATTATGCTGTCCACA  
504851 AAGTCCTAAAGAAGAACTCATCATTATCCATAAAGTTTTTGGTTATCTG  
504901 GTTTCTTTTTTGGTTCTTTTAAAGAAACAACTACTTGCCAACAGCTTTA  
504951 TAAATTCATTAAAAAACAACTAATTTCTTGAACTGTTTTTGAACCTT  
505001 AATAAACTTAGCGCGTGACACCATTTTCATTGCATTAGTTATCTTAATGG  
505051 TGGATTTTACTGTATTCAATCTGCGCTTAATTTCTTGATATAAAGCCATT

505101 AATTAAGTTCCTCAATACTACCAAATTTGGTAATATCATAATCTGTTAAT  
505151 GTACTGATAAAACGTTTCACAAGCATTTTAAAAGCGGTTTGTAGTTTACT  
505201 TTCTAAATCCTCAGTAAATTCTTTTTTGTAGATAACTCTTAAACAGAG  
505251 GATGGGAACCATTAATTTCTTCTGTTATCCTTTGTTTAAATTTAGCAATT  
505301 TCATCAACTGGAATAAACTTAATGAAAGCTTTGTTAATAGCAAATAAAAA  
505351 TAATGCTTCATGGACTTGAGAGTAAGGTTTACCATTGTTGTTAATCA  
505401 TTTCCATTACTCTTTTACCATGCTCTAAAACCTTTTTTGTATTTTCATCA  
505451 AGATCACTACCAAATTTGACTAAAACCTATCAAGTTCACTATACTGAGCAAG  
505501 TTCTAGTTTTTAACTGCCAGTTTGCTGTTTAAATCGCTTTGTTTGTGCTG  
505551 CACTACCAACCCTTGAAACTGATAAACCAATTTGAATTGCAGGGCGTTGT  
505601 CCAGCGTTAAATAGACTACTAACCATAAACAGTTGGCCATCAGTAATTGA  
505651 AATAACATTTGTAGGAATATATGCAGAGATATCACCAGCTTGAGTTTCTA  
505701 TAATTGGTAAAGCTGTAATTGAGCCACCACCATTTTCATCATTTAATTG  
505751 CATGCACGTTCCAAAAGTCTTGAATGTAAATAAAAAACATCTCCTGGAAA  
505801 AGCTTCTCTACCAGGTGGTCTTTTTTAAACAGAGTGAAAGAGTTCTGTAAG  
505851 CAACAGCATGCTTAGAAAGGTCATCAAATACAATCAAACATCCTTTCCT  
505901 TTTTAAAGTCAATATTCAGCAATAGTTATTCCTGTAAAAGGACTTAAATA  
505951 AACCATGGAATCAGAGTCACTAGCTGTAGCACAAACCACTGTAGTGTATT  
506001 TCATTGAATCATTAACCTCAAGTTGGTGTACAATTTGTGCTACTGATGAA  
506051 TTTTTTTGACCAATTGCTACATAAACACAATAAACATCTTTATCTTTTG  
506101 ATTAATGATAGTGTCAATCGCAATAGCAGTTTTACCTGTTTGTCTATCAC  
506151 CAACAATTAATTACGTTGTCCTTTACCTATAGGAAATAAAGCATCAATT  
506201 GTTAAGATTCCAGTTTCAAGTGGTTGGTTAACACTTTTCCTTTTCATTAC  
506251 ACCTGGAGCAATTTTTTCTATTTGATCATATTAGTAGCTTTAATATCAC  
506301 CTCTACCATCAATTGCTTCACCAAGTGCATTGACGATTCTACCAAGCATA  
506351 ACATACCAACAGGAGTTTTTCAATTACACTGTGGGTTCTTTAGCGGTACT  
506401 GCCTTCTCGTAACGAAGAATAGTCACCAAAAAGTGCTATTCCGACTGTAT  
506451 TTTGTTCAAGGTTTAATACTATTCTTGAATATTATTTCAAATTGAATT  
506501 AACTCATTTAATAAAGCATTTTCAAGTCCACTAACCTTGGCAATTCCATC  
506551 AGCAACACTAATGACTTGACCAATTTCACTGTTAAATATTTTTTGGAAAT  
506601 ACTTTTTAATTTAGTTTTGATTAAATGCTACGATTTCATTTAGTTTATCT  
506651 GCCATAACTTCTCAATTAACCTAAATAAAATGGGCCATTATGCGTTTTTAA  
506701 TTCATCACGCACATTTTTTTCAAATAAATGGGAAGTTGATTCTATCCTAA  
506751 TTCCTGAAATTAAACTGCGATCAATCTCAGTTTTATAAACAACCTTTGTT  
506801 TAAAAAGTTTTTCCATTATTGCAATAATTTGTAAAGTTGTTTTGAGCT  
506851 TAATTCAAAGCAGTAATTATTTTGATAAATTGAATGTGTTTTGACTTT

506901 CAACATTATCAAAAAAATACTTAATTGCCTGTTCAACTAAAGTAAAGTAA  
506951 CCCTTTAAAAATAATTACTTTTAAAAAATCAACAAAAAAGTTGACAAAAATG  
507001 ATTTTAAACAACCTTATCAACAAGTCTTATTTTATCTGGTTTTGTAGTG  
507051 TATAAGAATTAAAGTAAGAACGATAATGAACCATCTTTAAATACGCATT  
507101 AATTCAGAAAAAATGGCACTCTTCATAAATTTCTTTACTTGTTTTG  
507151 CTCTTCACTTAATTGAAAAAGTGCAGTTCCAAATGCTTGTGCATTAAATCA  
507201 TCTTCTGTTTCGTTAGCTTCTAAATCTCTAATAAACTTATCAATAAATTC  
507251 TCTATCTGATTTTTGATCTATTTTCTTGAGAATTAGTTCTTGTGCAGCCA  
507301 ACATAGCCAATTCCACACTCTCTTTAATAGATTGTTCTTTAAGAGAACGT  
507351 CTTTCTTTTCAATTCCTGACGAGCTTGAAAAATCATTAAAGTTAGCTTG  
507401 GCGATTTGCTGTTTTTCTATTTCACTTTTTAATTGCAAAGCTTCATAGT  
507451 TAGCTTGATCAACAATTTCTTTAGAACTATTAGTGCTTTTTCATGCCTT  
507501 TGATTAGATTCTTCAAGTAGATTTCTTGCTTGTTTTCTAATTCATTAGC  
507551 TTGTTTGATTTGTGCTTCTAGTAAATTTTACGGTTATTTAAAAACCTTT  
507601 GAGTTGGTTTTCAAAACAAGAAAATCATCAGTGTTAGTAAGATGAAAAAT  
507651 GCTAGTAAATGAGTAATAAATACCCAAAAGTTAGGAAAAAGTTCATTTAT  
507701 TACTGAACCTACTCTTAATTTCTCTAACATTCTCAGTACAAGAAACCAAAA  
507751 ATAAGCTGAGTGTAATAAAGCTAAAACTAATAAGCTTCATTTAAAGACA  
507801 AGTTTTTTTGCCTTTACCATCCTTAAGCTCCTGCTACAAAAATTAAGATA  
507851 AAGGAAATTAAGTCCATAAATTGCTGTAGATTGAGAAACAGCAGAACCC  
507901 AATGAAAATTAGTTTAAAAACCTGTTTTTCACTTCAGGATTCTTGCTA  
507951 TTGCCTCAACAGCTTTACCAAAAATATAACCTTGTCGAATCCCTACAGTT  
508001 GAACCTGCAATCATAGTAACACCAGCACCTATATAAGCACCTAGCTTAGC  
508051 ACTAGCGTTAACATCCTGGGTAGTTTGAGTTGTTGTAATATAACACCAA  
508101 CTGTAGCTAAAATTTCAATTAACATGTTCCATAACTAAATATTTTCTTGAA  
508151 TTACCTTTATGCCTTTAAAGTGTAATTCACCTGCATTATTATTTCCAAA  
508201 CCTTGATTGCGCATTTTAGCCCAATAATTATAAGTCAACATTACAAAAAC  
508251 ATAACCTGCAATACACCTGCAATTACATCAAAATAGATGTGTAATACTG  
508301 GGGTTATTAAACCTGCAAAAAGTTCCTAAGCTAAGTGCTAATGGTTGG  
508351 TTATTAATACTTGAAAAAATAAAAATTCAAAAGTTATAAAAAAGCGCCAA  
508401 AATAACTGTGCCCGCTAATATGTTTCCCATAACCTTAATGAAATAGAAA  
508451 AAAGCGGTGCAATCCACTCAATATACTAAAAGGATTTGGAATGAAAGTA  
508501 GAATACTTTTTTCTTTAACAGTAATCCAAAGGCAAACTCTTTAAAAAA  
508551 ATTCATCTTTTGGTATCTAATCCCCATAACAACAATCCCAATAAAAGTTG  
508601 CAAGTCCTAAAGAAAAAGTAAATGTTAAAGATGATGTTGGTGGTGAAATA  
508651 CCACCAAGCAAGCTAACTAAGTTGCTTGATACTATGTACAGAAGCAACAT

5

10

15

20

25

30

35

40

45

50

55

508701 TAAAAAGTAGGGAGCAAATTTCTTATTTTCCTCTCCTAAAAGATCTGCTG  
508751 TTGTATCTTGTACCCAAACAAACAACATTTGAAATAAAAGCAAAAAATAT  
508801 GAATTATTTTAAAGAATCTGCTTTTTTAACTTAAGCTTATAAAAAAT  
508851 AAAAAAGTTAGAAGCAGTACAAAAACAATAAAAAATACCAAGAATTTGAT  
508901 CAGTAGGGGCAAATGGTTTTCAACCGCTAATTGGTGAGATATCAAAAAATA  
508951 CTTTGATTGGAATGAAATCTATTTGATTAGTTTCTTTTAAACTATCTC  
509001 CCGTGGCGACATGTTTTCTTTTCGATTTAGATATTAAATTGATAAAAAA  
509051 TATTCTAAAGGTAACCAAACAATGATAACACTAAATTTAGTATTGGAAA  
509101 AAACAATGTTGAAATTATTGTTGCAATAGTGTAAAAATTGACGGAGTGA  
509151 CAACAAAAGAAATAATCACAGGAATTAAATAAATTAAATATCTAGCTGTG  
509201 AAAAAAATGCAAAGAATGAACTGCTTTTTGCTTTTGTACATTTTCAA  
509251 ACTTGCAAAGAAAGATGCTAATCTTAAACTGATAGTGAATTTAAACAG  
509301 CAAAAGGTAATGGCAACATTCAACCAAATAAAATGTCCAAATTATTGCCT  
509351 TTTGTTAAAAACAACACTGCTATTAAAATTAGTACAAATAACCAAGCTAC  
509401 AAAAATAATTAAGGTAATAATTTTGCAACCTTCTATTGTTTCAATTGA  
509451 ACAAACCTTTTAGATGTTAAAGTTTTTAGGTTAATGTTTGTAAAGGTAT  
509501 TTCAACCTAAGTATTTTCCTTTATCACCAAGTTCAATTTCTATGTACAAC  
509551 AAACGATTGTATTTAGCTATTCTTTCTGAGCGTGACATTGAACCGGTTTT  
509601 AATTTGACCAGTTTGGGCAGCAACTGCCAAATCAGCAATAGTTGTATCTT  
509651 CTGTTTCACCACTGCGATGTGAAATTACTTGACTCCAGTTAGCTTTTTTT  
509701 GCAACTTCAATTGTTTGAATCGTTTCACTAATAGAACCAATTTGATTAA  
509751 TTTAATCAATATCGAGTTTGTGTATTTTGTGCAACACCTTTTTTAGCAA  
509801 GTTCTGCATTAGTACAGTAAGTGTCATCACCAACAATTTGAATATGGCTA  
509851 CCTATGGTTTTAGTTAATTGGTTCATCCCTTCTCAATCATTTTCACTCAA  
509901 ACCATCTTCTATTGAAATAATTGGATATTTTTTGTTAATTTTCTAAGT  
509951 AAGCAATCATTTCTTTGCTTGTTAAACTCCAATCCTTTGCATTAAGGATA  
510001 TTAGCTTTTATTCCTTTCTTGAAAAACATAAAGTTTTTATCTTCGTCATA  
510051 AAACCTACTAGCAGCAACATCAATGGCAATAGCAATATCATCTCAAGGCT  
510101 TATATCCAGCTAATTTAATGGCTTCAACCATGATGTCAAGTGCATCTTCT  
510151 GCAAGTTTAAAGTTAGGCGCAAATCCACCTTCATCTCCTTTATTTGTGTT  
510201 TAATCCACGCTTTTTTAAAGATTTTGTAAAGCATGAAAAGTTTCACTAG  
510251 CCATTTTTAAAGCTTCATGCATCTTTTAGCACCTAAAGGCATGATCATG  
510301 AACTCTTGAAAATCAATATAGTTATCAGCATGAGCACCACCATTAAATTAC  
510351 ATTTAACATTGGCACAGGTAAAAACAAAATTTGTTGTATTTAATCCAAATTA  
510401 ATTTATTTGAAATGTATTGAAATAATGAGCTGTTTGTGCTTTTGTCTGCT  
510451 GCTTTTGATACTGCAAGTGAAACAGATAATATAGCATTTGCTCCTAATTT



510501 TGCTTTGTTGGGAGTATTGTCTAGTTTAAATCATTGCTTGATCCACTGTTA  
510551 ATTGATCAAAATGCATTTAAGCCAATAAGCTTAGGGGCAATAACTTTATTA  
510601 ACGTTATCAACGGCTTCGTTAACGCCTTTACCAAATAATTTTTTGGATC  
510651 ATTATCACGTAATTCAATTGCTTCTTTCTCACCTGTAGAAGCACCTGATG  
510701 GAACCATCGCTTCACCTACATGACCAGATGCCAATTTAACAACACAAGCT  
510751 ACTGTTGGAACACCCCGAGAATCAAAAACCTTGATAAGCAAAAATATCGGT  
510801 TATTTTTGAATTGATGTTTAGATTTGAACTTCCCATATTAAATAGAAAAA  
510851 TATTGTTAATAAAATTATTATATGTTTTAAGATTCTATTAAATCAAGTA  
510901 ATATGAAAGAAATTTATTTTGGTGGTGGTTGTTTTGAGGAATAGAAAAA  
510951 TATTTTCAACTTATTAAGGGTGTTAAAAAACATCTGTTGGTTATCTCAA  
511001 CTCTAGGATTAGAAATCCTAGTTATGAGCAGGTTGTTCTGGTTATACTA  
511051 ATGCTGTTGAAGCTGTAAAAGTTGAATACGAAGAAAAAGAAATTTCTCTT  
511101 TCAGAATTAATTGAAGCACTTTTGAAGTTATTGATCCAATAAGAAA  
511151 TAGACAAGGTAATGATATTGGAACACAATATCGTACTGGTATTTATTGAA  
511201 CTGATAGCAGTGATGAAAAATAATTAATGATAAGTTCTTAAACTTCAA  
511251 AAAAATACAGTAAACCAATTGTTACAGAAAAATAAAAAAGTAGAAAATTA  
511301 TTATCTTGCTGAAGAATACCATCAGGATTATTTAAAAAAGAATCCAAACG  
511351 GTTATTGCCACATCAAATTTGACTAATTAATATTTTCAAGATTTTAAATA  
511401 AATAAAAAGGATTTAATGATGTTATAGCaATAATCATTAAATCCGTTCAAT  
511451 ATGTTTAACAGAAGCTACAAGATCAATTAAGAAAAATCCTTTCAAGTAACCT  
511501 CATTTTTATTAATGGTTTCATAGTATTTTGTAAATACAAGGCGATATTGG  
511551 TGCTCAAATTCAATAATAGTTTTGGTTGCATTTTCAAATTGTAATGTAAG  
511601 TGGCTTTTCTTTATCTTGTAACCTTTCAAAGGTTTTCTTAAGGTTATTGA  
511651 GCGCACTTTGATGCAAAGTAACTAGATTATTAATAATCCTTTATATCAAGA  
511701 TGCAAATAATGTTCTATAAACTTAGTTAAATTTATTAGCATAATCACAAAT  
511751 GCGTTCCAAGTCACGACTTGACATAATTATTGTGATTGTTAGGCGTAAAT  
511801 GGCTAGCTAATGGAGAATTTTTAGAGATTGTCAAATTGATTCATTAATT  
511851 AATTTAAATTCAGACCTATTAGATTGGTCCTCCATTTTATAAATAGTTTT  
511901 AATCAGTTCTTTGCGTTTTTCTAAATTATCTTCACAAAGTAATTGATTTA  
511951 ATGTTTCATGTGCATTGATTACGTGCTTAAATACTCAAAAAAAGCTTT  
512001 AATAATTTCTTTTCTGAACGCTTTAAATTTGGTAATTAATGTTTTCCAT  
512051 AGCTAATTTTCCCACTTATATAACTATTTGTTGCTTTTTGCTTAGGCTT  
512101 TGTAAATATCTGtTTTGTAGTGCCTTGTTCAATTACTCTCCATCAGCAA  
512151 AAAAAATCGTTTCATCAGTTATTCTAATTGTTTGAGCCATAGAGTGAGTA  
512201 ACAATAACAATTGTGAATTTTTCTTTTAGTTGTTGAATTAGAAGTTCAAT  
512251 AGAGTTTGTGGCAATTGAGTCTAAAGCACTGGTAGGTTTCATCCATCAAAA

512301 GAACATCTGGTTGTAAAGCAATAGCACGCGCAATACACAAGCGTTGTTGT  
512351 TGTCCACCAGAAAGGGTGTTCATTCTATGTAAATTATCTTCACTTC  
512401 ATCTCACAATGCTGCTGATATCAATGCCTGTCTTACTATTTTCATTGATAG  
512451 CATTTTTATTGTGAATACCATGTGCTCTTATGCCATAAGCAATGTTTTCA  
512501 AAAATAGAAAAATTAAAGGAGTTAATTTTTGAAAAACCATGCCAACACT  
512551 AGTGCGCAATGTTAAATCATTAAATAATTCCTGAATTGATATTCTTACCAA  
512601 GAAAATATATGTCACCTGTTCAACGTGTGTTTTTCATTTAAATCATTTAAT  
512651 TTATTTAAGCACCTAATAAAGGTGGATTTACCGCATCTGATTTACCTAT  
512701 TAAAGCAGTTATTTTATTGCGTTTAATGTCAAGATTGATATCAAATAATA  
512751 CTTGTTTGTTTTTGTTATATCAGAAGTTGAAATTTTGAATTTCAAATACA  
512801 TTTTTTTCATCAAAATCCTTTTTTAATGACATTATCTTTGGTGTTTTTAAT  
512851 CTTTATTAGACGGTTTTAAATTTCAATTTTCATTCTTAATACGGGAGATTT  
512901 CATTTGCATCTGTTTCATTATTTAAACCAGTAATTTCTTTTTTATATTCT  
512951 TTGATTTGTTGTTTCATAAAGCTTTTCGGTAATGCTTAATTTTTTCAAGCTT  
513001 CAATTGAAAATTTTTTCAAAGTGCTTTTATGTTCTTTTCCATAATTTAAA  
513051 GGACTGAAATTTACTTTTTAATTACTAGCCATTTTGTGTTATTTAACAAAA  
513101 ATAACTCGGGATTAAATAAGAACTGAAAAAGATTAAAAGAATTAAGAAA  
513151 ACAACAGAGACCAATGATGTTTCTAACATAACACTTATTGCATTGCTATT  
513201 AATAGAAAATAACTGTCCATATATCCTTGTGTTAGTGTTGACCTGGCA  
513251 ATGACAAATGAAATAAATTACTAGATGATAACCCTGAAGTGATAAAGAAG  
513301 GGTGCAGTTTCAGCAATAATTCTGTTGATTGACAAAATTAATGCAACTAT  
513351 TAATCCTTTCAAAGCACTAGGTAAAACATTTTGAATAAATTCACGTT  
513401 TACTTATACCTAAAGCAAAAGCACTAATTCCTAAATCCCACTGACATTA  
513451 TTTAGTGCTTGTGACAAGTCTTATAAGGAAGAGTAATATAACAACACT  
513501 AATAGTTAGAATGCCTGCTATTAAACTAGTACCATTAGCTCCTCCAGCAC  
513551 TTAAGTGAAGACTCTTAAAAAGAAAGAAAGTCCAAATAATCCATAAATA  
513601 ATAGATGGCATTGAACCTTAGTGAATCAATTACAAAGTTAAAAACATTTTT  
513651 AACCACTTTTGAATTATTGTACTCGTTAAGTCAAATTGCAATTAAAAGTG  
513701 CTAGTGGAAAAGTAATGGTGATAGTAATCAAATAAATTACTAGAGTATTT  
513751 ACTAGTGCTCTGCCAGTTGAATCAGCTTCAAATGAAAAACAGTAGAACC  
513801 ATTATTATTAATAGCAACACTTCCATTAATAAATACAAACAGCAAAATTG  
513851 CTAACACAAATCCAAAAGCTAAAAAGTACAAATTAATTCCTGGAATATT  
513901 TTTAAAAATAATTAAGTTTTATTCAAACAACACTTTGAAGCCTTTCTTT  
513951 AAAAAAAGTGAACGTTTCATTGATGTTGTTTACTTTTATTTTTTTAACAC  
514001 TTTGCTTGTGATGTTAAATCAACAAAAGTGCACTAATATTATTGGGA  
514051 ATGAATCACCAACTTGATAAATAAAATTACTAATCTTTTTTAAAAAGGG

514101 ATAGCGTTCCAGTGTTTTTGGATTAGCTGATCAAATGGCAAAGAAATTTA  
514151 ACAATGAAACTAATATCAAAATTATGATTCCAAAGATATATAAAACACCA  
514201 TTAATCTGTTTCATCTCCATTTTCTGAAAAATAAAAAGTGGAAATAACTGA  
514251 TCCCAGTGTTTTTAAATCAGAAGTAAAAAACGATTGTTGTTAATTACCT  
514301 CTTGATAGTTAACACTCTGCAAAACAAAGTTAACAGCCATTGTTTCACTA  
514351 ATTGCTCTCGCAAAGGCTAAGGTCAAAATAACTGTTAATTGTGGTTTAAT  
514401 TTCTTTTAAATAATTTTGTAGATCGCACTTGTTTTATTTTCCCCTAAGG  
514451 AAACAACAACACTAATTAGATCGTTATTTACATAAGTTAATGTATTTGTT  
514501 GTTAATGAAATAACAATAGGAATGATCATAAAAGAAAGCATAGCTATCAC  
514551 ATTTAAAAGTGAAAGCGCGGTAATTTCAAGATATCCCGAAAGAAAATGC  
514601 TTAATATTTGTGATGCAAATAATCCAAAAATTACAGATGGTATTCCTGAA  
514651 AGGATATCAATAATAAGTGAAAGTTTTTTTCTTATTTTGGTTTGCATCG  
514701 ATAAACAAGGAAAAATGAAGTTCTAACCCCTATATAACTAGCAATAATTA  
514751 AAGCTCCTATTGATACAATAAACTTACCAATAAGGGGAATCAAATTCCT  
514801 GCCTGTTTATTACCTAAATTAAATTCAAGATTAAACAAGGACTTTGCAAA  
514851 ATCAGGTCCAATTTTTTGTGCTTCTGTAAAAGAAAAACAAAAAACTTA  
514901 TAAATAAAACTAAAAACAAGAATGCTAAAGTCTTTGAAAAGATTCTTAAA  
514951 AGATTCTCTTTTTTTAAACGTTTTTTAATCTTCTTTTGCCTAAAAAGCT  
515001 CCAAAGATAGGATTACTAAAAGCAAAGTCATCAACTCAAAAATTTTCTAA  
515051 ATTCATTGGTGATGAGTCATTTGTTTTAAACATCTTCTTTTCTCATCTT  
515101 CAGTTAATTGCAAAATACCAAATTCATCATAAATATTTTAAATTACATCT  
515151 TTTTTCATTAAAAATAATCAATTAAAAAAGTTTTAATTTCATCAAT  
515201 ATTCTTATTCTCTTCAGAAAGTGAACTATTGAATTTAAAGGACGTACTC  
515251 ATTTATACTCATTTTGGGAAACAGTTTGATTAGAAGGCAAACTTCCTTA  
515301 TTCTCATATTTAATTGGTAGTATCTCAAACCATTAATTTTAAATAGCTTG  
515351 AAGGTTGTTTTGAATAAATCCTAAACTAAGGTAAATCATCCGAAAAGAT  
515401 TAGGATCTTGTAAGTTAGTTACAAAAGTATTAAGGCTTCAATATTTGTT  
515451 TCACTAGTAGGTTTAGCAAGAGGTCCATAATTAATAATTCCTTCAAAAT  
515501 ATCTCTAGTTTGAGAATCTAAAGTTTTATCTGATTTTAAGGCGGAAAAAT  
515551 TTAAAAAGCTTCTGCTGTTCTGAAGCAAATGACCCACCAGTTCTTGGA  
515601 AAACCTGTAAAGGGTAATCTTTTTCATTTGACATATTTTTGTATCCTT  
515651 TTTTACAACTTATCAATGTTAATTGTTTTAACACCAGCAAATAAGTCGT  
515701 AGAGATCATTTATATTATCTTTTGTTAAAAGTAACTTACCTTTAACTCC  
515751 TGTGGTGCCTTATAAATTACTGCAATAGCATCTTTGCCAATAGTTAAAGT  
515801 TTTGAGCTTTTTATCTCTTCATTTTTTTTTCATTCTCTTTGTCATATTCCT  
515851 TAGGGTTTTAGAGACATTCCGATATCAGCAAAGCCGTTAATGATTGCT

515901 CTGATTCCAGCATTGATCCGCCTGCTTGCACACTAATTTCAACAAGCTT  
515951 ATCATTGTCATTATTTTCATTTAGAACATAATAAGAACTTAATTTATTTA  
516001 GTAAAGGTTGAACTGAAGAAGAACCAACAGCACTAATCAGGTTTATGTTA  
516051 GCACAACCACTAAGAAAAAAGCAGATGCTAATGTTAGTAGCGTCAATTT  
516101 AAAGAAATTTCTAACTTTAGCACTTTTAAACAGATTAAATCTTTTCTA  
516151 AAGAGAATTGCAATTGACACTCAGGTTATTATTTAGTCTAGTTTTTTCAC  
516201 AAGCCAATTAATTTAAATGAAATGCATTTTTATTAAATTGCAAATTTAATT  
516251 TCTTTTCTTAACAATTTTCTTTTTTCTTCATTTTAAAAACAAAACAGCAG  
516301 AACTTATCATTAAGCTAATGATAATTCAAAAATGACTCATAATATTAAC  
516351 TCAACATTTGTATCTTGTTTTTAAATTCATTTTTTCTAACTTATCAAC  
516401 TTCATAGGATTTATCTTGAGATTTAAGATTAAATCTGGAACCTCTCTTGA  
516451 ATTGCAGGTTATTTGTTTTAGATAAAATGATAATGCTTTGAAAAGTTGT  
516501 GTTTGATTTTCACTAGTAATATCAAATCAAATAGAATTATCAAAACCATT  
516551 GGCATCTACAATTAAGAGTGTGTTGATTATTTGTTATTTTAAATCATAGC  
516601 TAATACTAAATACTTGGTTATCATTATTAACACCTTTAATAAATAATTTT  
516651 TTTGATCTAACATCGACATCAAAAATAAATTAATGATTTTTATTTTC  
516701 TACTAAATGGATGTTAATAAATTTATCTTTAGGTTAAAGCGGACGTTTT  
516751 TAGTTGTTTGCAATCTTTTTTCACTTAGAGTAATATTGAGTTTATCAACT  
516801 AGTAATTGTTGTCATTTAACTAAAAGGTTTCATGAAAATCAAGTTGATA  
516851 ATCCTCTAGAAATTTAAATGAAGATGACTTTAAATCTAATTCAGCAATTT  
516901 TTAAGTTATCAACTGATAAAAATACCTTGCTTTTTCTAACTTAAATCCC  
516951 AGGTCATTTTTATCAACAAAAGTTTGTTAGTATGAAATTTAAATAAATA  
517001 TGTTCTTAATTTAGGGTTTTTTTGATTTTGTGATAGAAAATACATTTGT  
517051 CTTTAATAATTTCAGAATCACTTTCAGAACCATATTTGAATAGTTCATTG  
517101 CTATTATTTATTTCTGCTAAAACATAAAATATACCTTTCTTTTCATTAGT  
517151 AGGCTCTAGATGTTGAAATATTTTTAGGGTTATCCACAAATGTTAAAG  
517201 AGTTACTGTTGATATCTAAATCAATATTCTTATCCTTAGATTTAAACTA  
517251 TTTTGATAATGAAAGCCATTTGTCTTTTTTCATAATCATTAACTTTTC  
517301 ATTACGTTTTTTAAGTTTCAGCAACATTAAAGTTTGAACATTTTTATTTA  
517351 GTGGAATACGAAAATCTTTAGCAATTCAACGCTGTTCATTAAATCTTTT  
517401 CTATATTTAAATTTGTATTCAAAACCATCCTTAGTTCCTTTTGATAGTTGA  
517451 AAGTTTTTTAATACTGTCAAACAGTGGTTCAACACTATAGTTACTAATAT  
517501 TTTCTGATTCATATCCATCTACAAAAAATTAAGTGCTAAAAATTCAATA  
517551 TTCATTTTCATTATCTGCTTTCTGTTTTCTGTAAAAACTCCTCAATTGA  
517601 ACTTAAATCAAAATAATTCTTGTTATTTCTTAACAATGTTATTTCAATTA  
517651 CAGAATTACCAATTTTACTTTAACAGTTAATGTTGATCTATCAAAAATG

517701 GTTTTGACCATTCTTGGTAAATTTCTAATAAAGAATAGTTCTTCTTTATT  
517751 GTTTGGTGACATTTGCAATAGGTTGTATAAATAATCTAAATTTGGATAAA  
517801 AATTACTTTGATTATTGGTTGAAATATTAAAGCTTTTTAACGCTTCATTT  
517851 TTATCAATTGATTCATCAATTCTTTGATTAAATAAATAACTTCTTTAAT  
517901 TGCATTTATGAATTTATCTTTAAATTTAATAGTTGGTTTAAATTTTGTAC  
517951 CTATTGTTTCTTTATTTAGAGTTTTTTCAGTTTGACTAACAAGCGAATTA  
518001 ATATCAAATTCCAACTGTGAAATTCAAAGCTTTGAAAGATTACTGAAACT  
518051 AATTGGTAAACTTCATCAGGATTATTTTGCCTTAGATAAAAACTTATTT  
518101 GATGATGAACAACCTTCTTGTTCAGGTAATATAGGTGTATGTTAAAAATA  
518151 TCCCATTACTGTTGAATGCTTCACGTCTACTATCTTCAGTTTCTGGTCT  
518201 AACTACTAATCCATTACCTAGTCTTAATATCGTTTGAGTTATTTACGAT  
518251 TATTAGTAAATGCTTCAATGATTTTTCTATCCTTTTTTCATTTTCTCTTTA  
518301 AACTCATTTTATACTCATCCAATGAGCATCAACTTGTTTGTGCTGTTAAT  
518351 AGAAAAAATCAACTGCTTCTACCAGGAAAAGGTTTCGTTTCACTGAGCGT  
518401 TATTCTGTTCAAAAACCTGGAGGAACCTTCACTAGTTCTAAATCTCATCAG  
518451 AAACGATAAGCTCTAATTGGTGTCAATTGCTAAACCTCATCAGAAATCTGG  
518501 AGCTACAAAAATATTATTTTTTCAGTCAGCAAAAAATCCTCTTGATTCTT  
518551 GGCCAAGATAATATCACATAGGTGCATTAAAAATCAATTACATAATTACCA  
518601 TTATTACCTTTTCTTAATCATTTAATATTCTAATAACATCTTCTGGGGT  
518651 TGGTTTAATCATTCCTTAAAGTCGATCCTCACATGTGAACAACTTAGCTT  
518701 CAATAAAATATGCTTTTTTATGACTGGGCTTTGTAAGGTCTCAAAAATAA  
518751 GGATTATCAGGTTTATATCAACTTTTGTTCAGAACCCTCTGGATTTGT  
518801 ACCAGTTATTTCTATATTCCTAGAAGGAACCTTCGGTTCATTTTTCATTAG  
518851 TATGACCATCTCTTGGAAAAAATTAGAAATTGCTTGACTATGAAAATAA  
518901 AATCTCTGCTCACTATGGATATCAGATGACCATGAGTTTCTAATTCAGG  
518951 GTATCTAAATGTAGATGAAAATGCATGTGCAATATAACTACTCTCAATT  
519001 TTAACTTTATGTTCTTTAGATAATAAATATTGTTGTATCAGTGAAAGTTA  
519051 TTATCTCTAATAATTTGTTTGTAAATTATCACTATATTTATTAATAATTC  
519101 ACTTCATTCATTGCAATAAGTTTTTGCAAAATAATTATTTTGATTAGGTC  
519151 TTTGAATTACTTCATTATCAAAATTAAGCTTTTTTCGAAAATAATCGTTT  
519201 TTTAAATTAAATCCAGCTGTATAGCTTCTGTTTTGAATTGTGTTTGGAGA  
519251 GAGATAAAGATTAGTATCTACCAAGTTTTTTTCAAGTGAAGCATTAGCTA  
519301 AAGCAACGGGAAAAAGAAAAGAACTAATAAAGGAATAAAAAGATATGAA  
519351 CGCATAATTTATCTCATTAATAAATGTGTATTTAATGAAATATTGACAA  
519401 TTTTTATTGCTAGTTCTTGTTAAAAATTATCTCTGTTTTATTTTTTATC  
519451 ATCTTTTGTTTTTTATTTCACTTATGAAAGTAAATAAAAAACAGTGATAAA

519501 CAAAACATAAACTACTAAACCAATAATCAAATATACTATAATATCTGTTT  
519551 TTTTATCTTCACATATTAGATTGAATAATTTTGTCTATTTGAAACTATAG  
519601 CTGTTTTTCTTTAAGCTAAAATTAGGTTCTTTTTTAAATTGAAATTTTTT  
519651 TAATGAGAGAAATAACTTAAGCTCATTTTTTCAGTTTCTGATTATTTTTCT  
519701 TATCAAGATCAAACCAATATATTTATTTAAGTAGTTATTTGTTGTTCTA  
519751 ATTTGCAATTCATTTTCATTTTTTGATAGCAATATCATAACAAGGCTAGT  
519801 TAATCTATTTTTACTTATATTAACCTCAATATTGAGCTGATTTTTTAATTG  
519851 CATCAACATTTAAATAAAAATGAAGCGAACTATTTATCTTTAGAGTAGTT  
519901 AATTTGATCTCTTTAGGAAAAAGATCTAAGCTAGATTCTTTTTTATCTAT  
519951 TAAAAGATTCAATTCACCTTAAAGCCAAATTTAGTTTTTTTAATTAATAGTT  
520001 CTTTATTAGCTAAAGAAAAATAATCATTTATATGAACCTCATAACTTTCA  
520051 AAAAAATGAGGTATTATTTTTCTTTTGGATTAAATTCATCTATTTCAACATT  
520101 ATTAACAATTACCCCTTAATTTATCACCGCTTGATTTAAATCAAATATCAT  
520151 TAACATTTAAACTAACTTTTTTGGTTCTCATTTGAAAAAGATAAGTTCTT  
520201 ATTCAGGAAAGTTTTTATTTTGTCTAAGAAATACATCTTATCTTTAAT  
520251 GATTTGCTATCATTTTTTAGAACCCCATTTAGTTAAATCATTACTGTTAA  
520301 TTATTTGTGCTGAAACATAGAATATACCATTTTTTAACACTGGGCTTAATT  
520351 AAAGATTTTTTAATTAATTTCTCAGGATCTTTTATGTATTTTATTGTAGC  
520401 GGATGAAATATTTAAATTGTTTTCTTTTGAGAAGTAAACTATTTTTAA  
520451 TTGCATATGTAATTGGTTCTCTTTGATAACTATTTAATCCGTTTTTTTCA  
520501 ATGTCATTAACACTGAAATTTTTCTGATTTGTAACAATAGGAATTAATA  
520551 ATGATCTTTTAAATATGATGTTCAATGTATTGAGATCTAAACTTTAAAC  
520601 TATATTGAAACCATTTTTAGTTTTCTGAATAGAAGGCAAATTTTTAACT  
520651 GACTTAAAAAAGAATCAACTGGTTGATTTTTTAATGTTTCATCCTGTTTT  
520701 ATTCACAACAATAAAATCAAAAGTTAAAAACTCAATTCATaAAAAATTAA  
520751 TACCAGTTTGATCAGCATTTAAGAAATTTCAACATCACTTAATAAAAAA  
520801 ACGTTACTGCCATTTTCTATAAAAGTAATTACTTTATTTTTGCCACCTAT  
520851 CTTTATATTTATCGTGATGGTAGTATCTTTAAAAATACTTTTAATTAGGT  
520901 TGGGTAATATCCGAATAAAATTTAATGTTTTCTCTTGTGTTTGGATTAAATG  
520951 TTAATTAAATTACTTAAGAAAAATATTGCATCAATTCTTCATCTTTTGG  
521001 TTCAAAATCAAATTTAGATTCTTCCTGTTTTTCTAATAAAATCTAAAGCAA  
521051 ATTGAAAAAAGTTTTATCTTTATTTGCTAATTGATCAAACTCTTGATT  
521101 AGCTTACTTACCATTTCAATTGCATTAGAAAATTGATCACTAAATTTAG  
521151 CTTTGGTGTTATTTTTGATCCTATTAGTTCTTTGTTTAAACAGTAGTTG  
521201 GATTAGCTATTAAAGAATTTGAATCAAATTCATTTGGTTAACAATGATC  
521251 TTAGCAAGTTGATTGTTGCTATAGTTAATTGATTTTGTGATTGAAAATC

521301 ATCTTTAACTAGATAAAGATTAGTATCAATCAACTTACTTTTTATGGAAG  
521351 TGTTAGCAAATAATAAGGGAATTATCGCAAAGGAACTCACTTTAAATAG  
521401 CGTTTTTCATGACATAATAAGCTTTATATTCCATAAATTAAATAAAACTTA  
521451 TTAAGTGACAGTTTTTTTTACTAACGCTTAGTAAATTGTGGTGACGCTCTA  
521501 GCACCATATAAACCAAATTTTTTGCGTTCCTTAGCACGCTTATCACGTGT  
521551 TGTTAATTTTTTGGTTTTTAATAACTTTTTAAGATCTGGATTAAATTTTA  
521601 TTAAAGCACGAACAATACCTAATCTAATGGCTCCTGCCTGCCAGTAAAT  
521651 CCTCCACCTTTAACAACAACATTGATATCAAAGTTATCCTTAAGTTTGGT  
521701 TAACTCTAAGGGTTGTTCATATCTTGAATCACCAATTTATTGGAAAAT  
521751 AATCGCTAGGATTACGATGATTAATGGTTATTTTACCCTTATCTTTGCTT  
521801 TGATATAAATAAACTTTAGCAGTAGAAGATTTACGACGACCAAGTCCATA  
521851 AAAAGATTTTTTATCCATATCTTTTAACTTCAATTAAGTAATGTTGGTTT  
521901 TTGTGCTTCCATGTTGTGCTTATCATTCTTAAAAACATGTACTTTAGTTA  
521951 TTAATCTTCTGCTTAAACGATTATCAGGTAACATTCCCTTAACAGCATTG  
522001 AAAACAAGTTTATCTGAATTTTTGTTTATCATATCCCTTCCACTAGtTTT  
522051 TTTAATTCCACCCATGTATTGAGAGTGATGATATCAAACTCATTGTCTT  
522101 TTTTATTTCCAGTTAAAACCACTTGATCACTGTTAATAATTATTAGATGA  
522151 TCTCCACAATCTTGATTAGGAGTAAAATTAGCTTTATTTTTTCTCTAAT  
522201 TAAATTTGCAGCTTTAACTGCTAATTTGCCTAAAACCAACCACTAGCGT  
522251 CAACAAGATACCACTTCTGTTTTTAATGGCTTCTTCTTTGTAAGCATC  
522301 GATGTTTTTTGCATATATTTAGATACAAAACCGCATTCTATTTTAATATT  
522351 ATTACTTTTCTTCAAAAAGTCCTTTAAAGTATTTATCCACCATTTTTTGT  
522401 GATAAAGAGCGTTTCTTTCTTTTAAAAAAGGCTTAGCTAAGTTTTCCAA  
522451 TTGGGTAAAGTTCAACACTTCAGTTTGATACTTTTGATTTTTTGTTTCTT  
522501 CAGTAATTGTTGTTTTATATTGATGCTCACTAAAAGATGCTAAGAATAAA  
522551 TTTTGGTTAAAAATCTGAAATATAGTTGCTTGTAATTACCTTCTTCTAT  
522601 TGCCTCTTTTCAAAGTCTCATAGCAATTTTTTGATCTTCAAATAAGATAA  
522651 CTATCCCAAATGAAGAAGCTTTTACTATTTTGGTTGCTTTCATATATCA  
522701 CGAGCACTATATTTGTCTATAAAGTTATTGAAATAACTTAAATTATTCTG  
522751 TTTATCTTTATCATTAAATTTAGTTTGAAAAACACTTAAAGATTTTGAA  
522801 AATGATTAATTCAATTTATTGTCATTAAATGCATTAATTGCAAGAGCAATA  
522851 TTGGCAAGATTTAGTTTGCTTGATCTAAGAATTTGTTATTAGTAACTTC  
522901 ATCATTTTTAGGTGTCTTTTCTGATTTATCTATAAAAGATTTTTCAAATA  
522951 AAGAAAAGTGCTTTTGGTCTTGTTTGATTTGATTTTTTTATTTTTTTC  
523001 TTTTCCAAATATTCAGTTTCTAAGTGATAGAGATTTTTTCATTACTTGGTGA  
523051 GCTTATTGTTAAAGGTTTTTGATTAAAAAATTCATTATAGCTAATAACAA

523101 TAGCTTTTAGCCTATCAATTAAAGTTAATTGACTTAAACCAAATAGTA  
523151 TTTTCTTCAATGGCCTTAATTAAAAACGCATAATGCTGCTTTTCAAAATT  
523201 AAGTGTCTTCTATCATTGTTTTTTTTCAGTTGAATCTAAACATTAATATTTT  
523251 TTAGTTTTGCATACGCATATAAAATTAAGTGTAGCGCAAACAACTCTCTT  
523301 AAGAAGTAAGTGAAATTTAGACCATTACTTTCAAATCATCAAGCAAGTT  
523351 AAATGCTTCTTTTATATCTCCTGATAAACTGCTTTAATAAAAGTAAATT  
523401 TTGCATTTCTATCAACGATATTAAATGTTTTTTCAACATCAGTAATACTA  
523451 ATTTTTTCACTATCAGAGAAATTGCTAaTTGATCTAGTAAGCTAAGCCCA  
523501 TCACGCAATGAACCTTGGGATAAATCAGCAATTTTTATTAATGCATCTTT  
523551 CTCTATCTTAATCTTTTCTTTTTTGTCTATATCATTTAATCTTTCAAGGA  
523601 TTAAATCACTAGTTATTTTTTTAAAAAGAAGCTTTGACATCTGGACAAA  
523651 ATTGTTAATGGAATCTTGTTAAATTCAGTAGTTGTAAAAATAAAAAGAAC  
523701 ATAAGGTGGTGATTCTTCTAAAGTTTTTAAACAAGCCACCCCATGATTGGG  
523751 TGGTTAACATGTGTGCTTCATCTAAATATAAACCTTTTTTTTAAATGTG  
523801 AAGGGATGATTGAAAACATTTTCTACCACTCTCTAATATCATTAATACC  
523851 ATTTTTAGAAGCTGCATCTATCTCACTATATCAATGGCACTATTAGTGT  
523901 TAATACTTTTACACACATCACAACCTATTACAAACATCAATTTGATCTCAA  
523951 TTTAAGCAGTTTATCGCTTTTGCTATTATCTTTGCAAAAGTAGTTTTACC  
524001 TGTTCCCTCTTTCACCTGAAAAGATATAACCATTAGGTAGTTTATCCCTGT  
524051 TAATAGCATTACCAAGATTTTTCTTATCGATTCTTGTCCTAGGGTTTGT  
524101 TTGAAATTGATTGGCCGATATTTTTGATAAAAACTTGGTGCATAATTTT  
524151 TAAATTGAATCTGGTTTTTAAATTTTGGACAAATATTGGGCAGTATAAGA  
524201 TTTATTAAGTTGGTTTTATAAGTTGTTTCAAGTGTTCCTTGAGCAACAATTT  
524251 GACCACCATTGTCACCACCTTCAGGACCTAAATCAATGATATAGTCAGCA  
524301 ACCTTAATAATATCTAAGTTATGTTCTATAACAACCTACTGTATCACCATT  
524351 CTTAATGATTCTTTGAATTATGTGAATAGTTTGTATATCTTCTAAAT  
524401 GTAAGCCAGTAGAGGGTTCATCTAAACAAACAAAGTTTTACCAGTAGAT  
524451 TTTTTTTGTAAAAAAGTTAGATAAAGTTAATCTCTGTGCTTCCCCACCTGA  
524501 AAGAAAAGTGACATTAATACCTAATTGCAATATTCTAAACCAACATCAC  
524551 ATAACAACCTTAGTTTACGTGATATATTGGGATAGCTTTAAAAAATTCA  
524601 TAAGCTTCTTTACAAGACATTTGTAAAACATCAAAAATTGATTTTCCCAA  
524651 ATATTTAATTTCCAGTGTGTGTGAATTGTACTTCTTGCCATTACATACTT  
524701 CACATTTGACATAAACATCAGGTAAAAAATGCATTTCAATGCGAATCACA  
524751 CCATCACCAAAACACTTATCACACCTACCACCTGGAACATTAAAGAAAA  
524801 TCGTGAATTTGTATATCCTCTTGCTTTAGCTTCTTTTGTGTTGGCAAATA  
524851 AATCACGAATATCATCAAAAACACTAATATAGGTTGCAGGATTAGAACGT



524901 GGTGTTCTACCAATTGGGTCTTGAGAGACAACAATTATCTTATCAATGTT  
524951 GTTAGCACCAATTATTTCTTATATGTATCTTTTTTAACACCTTTACGAT  
525001 AAAGAATTCCTTCTAAAGCTGGAACTAATGTTTGATTAATTAAAGAGGAT  
525051 TTTCCAGAACCTGAAACCCCTGTTATCAAAACCAATTTATTTAAAGGAAT  
525101 GGTGACATTAATATTTTTCAAATTATTAACCTTTAGCACCTTGATAATAA  
525151 TTGTTTTACCATTACCACTATGTCTATTTTTTGGAAATGGAGATTTGTTTT  
525201 TTACCACTAAGATATTGTCCAGTAATTGAGTTTGAGTTTCCATTACTTG  
525251 TAAAGGTGTACCGCAAGCAACTAATTCACCACCTTCATTACCTGCTTTAG  
525301 GACCAATATCAATTAAATAATCTGCCGCTAACATTGTTTCACTGTCATGC  
525351 TCAACTACTAATAAGGTGTTACCTAAATCACGCATTACCATCATTGTTTT  
525401 AATTAAACGCATATTGTCTTTTTGATGCAATCCAATAGAAGGTTTCATCCA  
525451 TTACATATAAAACACCAGTAAGTTGAGAACCAATTTGGGTAGCTAATCTA  
525501 ATTCTTTGTGCTTCTCCACCTGACAGCGTAGAAGCTCTTCTTGCAAGATT  
525551 AAGATAATCTAAACCAACATTTTTAAGAAAAGAAAGACGATTAATAATCT  
525601 CTTTTAAAGCTAATTCACCGATCTTCTTTTGCTCATTTAACTCTAGT  
525651 TTTAATAGAAAATCAATACTTTTATCAATGGAAAGTTCAGTAAAGCTAAT  
525701 AATGTCAATTCCTCCTAACTTAACACTTAAAGCGTCTTTTATTAATTTTT  
525751 TTCCATGACACTTTTTACATGTTATTTAGACATGTATGCAGAATATCAT  
525801 TCTCTACTTACTTGGCTGTTTGTCTTAGGTGTCTTCTTTAATTAAATT  
525851 AGCTATCCCTTCATAATGCTCAAAGCGGATATTCTTAGCACCTGAATTGG  
525901 AAATTGTTTTTATTTCAATAGGTTCACTTCTCTTCTAAAATTAAATTA  
525951 AGTTGTGACTTATCTAACTGTTCAATTGGTTTATCTAATGGAATTTTATA  
526001 GTGATTAACCTAAAGATAAAAAGCGCTGTCAATCCAAAGAAGTTCATGCA  
526051 CAATATTTTTAAAAATATCAATGGCTCCTTGGTTAATAGAAAGTTTAGAA  
526101 TCAGCAATTATCTTGTCTACATCAGGTTTATACTAAAACCAAGTCCTTT  
526151 GCAATATGAACATGAACCTAAAGGGGAGTTAAAGGAAAATAATCTTGTT  
526201 CCAATTCACCTAATAGAAAAACCACATTTATCACAACCATGATTTTTGCTG  
526251 AAATTTAATATTGTTCCATCTTCTTAAGAACTTCTATCTTGCCATTAGT  
526301 TAACCTATCAATGGTTTTCAATGCTATCAACTATCCTTGAATAAGTTTGAT  
526351 TATCTTTATTGATGATAATTCTATCGATCACTACACTAATGTTGTGTTTA  
526401 GTATTTTTATCAAGTTTAAATTCATCATCTAAGGTGTAAATCTGGCCATC  
526451 AACTAAGACTCTAAGAAAACCTAATTGCTTGTATTAAATAAATTCATTG  
526501 TAAAAATGCCGCGCTGATTTTTAACAGTAGGTGCTAATAATTGCACCTTT  
526551 GATTTATTAGGTAAATCAAAAATCTGATTAGCAATTTGGTTAATTGTTTG  
526601 CGTTTGAATAGAACCATGACCATTAGGACAATAAGGGGTCCCAATTCTAG  
526651 CTCATAAAAGTCTTAGATAATCATAGATCTCAGTTACTGTACCCACAGTT

526701 GAACGTGGGTATGTGAAGTGGTTTTTTGATCAATGGAAATTGCTGGTGA  
526751 TAATCCTTCTATAAGATCAACATCAGGTTTATCACTGTTACCTAAAAATT  
526801 GCGTGCATAAGAAGATAGAGACTCTAAATATCTTCTTCCCCCTCAGCA  
526851 TAAATTGTGTTAAATGCTAAGGAAGATTTACCTGATCCTGATAGACCAGT  
526901 AATAACAACAAATTGATTTTATAGGGATATCAATGTTAATGTTTTTAAGGT  
526951 TATTTTCTCTAGCACCTTTAACCCCTTATAAAATCATTATTTTTTCATTCC  
527001 GGTTTCAAAGTCAATGTTTTTAATTGAAAAATTTTAACTAACTTATTAT  
527051 TAGGATCATTGAAAATAAGCGCAATACCTTGTTTATTTTGATATGAGATC  
527101 AAAAGTCCACGAATGAAATTATAAGCGTGGTAGTGAAATCATTGCAGCA  
527151 GTTTATCATTAGTAACTTAGGATTTAACAAAAGTTTAAATAGCAAGTAAA  
527201 GCTTTAGACTTTTCATTTTTGTAAATTTTGTTTAAATCACTAAATAACATT  
527251 CAGCTGCTAATACCATTCTTTTTGGTTTGATTATCAATAAATTAATGTT  
527301 GTTAATAAAGTTAAGTTTTTTAAGATTTTTTTGTGATCTTAAAAAGAAAT  
527351 TAATTGTTTTTAATTGTGAATTCAAAACATTAAGATAAAGCTTATTTGAA  
527401 GCTTCTAAACGATTGATATTGCACTCTTCTGAATCAATAAAAAAGTTCT  
527451 CTTAATTTTCTGTGTTGTTTTTTAAGTCTTAAGTGAATGTTTGTGTTA  
527501 AAATACAATATCTTTTCATGATGAATTTAATCTTTTGTAACTTTGTATT  
527551 GTTTCATCGCGAAAAATTCACCTTAACTAAATTAATGTCTTTTAAAAGTAA  
527601 TTTGTATTTTGTGTTGCATTTTTTTAGCTTTTGTGTTAGATCATTCTTGG  
527651 TTTCTTTATTTGTTGTATCTGTTGTTGAAGAAAAACCGCGTGATGCTAAC  
527701 AGGAAACTAACAGGGGTTTCAAATTTAGATCTAAATATTTATTAATAAC  
527751 TTTGTCAACTAGAAAATTTCACTTTGGGGAGTTTAAATCATTTTTTTAACT  
527801 TATCTTTTAGCAAATAAAATGTGGTTCACCTACGTCCTTCATTTCAAATA  
527851 AAATCATTAGAACCACAACCTTAAAACTCATATTTATTAAAGAATTGTTG  
527901 AAATTTTTTACTTAGGCTATTTCAAAGTGAAATAAGAACAAAATACAAGT  
527951 TATTTAACTCATATTTTTGTGCTAATTTTTTGATAATTAGCTAATAAG  
528001 CTTTCATAAAAAATATTGCTTTATTTGAAATGCAAAGTTAAAGTCTCCAA  
528051 ACTTTTTCTCATGCTGATTAAACCAATTGCATATGCACTGTATCAATAA  
528101 ACTGTTTGAAAAGTGTTTTTTGGATTAGAACTGAAAAGTGTATTATGC  
528151 TTACCTCTATAATGATTTTGAATTAATAAGATGTTTCTTTTAGTTCATT  
528201 AACCAATTTTTCATGAACATACAAATTGTTTGATTGTTTAAACAAAATTTT  
528251 TAATAAAAGATAAACGTGCTTTGATCAAAAATTCATGAACCTCTTTTTTC  
528301 GTTAGAATGAAACGTGCAGACATTATTTTAAGTTCTTGATTAATTGTCTG  
528351 GTACTTTTCAGTCAAATTAGGACCTGATTTTAAGCTGATAATTTCTTGAT  
528401 AAAGATTTTGAATATTAGCAAAGATTTTATTGACTAAATTAATACTTTCA  
528451 TCAATAGTTTCTACAAGTAATTTTGGAGAAAGTAAATCCATTTTCTTAAT

528501 TTCTTTCAAAAGTAAAATTCTTGTTTTTAATCCGCTTAGATACAATCTTTT  
528551 TTTCTAAAATTCTTTTCTATAAAAAATAAAAAACTTCTTCACTTAATC  
528601 TTTCAACCCTAAAAATTAAGAAAAGGTGAATGAATTAATTAATTGCAA  
528651 AGCATTTTTTATGTTGTTTTGAGAATGTTTTCTTAGCATCAAAAAGTCTTT  
528701 GTTAGCTCTTTCAATTTGCAATTTTCAAAAATACTGTTATCTCGTGAT  
528751 TTAGCTTCATAAGCAGCTATTTTCAGTTTGTTTTTAAGTTATTTTTTTG  
528801 TTCGTTCAATGCATAGTAACGCTCAAAAAAATTTTTATTACTTTGTTAT  
528851 TAAAAGTAAATAATTGATTGAAAAACATGCAATTAATAATCAACAAGTTCT  
528901 CTTTCGTTTTTTTTCAATTAAAGTTAAAAAATTATTGTATTCAAAAATCAAC  
528951 TTGTTCAAAGTAGATTGAATTAATAAATTTTGATGTAAAAAATGATTAA  
529001 TGACTTTACTAGTTTTTTGATTAACATTTTCAATTTTCAAAAATGAAAAAC  
529051 CTAAATAAATCATTAAAGCGCATTAAAACCTAAAAATCACTTTAACTGTTT  
529101 AGGTATATTCACTAAATTAAAGTAATTTTGATCTTTTTTATAACTTAAAT  
529151 CTTGTTTTAGAAAAATGCTAAATGAATTAGGAAATAACCACTTATTTTTTA  
529201 TTTCTTAAATCTATCTCTTCACATAAATTAACTTAATTTTTTTGAAGCGG  
529251 TAAATATTGATGGTTATTAACAAGCAAAAACCCAGAATAGGGTTGTTTAT  
529301 TTAAGTGTAAAATCTGTGAAAGGGTTTTCATTGTGCTTGATTTAAATTA  
529351 TCAATGAGATAGTTACCATACTTAAATAATGATAGCTTTGCAACCCCAA  
529401 ATAGTTAGCATCTAAAAAGGAGGTACGAATCATTAAATAATGACAAATCAA  
529451 CCCACTGTTCTAGATTATCAAAAAGAGATATTTTCTTTAGCATGTACCTT  
529501 TCAAAATTTTAATTGCTAATCTTTAAGGTACTTAAATAGAAATAATAGTTG  
529551 AAAGAATTAAGGGTGCTTTTGATGTCTCTTGGTGAATAAATTCATTACT  
529601 GCTCGTTTAATAGAAAACCTTCAATTCTTTTGAAATTTCTTTACCTATTCTG  
529651 TTTTTTAATCGTGGTGAAATCCTTAATATCATTAAATTTGTTTTTTAATTA  
529701 ATTCTTCCATTTTTGTTTTTAGTTTATCTTTTTCTGGTACATCTAAAGAT  
529751 ACTCCTAAAAAGAATAAGTTATCTCATTTAAGAATTCCTCTTTTTTTG  
529801 ATCAAAATAAATGATTATGATCACAACTCCAGATTCTGACATTTGATCAC  
529851 GTTCAAACATAATGCTAGCTCCAATTTCTTGTAATCCAGCAGAATCAACA  
529901 CACTTAGGATTTAATTTCAATTCATTTTTTTTGCTATCTAGTTTTTTGTT  
529951 TTCAATAGTTAAAATCTCACCGTTAAAAAGAATTAAGATTGATTTTGCT  
530001 CAGCGCCAGCTTGTTTTAAAACCATTTGTGAAGTTTATAAAATCCCTATAA  
530051 AGTCCACCAGTTGGAATAATATATTTTGGTTTTAAAGAACTAACTAAAA  
530101 CTTCATATCTTCATCACTTGCTTGATAGAAAGGATTTCTCTACCTAAGT  
530151 TGTAATAACTAACTTCATTACGTGCAATATCATCAAGGATTTGTGCTTCT  
530201 ATCTCTTCATAGCCAGCAACTTTAGGAGTCATAAAGATAAAAGTATCACT  
530251 CTTACGATAACGAATTCCTTCATCTTCGTTCAATTTTGAATAATT

530301 TAGCATACAACCTTATCAGGTGGTGAGGTGAGAACAACAATACTGTTGGTT  
530351 GAATTGTTAATCTCCTCAATAGAAATGGTATTTAAATGCGTGTTATTAAA  
530401 CAATTTTTGACGCACAATTGTGTTAAAGAGATGCACAAATGATTGTGAAT  
530451 AGATAATAAAAGGACGATTTTGCATCCTTGCAATCTGGGCAAGAGTCATA  
530501 ACACTGTAAGCATTTGAATCATAACAAGCTACAAATATTCTGCCTTTGGC  
530551 TGGAGTTATGATCCTGTTTAACTGTTCTAATGACTTGTGTTTAGGTGTTG  
530601 TAAAACCACTGTTTCTACCAACTAAACCAACTCCTGTTATTAATAACAAT  
530651 GTATTGTCAGAAAGTTTAGGGATAATTTGATTTAGTTGATTTTCAAAAGC  
530701 AATGTTCTTATCATTTTAAACAATGAAATCATCAATAAAAACGATGTAAC  
530751 CATTATCAGTATTTAAAGCAAATCCAAATGATGATGGTAAAGAACCTGAT  
530801 ACTTTAAAGGGGTAATAGAATGATTAGAAATTTGATTGTTTCAAGTGG  
530851 TTTTAATTCATGAATTTCCAATTTATCACGTGCAATATTAAGTTTGTTTT  
530901 CATTAATTTTGCCTTTAATTATAGAAGCGCCTATTGAACTTGTGTAAATA  
530951 GGAAAAAATCCTACTGTATGGaACAAAAATTCTAATGATCCTAAGTTTTC  
531001 AGTAATGGCATTACCTATAAAAAATACCTTTAACTCTTGCTTGATTTTCTT  
531051 GAATTCAACTAAATCAGGAATAATTTTTTTAACACCTAAACTGCTGTT  
531101 GTTGGTGTTAAGCTACCAACATTAAAGATAAACACATCATTGTCAATTC  
531151 AAGCACATAGCAATTTTTTACCACGTTTCATCTTGACCGCCGAGCGCAAAGA  
531201 ATTTAATCTTAGCCATTTTTTAAACCCGGAGGTTTAAATTTTTAATCAAAT  
531251 CACGGTAGGTTTCAATATTACGTTCTTTTAGATATTTAAGTAGCCGTTT  
531301 CTTTTTGATACCTTTGTATATAAACCACGCTTAGAAATAAAATCCTTTT  
531351 GTTTGCTAACAGGTGGTCTGTTAATTTTTTAACTGATCTGTTAATATAG  
531401 AGATTTGTACTTGCACACTGCCAACATCGTTTTTGTGAAGTTGATGAGCC  
531451 TTAATGATTTGTTCTTTATCAATTTTCATTAATTAATAAACACGTTGAAT  
531501 TATAACAAAATTAGAAAACGGCTCATTGCCAAGGTTAGAAGTAATAAATT  
531551 CTCCTACTTACTTATTACTTATAATAAAATATAGTTTTTATTTTTATTAAAT  
531601 AAATTCTCTCGATATTTTCGATATTTAAATCTATACATCTAAACAAATTA  
531651 ACAAAGCCATTTAACTTATGGACTCAACCTTTCATGAGCTTGGGATCTCT  
531701 CAAACTTTAATTGAAACGCTTAATGCGCTTCATATTAATAAGCCAACAAA  
531751 AATTCAACAAATCTCTATCCCTCAGTTTTTATCAGAAAAAACTTAATAG  
531801 TTCACTCGCCAACAGGAACCTGGTAAACTGCTGCTTTTGCAATCCCATA  
531851 ATTGAGAAGCTATTTAAAGAAGATCAAACAGCAAAACCAACTTTAGTAAT  
531901 TGCTCCAACAAGAGAATTAGTAGAACAGATTAAACCACATTTTCAAATA  
531951 TTGCTAAAAATAAAAACTAAGAATTATTAGTTTAAATTGGTGGTGTACCT  
532001 GCTTGAAAACAAATCAAAAAAATCAAAACAAATCCCCAAATAATAGTTGG  
532051 TACTATGGGTAGAATTATGGATCTTTTAGAGCGTAAAGCAATTCATTTTA

532101 GCGATTTAGAACACCTAATTATTGATGAAGTTGATTTAATGTTAGACCGT  
532151 GGTTTTAAAAAACAATTTTAAATTTACTAGAACAAATCAATTCCTTTAA  
532201 ACAAATTGCTGTTTATTTCAGCTAGTTACAACCAAGAAGCTATTAACATTG  
532251 CCAAGCAAATTACTAATAATGGGATCTTTATTGGATCACCTGAATTTAAT  
532301 AAAGACGCAAATACCAATAATGATAAACTAATCAAACAATTTGTTTGTTA  
532351 TCTATTTTCAGATCAAAAAAGCAAGCTTTATACAGCCTTATAAAAAACAG  
532401 CACAAGTTAAGTCAATCATTGTTTTTTGTGACACTAAAAAACTAGTTGAT  
532451 GATCTTCATGTATTTTAAAGAAAAATGAATTAAGAACTTTTGCACTTCA  
532501 TGGTGATAAAAAACAATTTATTAGAGAGAGAAATCTTAAATCTTTGCCA  
532551 ATACAAAACAACCCACGATTCTAGTAACACTGATCTTATTGGTCGTGGT  
532601 ATCCATGTTGAAGCAATCGATATGGTTATCAATTATTTCAGCTTGTTAAA  
532651 TCTAGAAGCTTATATAAATAGAATGGGAAGGACTGGCAGAAACAATCATA  
532701 AAGGGACATGTGTAACCTTCTGCACCTCACAAGAAAAGAAAGTCTTTCTG  
532751 AAAATGGTTGAGAAAATCACTGATAATCGAATAGCTGAATGTAAACAAAT  
532801 GGAAATAAAGTTAATTCCTTTAAAAAATAAAGCTAAAACATAAAAAAGGTG  
532851 GTATTTCACTTGATTGTGTTTCAGAAAATATATGCCAATGCAAAACCATAT  
532901 GACCGTAATAAACGTGTCCCTTTAGCAAGTGATCTTTTCAAAGTCGTAT  
532951 GCGCCAGCCTGAAAAAGCTATGCAAAAGCAAAAAATTCATGACAATGACT  
533001 GACAAAGTAATATGTAATAACAATTTATAAAATACTTGTATGGCAAAAAA  
533051 AGACCACTTACCTTAAGAGGGCCTTTGTATGGCAATAATCGTTCTCATT  
533101 CCAAACTATTACAAGAAGAAAATGGAATGTAAACCTTCAGTCATGCAAA  
533151 ATTAAGATACTAATGGTAAAGTAACACGGATTCTAGTTTCACTAAAAC  
533201 AATTCGTACCCCTTAAAAACAATAATCGTTTCTAATTTAAATTTAAGTTAA  
533251 ACTTAATCCATAAGCATATATGGATAAAAAATACGATATCACAGCTGTTT  
533301 TGAACGATGATAGTTCTATTAATGCAGTAaGCGATAACTTCCAAATAACA  
533351 CTGGATGCACGACCAAAAGAAAAATCTAAAGGCATTAATCCTCTGTCAGC  
533401 TTTTTTGCTGGTTTAGCTGCATGTGAACCTTGCAACTGCTAATGCGATGG  
533451 CAGCTGCTAAGATGATACTTTGAACAAGGCACTGATTAACATCAAAGGT  
533501 TATCGTTTAAACAAATCCTAGTGATGGTTATTTTGGCCTACGTGAACTTAA  
533551 CATTCCTGAGAAATTCCTCTCCTAATGAGGAAGAAGAGATTAAAGAAT  
533601 TCATTGATTTTGTAAAGTAAACGTTGTCCTGCTCATAACACTTTGCATGGA  
533651 ACTAGCAATTTTAAAGATAAATATTAGCGTTACTTTAGTCCACTAAAACCTT  
533701 ATTAAAAAGCGAAAAATACCTGTAATTTTGCAGGTATTTTTTTATTTAA  
533751 AAAAAGGATAAATTTAAGAAATTAAATTTTCGCTTTAGCAGTCGATAATTG  
533801 ATCATATGAAAAATAATATTAGTGATGTAAAGTTGGGACTGTTAGCAGCA  
533851 AAAATTTATTGAAATCTTGACGCTTTTATAGAGTTAACAGAAGATGACAT

533901 TATCTCTATTGCACTTCATGCAGAGCAAGATTCTAAGAAGCGTTTAAATC  
533951 CTGAATTTGGCTTAAGTTTTGACAACTATCTCAAATTAAATGGAGCAAAT  
534001 TTCATTAGATCAAGTTTTAGAAATGATGGTGAATAAAGTTGAATTGCTTGA  
534051 TTCTAAAAGTAAATACTCATTAGAAAAGCAAAACACAGTTCTAAATACAC  
534101 CTGAAAACATTTACGGAGTTTAGAATTTAAAGAAATTATTACTAAAGCT  
534151 TTTAATAAAGCTAAAAACGATCAAGAGAGAAAAGTTTTTCTTTATATGT  
534201 AAAGGGCTATAAAAACTTTGAGATAGCAAAAAAGCTCAATATTAGTCCTA  
534251 GAAGAGTGAGATATTTATTAGATCTTTTTAAAGCTACATCAAATTGCTA  
534301 ACAGAAAGATATGGATATTAAATAAAGATATTTTCTTTTAAAGAAATT  
534351 TTCTACTAGTTTTCTAACAGCACTATCACTAGTTAATTTCAATGCTTTTT  
534401 CAACTAATGATTTACATTCATTAATTGTTATTTTAGCAATAACCATTCTT  
534451 GCTTTAAACATTGAACTTGCACTCATTGATAACTCTGTTAACCCTAAACC  
534501 TAAAAGCAACGGTATTGCATATTGATCACTGGCCATTTCAACCACACATTC  
534551 CAGTTCAAACATTATTTAATTTACCACCTTCTACAAGTAAATTAAG  
534601 CGTAGTAATGCTGGATTTAATGGTTGGTATAGATAACTAACGTTTTTATT  
534651 CATCCTATCAGCAGCAAACTATATTGGATTAAATCATTGCTACCTATTG  
534701 AGAAAAAATCAACATGTTTTCTTAAGCAATCAGCTGCTAATGCTGCTGAT  
534751 GGAATTTCAATCATTATTCCTAATTTAAATTTCTTAGTTTTCAATAAATTC  
534801 TTGTTGAACTTTTGTTAAAAGTTGCTTAACTGAACTAATTCATCAAGAG  
534851 TTGCAACCATTGGAAACATAATTCCTAAATTTCCATAATCAGAAGCTCTT  
534901 AATAAAGCACGAAGTTGGGTCCTAAAAACAGCTTGTTTATCTAATGTTAA  
534951 ACGGATAGCACGATAACCTAAGAAAGGGTTATCTTCATGAGGAAATTGAA  
535001 AATAATTTAGTTTTTTATCTCCACCAATGTCTAATGTTCTAATTATTACC  
535051 AAATCATTTTTAGCTTTTTTGTAAGCAGTTTTATAAGCTTCAAATTGAAC  
535101 TGATTCATCAGGTCAATCTTGACTACTCATATAGAGAAATTCAGTTCTAA  
535151 AAAGACCAATTCATTCGTGTTATACTCAACTGCTAAATCCATATCTTTT  
535201 ACATTACCAATATTAGAAGCGACAATAACTTCATATCCATCTAAGGTTTT  
535251 TACTAATTTATTGGTATATTGTTTTAATTCATTTTGAAAGTTGGATTCCA  
535301 ACTCTTTTTCTGTTTTTCATTGAGTTATGTCTTTACTTGAAAAGTCAAAA  
535351 CCCACAATACCTTTTCTACCATTGATACCAACTGTTTTGCCATCTTCAAC  
535401 TTTACTGGTAATATTTTTTAAACCAACTATGGCAGGAATTTCCATAGAAC  
535451 GAGCCATAATGGCAGCATGACTTGTTTTACCACCACTCTCAGTTAAAAAA  
535501 CCCTTGACATACTTTTTATTAAGAGTTGCTGTTTGACTTGGTGTTAAATC  
535551 ATTAGCTACTATAATGACATCACTTTTAATCCTGATTAAATCATTAAGTT  
535601 TTAAGCTCAGTTAAATAACTTAAGAGCCTTTGGTGTAATCTAATATATCA  
535651 CTGGCACGTTCTTTAAATACTTATCATCCATTTCACTAAACATTAAAGC

535701 TGT TTTGTTGAAAAACATTATCAACAGCAATAACAGGATGGATGTTTTTAT  
535751 TTAGTTGTTGTTCTAATTGCTCAGTGATAGTAGGATCATTAGAATTTGG  
535801 ATGTGTGCATCAAAAATCATTCCTGCTTCTTGATTAATATTCTTAACAGT  
535851 AATTGTCTTAATCTCTTCAAGGTCTTTTTTTGCTTTTTTGAAAAGCACTGC  
535901 TTAAAAGCTTTTTTGCTTGGGTGGGTGTCATTTTGACATTTGTGTATTTT  
535951 TTAACGTCAAATTGAGGTGTTTGAATAATGAAAGCTTTTGCAACAGCAAT  
536001 GCCATCTGAAACACCAATCCCAATTATTTTTTTCATAGGTTAATTGTTAT  
536051 TTTTAAATAAGGATTTTGCAATCATCTCTTTGGTTTGCTAAGGTTAAGA  
536101 TATTCCAAGATAGTAGGAGCAATATTAGCTAAAATTCCAGTTTGATTAAA  
536151 GTTAACATTTTTGTGAGTACATACAAATGGTACAGGATTAATAGTGTGTT  
536201 TAGTAAGTGGATTGTTATTATTATCAATCATCACTTCTGCATTCCCATGA  
536251 TCTGCAGTTAAAAACATAGTTATTTGATTAGCTTTACAAAAATCAACTAT  
536301 TCGTTTAATTTGAACATCGAGTGCTTCAAGAGCTTTAATGCAAGCTTGAT  
536351 AGTTACCAGTATGACCTACCATATCAGGATTAGCAAAATTTAAAAACAGTA  
536401 AAATCAAAGTTATTAAGCTTTTCTAGTAGTGCATCAGTAATAGCTTTACA  
536451 TGACATTTCTGGGAGCTAAATCATATGTAGCAACTTTTAAAGAAGGAATTA  
536501 ATGTCTTTGTTTCATTGCTGAGATTAACTTCAAAACCACCATCAAAAAAG  
536551 AAAGTAACGTGAGCATACTTTTCAGTTTCTGCAATCCTCAATTGCTTCAA  
536601 ATTATTATTAGCAATTACTTCACCAAGACTATTTTTAATGGTTTGAGGTG  
536651 GAAAAGCAAATTCGCTAGGTACAATCCCTCATAATTCATCATTGTTACA  
536701 AAAAAATAATTTTCTTTTCGTTTCAATTCAGGTTGATAGTTGTAATAATT  
536751 GCTGTAAAGATCAAATGGGACATTTGTCTTGCTCTATCAGGTCTAAAT  
536801 TAAAGgAAATAACTCCATCATTATTGTTTAAATGCAAACTGATCAGAATTT  
536851 AAATTGGCATTAAATGCAGGATAAAATAAATTCATCAGTAATTTGGTTCTG  
536901 ATATTGCGTTTCAATATAACCAATTGGGTCAATTGAATTTATTTTTTGAAA  
536951 CTCCTAATAAAGCTTTATAAGCAATCATTTACGATCCCAGCGTTGATCA  
537001 CGATCCATTCCATAGTATCTTCCCCCAATAGTTCCAATAACAACATTAGG  
537051 ATAGTTTTTTAGAAATATCATTAAATTTCTCAAGATCTTGTTTTAAGCTAC  
537101 AAGGTGCTACATCTCTACCATCACCAAATAAATGTAATACTACCTTTGCA  
537151 TGTTTTGAAAACAATTCAATGAGTGCTAATAGATGTTCAATTATGACTATG  
537201 CACTCCTCCATTGGAAAAATAACCCAATTAAATGGATTTTTGAATGGTTTTT  
537251 TTTCTACATGTTCTATGGTTTTTAAAAAAGCTTTATTTGCAAAAAAACTA  
537301 CGATCCTTAATATGTTGATTAATCAAAGAAAGTCCAGTATAAACAACCTCG  
537351 ACCTGCCCCAATATTTAGATGACCTACCTCAGAGTTACCTATTTGACCCA  
537401 TAGGCAATCCAAGTCTTCCCCAGATGCATCTAAAAGTACACAAGGATAT  
537451 GAATTGATTAATTCATCTAGCATTGGGGTATTTGCATTTTGTACTGCATT

537501 ACCATAAATAGCATTTGAGATCCCATAACCATCAAGGATTGCTAATAAAA  
537551 CTTTTTTATGCATATACCCTAGCCATTTCTAAAAAGTTTTTAATTTCTAA  
537601 AGATGCTTTACCAACTAAAAATCCATCAATTTGTTCCATTATTGCTAGTT  
537651 TTTGGATATTATTATGATCAACTGATCCGCCATATAGAATTGAGATATTG  
537701 TTAGCAACATTTTCATCATATAAGTCATTAATATATTCCCTAATGGTTTT  
537751 AATGGTTTGATTTGCAACTTCAGGAGTTGCTGTTTTACCTGTCCCAATTG  
537801 CTCACAAAGGTTTCATAAGCAATAACTAAATTTTAAATTAAGCTTTTGTC  
537851 ATCGTATCTAAGCAATTAGTAAGATCAGTTTTAAGAAAGCTAATCTCTTG  
537901 TCCTAAAGCCTCACCAATACATAAACTACTTGCATGGATGCTTTTAGAC  
537951 AAGCAAAGAGCTTTTGATTAATAACTGCACTGGTTTCGTTATAGTATTTT  
538001 CTTCTTTCAGAATGACCAATAATACTGTTGTTAACACCAATGTCTTGAAG  
538051 TTGAGTAAAGCTTACAGTTCCAGTATATGAACCACTTCAATAAAGTTAG  
538101 CGTCTTGCGCAAATAAAAGGAGACTATCACTAATTATTTTTTTTATTTCA  
538151 GTGAGATGAACATAAACAGGTGCTATCCCAATTTTGGCATTGTAATTAAG  
538201 TTTATTTTGTGAAATTGTTCAACAAAATACTGCGTCTTTTAAATTTT  
538251 TATTTGTTTCCCAATTGCCAATTAAATACCTGTGCGCATATGAAAGATT  
538301 TTATAAGTTTTCAAAAACCATTTTCTTTTCCAATAATTGATCATTAGT  
538351 TATGACTTGTTTTCAGTTCCATGTTTTGTTTGCTTATTGGTACGTCTATC  
538401 ATAGATATAGCCATCAAGCTTTTTAATAAAAGTAATGGAAAACAAAGCAT  
538451 CACGATCAAACCTTCTCACATCTTCTAAAAGCTTAGCAGCTTAAATAAGC  
538501 AAACAATTAGTTACAAGCACTTGGGTTTTTTGGCGTGAATATCCTCCTTC  
538551 AGCTTCAAACATTGTGATTGAAAATCACTGTTGATTATCAAGTAGATAGT  
538601 TACGAATTTTTTCTATGTGCTTACCATAAACTTCTACTTTTACAAATTGA  
538651 TACTTAGGGAATAAAAAAGTAATAATCCCAACACAATGTTTCATCAA  
538701 TAGAGTAAAAACGAGGTTTGGAGATAAAAAGAAAGCAACTCCAAATGGCT  
538751 GGTGTTTATCATCACCAACATAAGATTGCACTGATAAACTACCAGTTAAA  
538801 TAAGTACCAATTACATAGCCAATAATAAAGCTAACTGTATTAATTAGCAT  
538851 CAAAATTCACCAATGTCTTTGTATTTTTTTTTCAGAAATATCAGAAATGCTA  
538901 AAAAGTCAAGACCGCTGTAGAAGCGTCAATAATTAATAAATACTGAATAA  
538951 AAAACTGCTTGTAATAAACCCCAAATAAGTCCATAAAAAAGTAAAGATAC  
539001 TTGTTTTTCAGCAGATTTTCTCAAAATATAAGTTGTACTCCCTTTTCAT  
539051 TAATTAATTTTCAAATCCACCATCTTTTGCTGTAGTTAAATTTGCAAAC  
539101 AAAAGAAGTTATCTATTCCAGGGATGTATGAAAAGAAAAACCAAAAAG  
539151 ATTTGAAACAGCTACAAAATAAAGGGTTAATAGGGTAAATTTTTTGGAGA  
539201 TTTTAAACCATCCAAAAATAAAGAAAGGAACATTAAAAAGAATTTGTGTT  
539251 AACCAAAAAATAGCATTAATATAGTTGCTGAATCAACATTAATATTTTG



539301 TGAAGTAATAAAAAAATTAACAAGACGAGCTAATCCTTGGCTAATGGAAG  
539351 CCATACCAATGTCATAAAGTCCTGAAAACGAAACAAAAATAACACCAAGT  
539401 AATCCTCAAAAAAAGCAACTATTGTCAAAATTACAAGTTGTAAATAAAG  
539451 CTTTTTAAGGTTGTATATAGATTGAACTTAAGAAATGATCCAGAAAGAT  
539501 GAATCCTTACAAAATTACCTGAAATTTTGATGTTTTTATCTTTCATAGTT  
539551 AAGAACAATTATTTTAATAATTTTGGTAATTAATAATTTCTTATTTACTA  
539601 TCTTATTAGTAATATTAAGCTTAGTGCAATAATGGCAACGAAAATAGAGC  
539651 TAATAAAAGAATTGCGTAAATCAACACAAGCAAGTGTTATGGATTGTAAA  
539701 CAAGCTTTGGAAAAAATAATGATGATTTTGAGAAAGCTGTTAAGTGATT  
539751 AAGAGAAAATGGCATTGTTAAATCAACCAAAAAATTAATAAGGTTGCAA  
539801 GTGAAGGAATTATTGTTTTAAAAAGCAATTTACACAAGGCAATTATGGTT  
539851 GAGATAAACTCACAACTGATTTTGTAGCCAAAAATCAAGAGTTAAAAGA  
539901 ATTTTCAGATTTAATGCTTGAAAAAATATTTGAAAAAGTAAATCCAAAAA  
539951 CAGAATTAGTTGAAATTGAAAAAATTCAAATTAATAATGATGAAAAAGTT  
540001 AGTGAAAACTAGCATTAAATGCTTCTAAACTGATGAGAAAATAGTACT  
540051 TAGAAGAGTAGTTGTATTTGAACTAAACTAATCAAATTTTCACCTATT  
540101 TACATGCCAATAAAAGAATTGGGGTAATTATTGAGATTCAAGGAAAACTC  
540151 AACGAAGATGATGGTAAGCATTTAGCAATGCATATTGCTGCTAATTCACC  
540201 ACAATTTATTGATCAAAGTGATGTTAATCAAACATGACTTCAAATGAAA  
540251 GAAATATTATCCGTTCCCAAGCAGAATTAGAGGTTAAAGAAAATCCTAAA  
540301 AAAGCAATTTTTTTAGAAAAAACTATTGAAGGTAGAGTTAACAAATTACT  
540351 AATTGATACCTGCTTAATTAACCAAAAATACTTAATTGATGAACTAAAA  
540401 CAATTGGTCAATTTTTTAAAGAAAAACAAGCTAAGGTTCTTAAATTTATT  
540451 AGGTATGAAGTGGGAGAGGGGATTATAAAGGAACTGTTGATTTTGTTAG  
540501 TGAAGTAAATGCACAAATCAAACAATAAAATCCGCCAAAGAATAATCATT  
540551 AAACCTTAGTGGTGCTGGGCTAACCAAGAAAATTCTCAACCCTTTTCTAA  
540601 TGATTTTTTTGAACTATTATTAATCAATTAAAAGTTTTTAAAGAAAGCT  
540651 ATCAAGTAGGAATTGTTATTGGTGGGGTAACATTATCAGAGGTAATAAT  
540701 TGCCAAGAATTTAACATTGCTGAATACCATGGTCATCACTTGGTATTAT  
540751 AGCaACAGTAGTTAATGGCTATTTTTTAAAGCAAAGTTAGATGCACATA  
540801 ATTTGAAAAGTGCTTTACTAAGTGCAATTAGTTGTCCTAGTTTAGCAGTG  
540851 CAAATCTTTCACAGCAAATATTGATAAAGCTTTTGAAGAGAATGACTT  
540901 TGTCAATTTTTTCAGGTGGCACTGGTAATCCTTATTTTTCCACTGACACTG  
540951 CATTAGCTTTAAGAGCAGTGCAACAAAAGCAGTTGCTATTCTGATTGGA  
541001 AAAAAAGGTGTTGATGGTGTTTATACAGCTGATCCTAAAAAGATAAAAA  
541051 TGCAACCTTTTTACCAACACTCAACTATGACCATGCCATTAAAAATGATT

541101 TGAAAATTATGGATATTACTGCTTTTACTATGTGTAAGGAAAAATAATCTG  
541151 AAAATAATTATTTTAAACATTAATGCTGAGAATGCATTATTAGATGCATT  
541201 AAACAAAAAGGTCGCTTTACTATAATTGAAAATAACTAATGACAAAAGC  
541251 ACATTACATTGATTTTTTTAAACAAGCAGCTGATAAAAAAATTCAATGAT  
541301 TAAAAGAAGAGTTAACAAGATTAGAACAGGTAGGCCAAATCCTAAAATC  
541351 TTTGATAATCTTTTGATTGAAAGTTATGGACAaAAAATGCCTTTAATATC  
541401 TTTAGCTCAAGTGACTATTAATCCGCCAAGAGAAATAATCATAAAACCAT  
541451 TTGATCCTAAGAGTAATACTAATGCTATTTACAGTGAAATTCAGCGGGCA  
541501 AACATTGGTGTTCAACCAGTTATTGATGGTGAAAAAATTCGTGTTAATTT  
541551 TCCCCAAATTACTCAAGAACTCGCTTAGAAAAATATTAAGCACGTTAAAA  
541601 AAATAATAGAGCAAATTTATCAAGAAGTGGGGTTGTAAGAAGAGATGCA  
541651 TTACAAATGATTAAAAAGATAATCACAATGAGGATTTAGAAAACCTTTT  
541701 AAAAGCTGAAATAGAAAAAATTAACAAAAATTATTCTAATCAATTAGAAG  
541751 AGATTCAAAAAGACAAAGAAAAAGAATTGCTAACAATTTAAATGAATGAA  
541801 AAAGCAAAACAATTCATCAAAAAGCGAACTTCAGTATTCATTGCTTTATT  
541851 AGTTGTATTTTGCTTTTTCTTTTAATTAGCGCATTTGCTGATGGTTTTAA  
541901 CTTTTGATCACCGTGATCAGCAGATTTCAATTCAGAACATTAAAAGTAG  
541951 AACAAGCAAGTGGTGTTACTAGTGTTATTAGTACTGAGATTAATGAAAAC  
542001 TTTAAAGCTGTTCTGTTTCAGCTTTAGCATAATCATTATTTTAATTGTTGG  
542051 GGTAATTGGTTCTCTGATGATTTGAGAGTTGTTCAAAACATACTAAAAA  
542101 ATAAACCAAACTAAGCTTAAGTTTAACGTTGTTAAATGCTGGAATAATT  
542151 ATTTTTGGGATGATTGGTACTTTTGTTGTTGTTTATTTTTACAAATGAAA  
542201 TGCAACTGTTAATGGTATTGAACATTAAGTTTTACTCTTTCTGTGGTTT  
542251 TACTTTGAATAATTTACATTGCTTGCTAGTAAACAAGAATTAAGTTT  
542301 AGCTTACAACCTTCATATAGCTTAGGAGCTATTGCTTGCTTTATTGCTAG  
542351 CATAGGTACTATTTACTTTTCTGTTATCAGGGGTTGAACTACAATCTTTT  
542401 TATTGATGAGTTTAGCAGTCAGTGTTGATACATTTCTTTTCTTTTGGGA  
542451 AAGCGCTTTGGTAAAAaTCCTTTAATTAAAATTTACCATCAAAAACATG  
542501 AGAAGGAGCTTTTTTTGGCATCATTAGCACCATTGTTGTTGTcGCTTTAC  
542551 TTTGTGTTTTATATTCAATTCCTTTCTTTGTAGCAAAGCCTACTTTTAAT  
542601 CAAACAAATGGAATAGCGCTCAATACACCCCAAAATTATGATAGCCATAA  
542651 TCTTATTACCAATATTTTTTTAATTGCCTTTATCTCTGGAGGAAGTAGTT  
542701 TTTATATCTACTGGTGGGTAAGCACTTTAGCTTTAATTTTTACAGGATCT  
542751 GTTTTTGCAATAGGCGGTGATCTTTTTTTTAGTTATATTAAACGCTTAAT  
542801 TAGTATCAAAGATTTTTCTAAGGTTTAGGTAAACATGGGGGAGTTTTAG  
542851 ATCGATTTGATTCAAGTTCCTTTTAAATTAGTTTCTTCTTTGTTTATCAT

5

10

15

20

25

30

35

40

45

50

55

542901 TTAATAGCAGGAACCATTTCCAACCAAAGGTTGTTGATGGAACCTAATAC  
542951 TTATTTTCAGTGCAATCACTAGTATTCAAAGCTAGTATTTAGAATTAATAA  
543001 AGTATGACTCCAAAACCTAAAGCTAAATAACAACATAAACTGAACCAAAAG  
543051 AACCAATTGATTCTTTGTTTGATTAAAAAAGGTGAAATGCTTGAAAAAG  
543101 AGTTAATTACACCTGAGGGAAAATATGAATATTTTAACGGTGGTGTAATA  
543151 AATTCAGGAAGAAGTACAAAGTTCAATACTTTTAAGAACACTATTAGTGT  
543201 AATTGTTGGTGGATCTTGTGTTATGTAAGGCTAGCTGATAAAAAATTTCT  
543251 TTTGTGGTCAAAGTAATTGCACATTAAATTTGTTAGATCCGCTTGAACCT  
543301 GATCTTAAATTTGCTTACTATGCTTTGAAATCACAACAAGAAAGATAGA  
543351 GGCTTTAGCTTTTGGGACCACGATTCAAAACATTAGAATTTAGATTAA  
543401 AAGAATTGGAATTCCTTTACATCAAATAAGAATGAACAGCATGCTATT  
543451 GCAAATACTTTAAGTGTTTTTGATGAGAGACTAGAAAACCTAGCTTCTTT  
543501 AATTGAGATTAACAGGAACTAAGAGATGAATATGCTCACAAACTCTTTA  
543551 GCTTAGATGAAGCTTTTCTAAGTCATTGAAAACCTAGAAGCATTACAAAGC  
543601 CAAATGCATGAAATTACTTTAGGGGAAATATTTAATTTCAAAAGTGGTAA  
543651 ATATCTAAAGAGCGAGGAGAGATTAGAAGAAGGGAAATTCCTTATTATG  
543701 GAGCGGAATTGATAACACTGGTTTTGTAGCTGAACCTAATACTGAAAAA  
543751 GACACAATTTCTATTATTTCTAATGGTTATTTACTAGGTAACATCAGGTA  
543801 TCATGAAATTCCTTGGTTTAAATGGCACAGGTAGCATTGCATTAGAACCCA  
543851 TGAATAATGAAATCTATGTACCATTCTTTACTGTGCTTTAAAGTATTTG  
543901 CAAAAAGATATTAAAGAAAGAATGAAAAGTGATGATTACCTTTTTTATC  
543951 CTTAAACTAGCAGGTGAAATTAAGTGCCTTATGTTAAGTCATTTCAAC  
544001 TGCAAAGAAAGGCAGGAAAAATCGTCTTTTGTAGATCAAAAATTAGAC  
544051 CAATATAAAAAAGAACTAAGTTCCTTTAACAGTGATTCGTGACACTTTGTT  
544101 AAAAAAATTATTTCCCGATATGACTGAAAGAACTAAATCTATTAAGGATT  
544151 ATTAATCAAAAACCTAATTCTTTCTTTCTAAAATTACTTTAATATCTCTT  
544201 TTCTTGCAAAATTAGATAATCTTTTCACACCAATTGAATAACCTGATTCA  
544251 AAATATCCACCATTATTTTGATAGATAAAATTAACAAATACAAAAATTTA  
544301 CTTTCTTTATTTTAAATTTATCGATAAACAGTTCCTTACAGCGCCAATATT  
544351 AGTAACACTTTTTTTGGTTTAGCATTACTTAATTTTTAGTTTCTTTAAC  
544401 AAATTGAATTGTTATAAAAAATGCGATTATTTTCTTGGATTTTAACTGCTT  
544451 AACTTTTTTTATTTTGATATAAAGTTAACTAATAGAAAAGTATTTATCTT  
544501 CTTTAGTTTTAAGATCAAAATATATCAGGTTTTATTTTAAAAAAATTAA  
544551 AAAATCTTATTAAAGCAATGTGTAATAAAAAAACGGTAAAAGATCGATTG  
544601 ACTTTCCTTAAAAGTTCTTGTTCTAATTTTCTTCACTTGTTCAATTTGTT  
544651 GAAAGTAATAAATCAACTTTTCATGAGAAGTACTCATGTCAATTTTGAT

544701 ATCAAAAGGAAAGTTAATTGAAGCAGGTATACTACTAAAAGTACTTTCAC  
544751 TTACCCTCCTATTATCTGTTGGAGGAGTATAAGTAAAGATAACATCACCA  
544801 TCAAAATTAGCTTTATCACCAGTAAAATCACTTTCACTTACACCCTTGT  
544851 ACTAGCTAAAAAGGATTTGATTAATGAAGTACTAGTATTGTCACTACCAA  
544901 CTATACCAGTCATTTTTAAGTGAATTTGAACCTTAAAAATCTAAGTTATTT  
544951 TTTCAACTGTATTGAAAATTAACCTTTTGACTTTTAACTCCTAAAAAC  
545001 TAAGGCGATTTGACCACTTATACCTGGATAAGTTTCATCAAAATATAAAC  
545051 CTTTTGCACTGATGTTAGGAGTAACATCTTCCTTTGATTTATTAACCTCA  
545101 AATGCTTTAGCAAATCTGCTATAATCAAGTGGTTTTTCTAATAGTTGATA  
545151 ATCTAATAAAGTTGTTTTTCAACTGGCAAATACAGTATTAATTACCTCTT  
545201 CCTTATCAGAACTATAACCTTTTTTAAAAAAGTAACAGCATTATTTTTT  
545251 GAAAGTTCTATATTGTTTCTCTGAAAATAAGCTTGTGCTTTTTCTAAACC  
545301 AGGATCAGTTGATGAACAGGCTACAGATAAAGTACTAAGTGAAATTAATG  
545351 GTAATAAAAAGATCTTTCTGAGTTTCATTACAAAATGGAATAAAGCACAT  
545401 ATGGTAAAAGATCGATAGTTTGATCTTGAAGTTTTGATCAGCTAATTGA  
545451 CCTACAAAATTACTTTGTAATAACTTTTGCATCAATTCATCTTTACCAAT  
545501 AATTTGTAACCTTAAATTGGTATTAAAATTAATTTTCTCAATAGAGTAT  
545551 CAAAAGTAGATTTGGAAAATAAATTACTGGAAGGTGGAGTATAAGTAAAA  
545601 ATTAAATCAGCTGAAATAGAATTTTTATCTTTTATATCACTATCACTTAA  
545651 TCCTATTTGACTCAAATATGATTTTGCTTGAGCACTGTCAAAGTTCCAG  
545701 TAGCTTGTAACCTTATTTGGACTTTGAAATCACGAGAACTGTTATAGTAA  
545751 AAATAAAATCTGTAAGTGGTTGACTACTCAATTTAATTACATTATTAAT  
545801 AATACTTGCAACATTTTGCCTGTATCTTTCAACTAAACGTAAGCCTTTAA  
545851 CACCAGTGCTCGGTTCAACATCTTCCTTACTCTTACCACTGCCAAATGCT  
545901 TTTACAAATCTACTTGGGTCTTGTTTTTCAAGAACTTTTCGTCTTGCAA  
545951 ACTAAATCTTCAAGCATCTAATAGAACGTTTGTAGCACTTTTTGAATCCA  
546001 CTTCAAACTATCTCTTAGTGAAGTAACTAACTCTTCTTGCTCTTGATTT  
546051 AATTCATATTTTTACTGAACTATTTCTAAGTtGGTTTAACTGGAAAA  
546101 ATTTGTTCCACTGCTTAAGTTAGAGCATGCTGTAATTAAGAACCTAATA  
546151 CCATTAAAGAAGAAATGATGCCAGCTTTTGTTCAAAATTGTTTTTTTAA  
546201 CATTTGTTAAGTTAACAGATTTtCTTATTTGTAATTTTTTGATCATTAAAT  
546251 AGAGGTAACTTCAACAACAATCATTTAGAAGTTTTGTTTCTATTTTTAT  
546301 CAATTAACAAATAGAAGGTTTCTATACTTAAAAAACAAAAATAATCACT  
546351 TAATTTTGAATTAATAACTTCTTGTTCTTGCAAGCCTAGATTATTGACAT  
546401 GAAACAGTTTTACTGCTTGAAAAGTTTCATTGGAAATCGATTCTCTACTT  
546451 AATCTAATCCAAGATTTTGAATTTGTGTTTTTATAAAAAAATGAATATT

5

10

15

20

25

30

35

40

45

50

55

546501 AGCAATTAAGTTTCAAAC TATTCTGT TTTTGAAAAAGTCTAACTAAAA  
546551 GATATAAAGAAGTCTGATTAAACAAAAATGCTTAAATCTTTTCCAAAG  
546601 TTTCTAAATAAAACTAATATTATTTTAAACAAAAAGAAACAGTACAAA  
546651 AAATGCAAATACTGATGCTTTTAACTAAATTTAGATCTAAGAAAACTAA  
546701 CACTCATTGCGTTTTAAGCAAAC TAAAAACAACATTAAGAATGATTTTT  
546751 CAAAAAGTTGCAACTATAATTTTAAAC TTTTATTGATTTCTTTTGTATTA  
546801 AAAACATTTGCACAACTTACTCTAAATTAATATCTTTTACTAATAATAA  
546851 GAGATTTTTTTTAAACTAATGGAATTACTAATTAAGTTCATAACTTAATT  
546901 TGCCATATTTCCCATTAATAAGTTCATTAATAAAAATTTACATGCTAAG  
546951 TTAGTGTTTAGTTCATTAGCTTTCTTAATTAAGCCTCTCACTTTAGCAA  
547001 TTTTCCAAAAAGTTAATAAAGCTATCCGCTTCAAATGGTAAAGCTGTT  
547051 TGTAATGTTTCTTAAGATAATTAAAAGCAAACATTCCCACTTCTTCTATA  
547101 TTAAC TACTTCTCTTCTAATAACATTAGTCAAACTAGTTTATATCCAAT  
547151 TtGAATTT CATCAATTCTTTTCAAAAAA ACTCCTGGGGTAtCACTTAATA  
547201 ATAATTCAGGGCTAATTTGAATCCAATTTAATGATTTAGTAATACCAGCG  
547251 CGGTTAGCTACTTTTAAGTGATTTTTATTTATCAAAGGTTAATTAACT  
547301 AGATTTACCTACATTGGGCATGCCAATAACTGCTAATCTAAATTGTTTGA  
547351 TTAATAAGCCTTTTGCTTTTAATTGTTGTCTTTTATTTGCAAATAAAGTT  
547401 GTTAATGTCTTTAGAACTTTTTTTTTTGAGTTTAAAAGGTTCTTTTAATGA  
547451 ACCAAATAAGATCTTTTATTTGGTTTGTATTGTGCTAAATCTGTCTTTA  
547501 ATGCCAGTATTAATTTTGGTTTATTTAAAAAATAACTAATTATTTCTGAA  
547551 TTATGAGTTAAAGTTGGTGCTCTAGCATCTACTATCTCAATGATGCCATC  
547601 AATTTGACTAGATAACTTTTTTAATTGATCATGGATCTTTTTCATGTGAC  
547651 CCGGGAACCAATTAATTTTGGCGGAGGTATATGTGTCCATCTATTCCCCT  
547701 GATTCTTGTAATAGATACCAAACAATCCTTGTCAATTTGTCTAATAATCT  
547751 TAATTAATGGGGAATTTCTACATACATGGAAACAGAACTATCATCTTC  
547801 TTTTGTAGTAAAGAATAACCACCAAGCGTTTCTTGAATAGATAAACTGTG  
547851 ATTAGCATTATCACTTAACAATGCTTTTCTAACTTCTTCAAGCTTATCAG  
547901 TAAATACTTTAATTTAGCAAAATTATAACGAGGGAAAAGATAACTAACT  
547951 ACTGTTCTGTTAACAAAATTGAAAAAAAAGTTGCAATTAAATTAGGTGA  
548001 GAAAAATAAACTAACTTCCCAAGCAGAATCACGATAATTATTGACATCTT  
548051 GCAACAATAAACTACCAGCAACAAAAGAACCAATTAGAATAGCAATAATC  
548101 AGAATAAACTATTTACATAAAAAAGAATTGATCCTACTGATCTATTTTT  
548151 CTTACGAGCATAATATTGGGTTAAGAAGTCCGCTCCCCCAGCAGAACCAC  
548201 CTAGTATGTAAAGTAATGAACTGATATGCCATTATAAAAAACCATAAATA  
548251 GCTGCATAAATAAATGTGGAAATAATTACATTACCTTGGGAAGTATCACT

548301 TCATAAAAAAGGGACAAAACCGGCACCTTTGATTAAATCTTTCGCTGCTT  
548351 TTCAAAAGTTAGTATCTGTTATAGAAGCTAACATTGGTGGTAAATTATCA  
548401 GAACCTGGAATAATACTGATTAAAAAACCAATACGTTAGATGCAACAAC  
548451 AAAATGGGTTGAAAGAATAGTAAAGTTTTTACCTATTTTTTTATAAGAAA  
548501 AAATAATTAAAGGGATGTTGATAAAGACATATAAAAGCCAGTAAAGGATG  
548551 TTAAAAATTAATAATCTTTGAGTTTCATCAAACTTTTTTAACAAAACAAA  
548601 CACTAATCTAGCAAAACCTTGAGTTAAAGAACTAATTCCAAGCTATATA  
548651 AACCTGTTTTTTGAATAAAAAATAAGTAAAAGAAAAGCATTAAATATGAT  
548701 AGTAAGTAACTAATACATACTTTAATGGTTTTTTAGCCTCATAAAGATT  
548751 GCTAAACATCAAAAAAGAGTTAGAAATCCTTACGCGTTTAGAACCAGATG  
548801 CGACTGTTATCTTTGATTCTTTTTTAAATAAGTTGTTAAAAAATTTTCATT  
548851 TGTAACAACTTTTTTAAGACTTTTTTCTTTAATTTTTGCTGACTTACC  
548901 AGATCTTTCACGCATATAAGAGATGTATGCTCTTCTTACTTTACCCCTGC  
548951 GTTTTACTTCTATGTCTATATTAGGGTTGTGGATTGAAAGTTTTTTTCA  
549001 ATAGGAATCCATCAGTGGTTTTCTTACCATGAAAGTTTCGCTAATCCC  
549051 TCTTCCCCTTCTTCTTAAACAGTTCAGTGAAGTTTGAACGAACTT  
549101 TTTCTTTTTCACGTAACCTTAATAGCAACATTAACCTCATCTCCTGCTCCA  
549151 AATTCAAGAACATATTCCTTTAACTGTTTTTGTCTACTGCATCAATTAA  
549201 TGCTTGTTTATTTATTTTTTTCATTTTTATTTTCTAAGTATTTTTGTAT  
549251 AAATCAGGTCTGTATTTTGCAGTTTTTAAGATTGCTGTTCTTTACGAAA  
549301 TGATTCAATCTTTTGGTGATCTCCTGAAAGTAAACTTCAGGAACCTTAT  
549351 CGCCTTTTAAATCGTATGGCCTTGTATAAACAGGAAAATCTAATAGATTA  
549401 TCATTGAATGATTACAAAATAAGACTCTGATCATTAATAACTCCTTTAAT  
549451 TAATCTAACAGTAGCATCAATAACACTTAGTGCTACAAGTCCCCACCAC  
549501 TTAAAACAAAATCACCTAAAGAAAACAATTTGATCAATATATTTATAAATT  
549551 CTTTGATCAAAACCTTCATAGTGACCAGATAACAAAATTAAGTGTTTCGTA  
549601 TTTTGTAAGTTTTTTAGCACAACTCTGAGAAAATTGTTACCTTCTGGGG  
549651 AGAGTAAACTACATGAGAATTTGGGGCTTTATAAAAAATTTAAACAATTA  
549701 ATAATAGGTTAGCTTTTTAAACCATGCCACTTCCTCCACCATAAGCCAT  
549751 ATCATCCACAGTTTTATGTTTATCATTGCAAAAATTTCTTCAATTTACTA  
549801 CTTCAAATTGAACTAAATTTGCTTTTTGAGCTTGTAACATAATAGAACTA  
549851 TTTAAGTAAGGCCAAATAGTGTTCAAAAAGTGTTAAACAGTGATTTT  
549901 CACTACTTTTTAGGACTTGTTTTCTTTCTTATTTTTACTTTCAATAAATTT  
549951 CTTCCACAAACCAGATTCATAAATAAAGAACGACTGTATCAGTTGGAA  
550001 TTGCCCTTTTATTAAGTCAATCTAAGGCAACAGTTTCATCTAATTTACAC  
550051 TTATTTTCCTTTAAAGCTGGATTTAGATGTCCAATTAAAGCGATATACTT

550101 TCCATTACGCTTTACTCGCGAATCAACCGCTACTATTCTATAAAGCGGAT  
550151 AGTGTACTCTTCCCATCCGCATCAATCTTATTTTGACCAATGATTTTTTTT  
550201 CTTAATAAAGCGGCTAATTATAACTTTTTAAAGTTCTATTTTATCTATGC  
550251 TTAAGAATAACTTAATCAGCTATTTTTTATTCGTCTAGTTAATAAATTTA  
550301 ATCATCCAATAAGGCCCGATTTTCATTTTGCATGTCATCTGCAAACCTCAT  
550351 TATTTTTTTAGATAAATAAGTTCTTATCTTTATATCTAACAAAGTCTTAA  
550401 TTATTTTCTGTTGTTTAGCATATTATTTTAAGGCGTTAAACTTGTTTTCA  
550451 GAATTAATGATGAAATAGTTGTTTTGCTATTCACAATAGCAAAACTTAA  
550501 TTTGAATTATGTTTTTGTATTATTAATCTGTTCAATATGTTCTTCTCAAAT  
550551 TAACCTATATTTTTATCGGTTAATTCTTTTTTAATTTTCATATAAGTAGAT  
550601 TAATGTAGTTCCTACTATTAACAAATTTTGTATTATTTTAAGGAATTCCA  
550651 ATAGTTTTTGTCACTTTCATTTGGGAGGAGAGATTTACCATTTTAAATTG  
550701 AATTAATTACAAAATTTTTTTAACAAATAATTAGTTGTTAATAATCGA  
550751 AATTATTAATTAGTTTTTTTAGCATTCTACTGTAATTGGATTTTTCTAA  
550801 TTATGAGTACTTTTCAATAAATTTGACCAACTTATTTTGTGGTGGATTAG  
550851 CGAAATATTTATCCATAAACAGATTAGTGTGAATTTGACCAAAAGCAATA  
550901 TTAATTAACCTGCTAAGGCAGCATTTCAGTGAACAATCAAATAAAAAC  
550951 TTCAATGTTATTTGTTGAAGTGTTATTGCTTGAAAAATAAAAAGTAAAG  
551001 GAATAAATACAAACAATCCGTGTGTTAAAGAGACAATTCAAGAATAAAGC  
551051 ACTCTGTTAGTATTTTGAAAATATTGTTGACTATTAGCGCCTGTGGCTAC  
551101 AAAGAAAACCTGTGCTTGCACTATTAATGAAAAGTAATTTGCTAAATCCA  
551151 AATTTTGATCTGAAACATCAAAAAAAGTAGATAAGATCTGTTTTCCAAAA  
551201 GCAACTGCTGTTAACAAATAGATTAAACTACCGAACGATATACAGATAAT  
551251 AACTGTATAAATGTTAATTTTTTTAATTTTCATCATATTTTTTTTGTCCAA  
551301 ACTTATATGATGAAACTGTTCTAACTCCTTGTAATAAACCAAAAATAGCT  
551351 GCTGAAGCTAAATTACTAATAGCAATAGGTCCAGTTAAAAGTGTCAGATA  
551401 AAAAAACATCATTTTTATCAGTAGTTGCTTTTGTCAAATTAACCAAAAAAC  
551451 TCTCATAAAATGTAGTAACAATAGAAAGTGATCCATTTCTAAAAAAGGAT  
551501 GCCATTCCATTAATGAAACTACAACCTAGTAGATTAAAGTCAATTTTGT  
551551 TAATTTAATAGTTTTTAAAAGTTAAATAAGTAAGATTTCTTTTGTTTAAAT  
551601 AAATTAGATAAATAATATAAGCTAAAAAATTAATTAAGTATCCTAGTATT  
551651 CCAGCCACAGCTGATCCTATTACTCCTAAAGAAGAATATCTAACTAATAA  
551701 AAAAACTATTAATATGTTAATCAAATTAGCAATAGGCGGAACAATTGCAA  
551751 TAAAAAGTTGTCTTCCCTCTGATTGTGCTAAATAAAAAACAACCTTGAA  
551801 AGCATAGGAATGATGTTAAGACCAATCAAAATATAAACATATTCAGATGC  
551851 TACATCAATAGCCTTTTTGTTAAAAAAGTGTGGAAGCTATTAGCTTGAA

551901 AATTTTGTTCAAAACCTTGATTGATCAAGATTATAATGCAACCATTCTTTT  
551951 GCAAAAGATAAAACCAAAAATTGGGTAATTAGTCCAAATACAGTTGTTGA  
552001 TATTAATCCGGTATTTCAAGCTTCCTGAATTTTATTTTGATCATTTCTAC  
552051 CAATTGCTTTAGAAAAATAACTCCAGTTCCTAGAGGAATAAAAAATATTA  
552101 ATGGCGTTTAACAAAACAATCAAAGGTTGACTAATATTTAAACAGTTTT  
552151 AATAAATTGTTTAAATATTAAGTCCAGAGCTTAAAAAACTATCACTTTTAT  
552201 AAAAAGCAGAATTTTTAAATTCATCAATTAAACTCTGATCAGTAAAAATA  
552251 GAATCAGGATTAAGTTCACCTCTAGGAACAACTTAATCACCATGATTTG  
552301 ATCTATAAATACATAAGCAGCACTAAAAAGTGCAAAGAAAAAGTTGGAA  
552351 CAGTAAATCTAAGAATAGTTAGAAAAAGCTGTTTTGATTCAAAAACATTT  
552401 TTAATTAGGAGTTGTTTTTCAAACGATCCCTTTTACTGTTCACTTATTT  
552451 ATTTTTAAAAAGATGGATGTAATCCTTGTATCCTAATTTTTCCATCTCTT  
552501 CAAAAGGAATAAATTTTTAAAGCTGCAGAATTAATACAATAGCGCAATCCA  
552551 CCTAATCACTCGGTCCATCATTAAAAACATGTCCCAAGTGGCTATCACT  
552601 GTTTTTAGCACGAACTTCAGTTCCTTATCATTCCGTGAGATTCATCACGGT  
552651 AGTTAGCAATTAAATTTTTATCAATGGGTTTTGAAAAAGCAGGTCAACCA  
552701 CAACCAGATTTAAATTTATCAGTTGAAATAAAAAAGTGGTTCACCAGATGT  
552751 TATATCAACATAAATTCCTTTTCAAATGCGGTTATATTCATTAATGT  
552801 AAGGTGGCTCAGTGTGAGCATTTTGC GTTACATCAAACCTGGAGTTTGGTT  
552851 AAAGTACGTTTTAGCTCAGCTTCACTCTTTTTTTGGTATTTACTCATTTG  
552901 GAATGTTGTTTATTTAAATATACATCAATAAATGGTTTTCTACTTTGAT  
552951 CTTAGGATTAATCTCAATTATACCCTCATTTTTTCTGTTTTAAATTAAGTT  
553001 CTTTTTCAGAACATAACATGCCAACTGAATCAAAACCAGCTATTTTAGTT  
553051 TTTTTGATAACTGTACCGCTAGGTAACACTCCACCTACTTGTACTAAAAC  
553101 TGTTTTCATACCAACTCTAACATTATTAGCTCCACAAACAATATCCAAGC  
553151 TTTTTGTCAAACCAGTGTTAACTTTACACCTTTTTAGATGGGTGTTTGCA  
553201 ATAGGAATAACTGAAACAACCTCACAAACAACAAAAGGAACTTTATTTGC  
553251 TAATGAAATAAGATCATAACCTAAAAGCTCACTTATTCTTTTCATTATTT  
553301 TTAATGAAGGATAGTTTAGACCTTCATTAAAGCGGTGTGATAAAAAAACT  
553351 TCTTAAAACCTTTTTTTGATATTAAAAAAGTTAAAACCAGTAATTCTATTT  
553401 GCATCATTAACAAAAAACTTCAGTCTTTGTCACTTTTGTGGCGTAAAGT  
553451 TGTTTCACTTCTACTTCTATGATGCCAAACATACAGTTTTTTAATGTTT  
553501 CTTTACGATAAAAGATAGAAACAAAATCTTTAGATATATCAAACATAAAA  
553551 GTTAGTTATTCTGTTTGTATTAAAAAGGCATAACTATTGATACCTGTGTG  
553601 TGTACAAATTACAGGTGAAAGCAAGTGCTCACTTACATCAACTGCATTGT  
553651 TGAGAAGCGTAACAAATTCTTGCTTTATGAGTTGATTTTTATCAGTTTCA



553701 AACATTGTTGTCAACAAAGCCGCTCTTCTGAAATTAACCTCTTTTTTTAA  
553751 TAGCTTTTTTCTAAAAATTGAACTGCTAACTTATGAGCACTGCTAGCAG  
553801 ATTGTGCTTTGTATAAAAACTGCAATTTGCCTGTTTCACCAAGGAACTA  
553851 ATTAAGAGATGAAATTTAAAGCTTTTGATAATAAATGACTTTAAATTAGA  
553901 TAATCTTCCTCCAGCTACTAACGGTTTTGTATCAGTTACAAATAAAATTG  
553951 CACCGCACTTATTACGGAAGTTATAAACAAATTCATCTAAGCCTGCTCTT  
554001 GAATACTGGTTGTTTTTAAGTCAAACCTTAATATCACTAATCAATCAAGC  
554051 TATTAACAACTTCAACTATCTGCTATCTAAAACATGAAACTTGTCTTCAA  
554101 ATTCTTTTTCAACAATCTTCAATTTAAATAGGAGGTTGAGATCTCTTTA  
554151 TCAATAGGGATTTCCTATGATAAGATCATAATCATTAAATTATGCTCTTAAC  
554201 TTTGTACGAACCTCTTCTTCAGAAGTTTGTGATGTTGAAAACCTTAACAC  
554251 CTTTAGGGGCGTTAATCATCTTATCAGTTAAGGTTTTAAGATCAATGTTA  
554301 AAACCTGATTTGAATGTTTCTTGGTGTTCAGCAATTGTTTCAATAATATA  
554351 AAGCGGTAAACATAGAGATGACTATTTTATCTTCCTTTAGATTACTGA  
554401 CAGAATCAACTAAAAAGCGATCCTCACTATTCTAGAACTTCTGTTACAG  
554451 TGCCTGCCCCTACAGTTCTACCACCTTCACGAATTGAGAACTTACTACCT  
554501 TTTTACAAGCGATAGGAGCAATTAACCAACAGTAATAGAAGCATTATC  
554551 ACCAGGTAGAACCATTTCAGTATTTTCAGCTAAAGCAATAGAACCAGTTA  
554601 CATCAGTGGTACGGAAATAGAATTGAGGACGGTAACCGTTTTAAAAACCA  
554651 GTGTGTCTACCACCTTCTTCTTTCTTTAAAGCATAGATCTCAGCTTTAAA  
554701 TTTCTTGTGCGGTTTAATAGAGCCTGGTTTTGCTAAAACCTGACCTCTTT  
554751 CAACTTCTTTACGTTCAACACCACGTAATAATACCCAGCATTTGTCACCA  
554801 GCCATTGCTGAATCAAGTTCCTTTTTGAACATTTCAATTCCAGTAACAAC  
554851 TGCTTTTCTAATTGGTTTTAAACCAACAATTTCAACTTCTTGACCTACTT  
554901 TGAGTTCACCTCTTTCAACTCTTCCTGTAACAACTGTACCTCTACCAGTA  
554951 ATGGTCATCGTATCTTCAATTGCTAATAAGAAAGGTTTATCTACTTCACG  
555001 TGTAGGAGTTGGAATCCATTCACTGCTTTAATCAAATCATGGATCT  
555051 TAGCCTCCCACTTTGGATCACCTTCCAATGCTTTTAAAGCTGAGCCATAA  
555101 ATAATAGGAGTGTCTTACCATCAAACCATAGGAAGTTAACAGATCACG  
555151 TACTTCTTCAGCAACAAGTTCTTGACCTCTTCATCACTAGCAATATCAC  
555201 ACTTGTTTAGAAAACTACCATTTTAGGAACCCCTACTTGGCGGGCAAGT  
555251 AAGATGTGCTCGCGGGTTTGGGGCATCACTATCAGTTGCTGAAACAAC  
555301 TAGAATAGCTCCATCCATTTGTGCAGCACCTGTGATCATATTTTAAATGT  
555351 AGTCAGCATGTCCAGGACAGTCAACATGGGCATAGTGACGTTTGTGAGAA  
555401 GAATATTCTACGTGTGCAGAGTTAATTGTGATTCCCCTTGCTTTTTCTTC  
555451 AGGGGCTTTATCAATTTTCATCATAACGCGTTGCAGCTGATTTTCCTTCCT

555501 TTGCTAAAACTGTACAGATAGCAGCTGTTAAAGTGGTTTTACCATGGTCA  
555551 ATGTGACCAATGGTACCAACATTGACATGTGGTTTGGAACGGTCAAATTT  
555601 CTCTCTTGCCATTTGTTTAAATTATGTTGTTAATTTTAAATAAGTTTAAAG  
555651 ATAAGCTGGAGATAATGCTTATAATCTTCAAGGACTTAAATTTAGTGAAA  
555701 ACAAACAATTGCCAAATTATTGGCTGATGAAAACAACCTTCCTTACCACA  
555751 AAAGACATTCTTAAGTTTCATTCCCTTATTTTTGGTCACTAGTGCTTTTG  
555801 TTTTAACTGGAATTGTTGAAAGTCTTTTAACATTTGGAACTATTATTGAA  
555851 CAAATTGATAAATTCAGTATCAGACTAATGTGATGTTATTAATTTATGC  
555901 AGTTATCTACACTTTTAATCCAAAAAGTTGATTGTTAAAAAACCAACAAT  
555951 TCTTTTTAAGTGCATTAGCTTATATATTATTACTTTTATTGGCTATAAC  
556001 CTAATTTTGTCAATAGCTGGTATAGCTTATAAATCAACAAATCCATATAA  
556051 GTTAACAAGTAGTATTTTTCTCCATGTAATTGCACCAATAGCATTCTTCA  
556101 TAGCAAGTTTTATCAAAATAAAACATGAGAAAGATGTCAATATTAACATG  
556151 TTCTTTAAAAGCCTATTATTATTCATGATCTATCCTTTAATATATGGGCT  
556201 TTATTTAGTAACTATTCCATATGTAAGGCATTATCTTTTAAATGGTAGGC  
556251 CATCTACTTATACCATTTATGGCAGCATTACAAATACTAAAAATAATCCT  
556301 TTTGCTTGATTAGTTGTATTTGCAGTTTATTTATCTATTTCCCCTTGAG  
556351 TTACTTAGCTATATATCTATTACAACCTAAGTTAATAAAAAAAGCCATAC  
556401 AACCGCAATTTAATTTGCCTTTTACATTAAATAAATGAAAACAAAATAA  
556451 GAAAAGCAGTTATTCCTGCTGCTGGGTGGGTGTTAGGTTACTACCAGCA  
556501 ACAAAGCAATTCCCAAAGAGATGTTACCATTGGTAAATAAACCTACTAT  
556551 CCAATACATAGTAGAGGAAGCAGTTAAAAGTGGCATTGAACAGATTCTTG  
556601 TCATTGTTTCATCCAAAAAACAGCTATATTAGATCATTTTGATTATGAT  
556651 CTGATCTTAGAAAAATGCCTTAATTCAAAAAATAAATTGCAGGAGCATAA  
556701 AGAGATTGAAGATATTGCTAATTTAGCACATATCTTTTGTAGACAAA  
556751 AAAATCAAGATGGTTTGGGAGATGCAATCTTGTTTGCTGAATCTTTGT  
556801 GGTAATGAAGACTTTGCAGTATTGTTAGGTGATGATGTTGTTTTAGTAA  
556851 AGAACCTGCTTTAAACAATGCTTGAAGCTTATTATGAACTAATTGTC  
556901 AAACAATCGGTGTACAAGAAGTAGATCCTTGTCATGTTGATAAGTATGGA  
556951 ATTATCACCCTGAAGGTGATTACAAAAATAAAGATCTTATTAAGGTTTT  
557001 AGCAATGACTGAAAAACCTAAACCAAAAGATGCTAAAAGTAATTTAGCAA  
557051 TCTTAGGGCGATATGTACTCAAACCATCTATTTTCAAAGCACTTAGAAGT  
557101 GTACCTTATGGAGTTGGTGGTGAGTTGCAACTAACTGATGGTTTAAATTT  
557151 TTGTTTGA AAAATGAAAACCTTTTATGCAAGAAAGTTTACTGGTACTAGGT  
557201 TTGATGTTGGCACAAGAGTGGTTTATTAAAGCAAATTTATTTACTGCT  
557251 TTAAACAATAAAGATATTAGTAAAAAGAAGTTTGAAGCTTTTAAATTT

557301 AGTTAAAGCTTAATACCATTTAAAGTTAAACCAAGGAAGTTTTCATTTCT  
557351 AATCAATCGACTAAAAGGACACATTTTCATGGGCTTTTTGAATTAGTTTTT  
557401 TACCAACTTCTTGGTCATTACTATTAGTAGTTAATTCAACACCAGCCTTA  
557451 ATGTGAAATAGTCCATTTTCTTGATGGAGTTCTACTTTAACACTTACAAC  
557501 TGGTTTTTTTGAAAACTAAATTGATGTTGTTGCATAACAACAATTACTG  
557551 CTTGAGAAAAACAACCTGCATAAGCAGATGCAAATAACTGCTCAGGATTA  
557601 TTTTCTGTTTGAACGTATAAATCAGGTTTGGGAAAACTAAGTTTTGTTTG  
557651 AAAACCATCTAAAGTTTAAACACTACCTTCTCTGCCAGTTTCAGTTTGTG  
557701 CAACAGTTTTATAAATCAATGCCATGTTAATTAATATAGATAATATTTTA  
557751 GTAAAAATGTTAAATAACATATTGCAATTTCTCAAAGAAAGAGAACTTTA  
557801 TTCACAAGCTAATTTTGAAACAGAACTAGATAACCATTTAAAAGAGAAAA  
557851 AAAATAACTTTTATGTTGGTTTTGATCCAACTGCTAATTCTTTACATATT  
557901 GGCAATTATGTTTTAATTCACATTGCAAAATTATTTAAAGACATGGGGCA  
557951 TACTCCGCACATAGTTCTAGGGAGTGCAACTGCTTTAATTGGTGATCCTA  
558001 CTGGCAGAATTGAATTAAGGAAAATTTTAGAAGAAAAAGAAATTGTAAAA  
558051 AACACCAAAACAATTAaaaaacaaatcaaacagTTTTTAGGTGATGTAAT  
558101 TATTCATGAAAACAAAGTTTGATTAGAAAACTTAATTACATTGAAGTTA  
558151 TCCGTGAATTAGGTGCTTTTTTTTCAGTTAACAAGATGTTAAGCACAGAC  
558201 GCATTTAGTGCTAGGTGAGAAAAGGACTAACTCTAATGGAATTAACTA  
558251 TATGATCTTACAAGCATATGACTTTTATTATCTACATAAAAAACCATAATG  
558301 TCACTTTACAAATAGGTGGAAGTGATCAGTGGGCTAATATTTTGGCTGGT  
558351 GCTAACTTAATTAAAAGAAAAAATAATGCTAGTGTTTTTGGATTAAGTGC  
558401 TAATTTATTAGTTAAAGCTAACGGAGAAAAAATGGGTAAAAGTAGTAGCG  
558451 GAGCATTATGACTTGATGAAAATAAACTAGTGTTTTTGATTTTTATCAA  
558501 TACTGGATTAACCTTGATGATCAAAGCTTAAAAAGACTTTTTTAATGCT  
558551 AACAATGCTTGATAAAAAAGTAATAGATGAATTGTGTAATTTAAAAGGCC  
558601 CAAAAATTAAACAAACCAAGCAAATGCTAGCCTTTTTTAATTACTGAATTA  
558651 ATCCATGGCACTAAAAAGCAAAAGAAGCACAAACGATCTGAACTAAT  
558701 ATTTAGTAATCAACCAGATCTTGATATTAAGTTAGTAAAAACAAGCACTA  
558751 ATCTAATTGATTATTTAGTTGAACTAAATTTATTAAAAGTAAATCAGAA  
558801 GCAAGAAGATTAATTAGTCAAAAAGGTTTGACAATTAACAATAAACACGT  
558851 TTTAGACTTAAACCAAATAATTGAATGAAAAGAAGAGTTACAAATTATTA  
558901 GAAAAGGTAAAAAAGTTTTTTAACAATTAAACTGTTAATTCTTAGCTA  
558951 ATTTATCTTTAACTTCTTTTTCTATTTCAGTTTCAACACTTTTTTGACTA  
559001 GAGCTTTTACTTTCTGGTTTTTTTGATTAATTTGTTATGAAGTAAATCAAC  
559051 AACTTTCTGCATTGAATTTAATGTTTTGAAATCATAGCTTGCTTGGAGTT

559101 TAATGTTTGTAAGTAGATCATCAAATGCTTCATTCACTTTTAGTTTAGTA  
559151 TCCATAAAGGTTGTAGGCACACTCATAACAAGTAAGTATGAACTGTGTG  
559201 ATTATAGACATTAAATTTGGCATATACATTCAAAGGATTAAAAAGCACTT  
559251 TATTTAATACCTCTGTATCTAAATTCTGAAAAGAAAAATTGAATCTTTT  
559301 TCAACAAAAAGTGAGATGTTTTCTTGCTTTTGTGTTTCAGTAAGTGCTTC  
559351 AAAGTGAAGGACATTCTTATTTAAAGAATAGTTAGCATCAGTTAAAAAGA  
559401 AATGATTTTCACTATTAAATTGCTGGTGTAAATAGCAATCAAGCAAGCTACT  
559451 TTTTCTGTTTTATTACTGCTTCTTTTAAATGCATAAATATGACCAAAAAC  
559501 AAATTCACTACCATCTTTATAAGTAACCTTAAATTGTCTTGGAAGTGTT  
559551 CAAAATTGTAAAGAGCAGTTGGATAAAAACTTGGTAATATATCGCTGCTT  
559601 ATAGGACCTTGTTCAAAAAATTCAAATGATTCTATTGCCTTGAAATTACC  
559651 CATCTCTTTTTGTCATAAATTAGTTCTGTTTTCTTTGTTAACTTTTTTTA  
559701 ATAGCTTGTTTCTTTTAAAAAGAGCAGCAAAATGGATAACAAATGCTAAA  
559751 AACAAAACAACACTACCTAAAAACAATTAAAAAAGTGATGCTATATTTGG  
559801 TATTTCAATTACGTGTATAACTATAAATACCAAATGAGATAGCAATAACAC  
559851 TAAAAAGACCACAAAGTCCAATTACTCTTAGAAAAGCATTGAGTTTATTT  
559901 GGTGTCAAAAAGAACTTGTTAAATTTAGTTAGATCTGACATATTTGTATA  
559951 AAAGATTGTATGAAATATAAACCAAAGCAAGCTCAACAGTTGTTTTATT  
560001 ACAAGATCTTTTTCTAAAACTGCAAGTTGCCAACTTAGCACGCATCT  
560051 TTATTAAACGAAGATAGAGCTCATCAAATTTTATATCAAGTATTTTGAT  
560101 CTTTTGTTTGTTTTGGAAATAAAAGTGCAAAAGTACTTTAGAAAATAAAA  
560151 AATCAGATCCCAAATTCGTTTTTGCTCTAACTAATAGTTTGTGTTTTTA  
560201 GTAATACTTCAGTTTGCTTTAAACATTTTTTAAAGTAATAACAAGATCA  
560251 TCATTACTGTCATTTAAATAAGTTTGTATGTTTTCAATTCAAATCAAAT  
560301 GTAGTGATATTCAGTGTCAAACAATTGGGGATTATTTTTAATTACTGTAA  
560351 AAAAATCAGTAATTGTTTTACTTTGATCATTTAGTACTTTAAACAATTC  
560401 CAAGCTTCATTACCATAACCAACTTCTATTGCATTTAATTCTTGCTTAA  
560451 TGATAGTAAGTTAACCAAGAAGTTATCAATAAAATCAACAACACTAACTG  
560501 TTTGTTTCACTTTCTGGTTTTACTTCAGATTTATTTAGTTTTTGCTTTGC  
560551 TTGTTGTTCTTGCTTTTGCAATAAGATTTCTGGTGGTAGTTTAGTGTTTT  
560601 TATGGATGAAGTCAATATCACTTTTCAAATAGTTTCAGCAATTAAAAGT  
560651 GCTTCTACAAGCAATTCTAGTTCCTTACGGTTACTCTTAATGATTGTTTT  
560701 TGCTTTCTTATACTGTTCTTCAATAATGAAATTAATCTCATTGTCAATAT  
560751 CTTTAGCAGTTTGTTCTGAATAAAGTTTTACATTAGAAGGGAGTGCCCT  
560801 TGACTTGGTACATATTGCACTTGACCTAATTTAGACATCCCAAGCTGGGT  
560851 TACCATTGCTCTTGCAATATTAGTTGCTTTATAAAAAATCGCTAGAAGCGC

560901 CAGTAGTAATTTCTAAATTACCATAGATTTCTCTTCAGCAGCTCTACCG  
560951 CCCATAGCAGTTGCTATCATTGCAAGTAAATCAGATTTTCTTTTAGGTT  
561001 AAGATCACCACCTCTTAGGTGTTGAAAGTGTGTAACCCCTGCTTGACCAC  
561051 GAGGAATAATGGTAATCTTTGTACTTCATCATTACTGTGGACATGTAAA  
561101 CCAACCAAGGCATGACCAGCCTCATGATAAGCAACTAGTTTCTATCTTC  
561151 ATCACTAATTACACGTGACTTTTTAGCAGGACCAGCTATTACTCTATCAA  
561201 TTGCTTCATCAATGTCATTAATGTTAATTGTGGTACGGTTGTCTCTAACT  
561251 GCTAACAATGTAGCTTCATTGATAACATTTTCTAATTGAGCACCTGAAAA  
561301 CCCAGGAGTTCTCTTAGCAACATCTAAAAGACTTATCTTAGAAGAGAGAT  
561351 TTTTATTTTCAGCATGAACTTTTAAATCCCTTCCCTTCTTTAATATCA  
561401 GGGAGATTGATTGAATATGTCTATCAAATCTTCAGGTCTTAATAATGC  
561451 ATCATCTAATACATCTAACCTATTTGTAGCTGCCATTACAACAACACCTG  
561501 TTCTGCTTGTAATCCATCCATTTTCAGCTAACAATTGGTTTAAGGTTTGC  
561551 TCAACAACAGAATAAGAAGAGAGTTCAACTCTACCCCGTTTAGAACCAAC  
561601 TGAATCAATTTTCATCAATAAAAATAATACAAGGAGCAGCCTTTTTCAGTT  
561651 TATTGAAAAGATCTCTAACTCGTTTAGCACCAACACCAACAAGCATATCT  
561701 TCAATCCAGAACCCGTTGATTGAAAGAAAGGAACACCAGCTTCACCAGC  
561751 TACTGCTTTAGCTAATAATGTTTTACCTGTCCCAGGTGGACCGTATAAAA  
561801 TTACCCACAGTGGGGATCTTGCTCCCATCTGGGCATATTTCAATGGATT  
561851 TTAAATAATCAACTATCTCAAGCAACTCATGCTTTTCTCTTGAAGTCC  
561901 AGCAATATTGGTAAATTTACAGTTGACTTAGCCAAGTTAGCTTGGGTTT  
561951 TGCCAATAGAAAAATATTATCTTCTCTCTGCCCCCTGCAGATATACCC  
562001 CTAGCACTTCTTCAAAAGAGTAAAAAGAAACTACAAAGATAATAATTGG  
562051 TAGCAAGCCAAACAAACCATTTAATACATCTCTAGCTCTAGTATCAGGAG  
562101 CAATGAAAGTACCAAGGGTTTCAAAACCTGCAATACTCTTTGTGTTATTA  
562151 CTAGAACCACCATTCATCATGGTTCATTACTATTAACGGTAATCTGACC  
562201 ATTACTTTGGTTAATTGATAAGTTAGCAATATTAAAGATAACATTGCCAT  
562251 TACTATTAACAGTTTTGTGAGCAGTAACAGTTAATGGACTATTTAAACCA  
562301 TCAAAGGTAATGGAAACTTGGAGAATGGTATCAGTAACATAAGTTGAACC  
562351 ATTTATTTGTTTAAATGTCAGTTCATTACTAAAACCGCTTACTTTTGCTG  
562401 TTAAAGTGCTGTACTACCTCCATTTAATTTTCAGCTTCAACTACTGCA  
562451 GTAGCAGCTCTTGGACTGAAAATATAAGCTAAAACACCAATAACAACAGC  
562501 TAAATGATGACTCATCAAAGACTTTTCAAGCAGTTTACGTGAAAAAT  
562551 TATTTTTTTCAGTAGTTGTTTGTCTACTAAACCCTTATTTCTTTTTTTC  
562601 ATCTATGTTAGTTTTTGACCGATTTGGGTTTTTTTGGTTTGAACATACATT  
562651 AACTGTAATTATACTGCCAATGGTAATGAACTAATAAGTGTTAATAAAG

562701 TGACGAAAATTATCTTTTATGTTTACTTAAAAGTGCAATAAAAGCCTTG  
562751 AACCAACGCATAAAATTTAATATCTGTTTATAGGGATTGCTGGTTCAAA  
562801 CACACCAACATAAGGTAGGTTACGATAAAAACCATCATAGTCAAGACCAA  
562851 AGCCAACCAAAAAATTATCTTTTACTTTAAAACAAGAAAAATCAATATTA  
562901 ATATCAAAGGCTTTGGGTTTAATCTTTTCAATTAAGCTAATTAAAGTTAT  
562951 TGATTTAGCATGCCTTGTTTTTAGAAGATCAATAACTAATTAAATAGATC  
563001 TACCACTATCAACAATATCTTCTATTAAAAGGATGTCTTTATCTTTAGGG  
563051 TCATGGGACATATCAAGCACAATCTTAGGTGGTTGTTTTGTACATGTGA  
563101 ACCATGATAAGAAGCAACTGCCATAAAATCTAGTTGGAGGTCAAACTAA  
563151 ATTTACTTATCACTTTGCCAAGGAAAGGGATGCAACCTTTTAGAATGCCA  
563201 AGAACAATTACCTTTTTATTATTAAATTTAGCATTGCACCAATTAAGTGC  
563251 TTTTGTACAGCCTTCTTCTATCTGTTGTTTCATTAATAACAATAGATTTAA  
563301 TACCCATCTTATTTAGTTTTTTGACGTTCTACTAAAACAACAGCTAAGCA  
563351 ATTAATTTCACTACTGTCTAAAGGTTTTCTAACTTTGAGATTAATTGTTA  
563401 ATTCTGAAATTCCTAAAGCACTACAAATAAAAGCAAAGATAGCGTGTTTA  
563451 TAATCATCAACCTTTTGCTCTTGAGGAATCTCTAAGGAGATATCAATATT  
563501 ATTGATAATTCAGTTTTTTCTGATGAAATTGTAAGTTCTTGCTAAGACTC  
563551 TTGGTGCTTCTTTTTTTGACGTACCTTTAAATTTGGACTGTTGATTTTCCT  
563601 TTATTGAAAACAATATGACCATCACCTAATGCAGTTGCACCAAATAAAGC  
563651 ATCAGCAACTGCTAATTGGATAACATCACTAACTTCATCACTGTTTTCAA  
563701 GATCATAAATATATTTAGAAATCTCAAATCAACACCGCCTAACCAAAAT  
563751 TTATTTTTACTTTCTTTCTTAATTTTATGTGGTATTTTTTGCTTCCTAG  
563801 GCCAACTCTTAACTGCATTGTTACAAATAATTATAATATCGCTCATCTTT  
563851 AAATAACAGTGTTGTTTTGTAATCCAAAAAAGTAAATTCAGGCAACAGT  
563901 TTTTGGACTTCAAATATCCTTATTTAGACAAAGCAAATTTATTAAAGTG  
563951 AACCAAAATAAAATTGAAGTATATCTCTAGATAAAATAAATATGAAAGGAC  
564001 CTAAAATTGCAATAGTAGGATCAGGTGCTGTTGGTACTAGTTTCTATAT  
564051 GCTGCAATGACTCGTGCACTTGGTAGTGAATACATGATTATAGATATCAA  
564101 TGAAAAAGCTAAAGTTGGTAATGTATTTGATCTTCAAGATGCTTCCTCAT  
564151 CATGCCCAAATTTTGGCAAAGTAGTTGCTGGAGAATACAGTCAATTAAAA  
564201 GATTATGATTTTATTTTCATTAGTGCAGGAAGACCTCAAAAACAAGGTGG  
564251 GGAACTAGGTTGCAGCTACTTGAAGGCAATGTAGAAATTATGAAAAGCA  
564301 TTGCCAAAGAAATCAAAAAATCTGGTTTTAATGGAGTTACATTAATCGCT  
564351 TCAAACCCAGTTGATATCATGTCATATACATATCTTAAAGTTACTGGATT  
564401 TGAACCTAATAAAGTAATTGGCTCTGGTACTTTACTTGATAGTGCAAGAT  
564451 TAAGATATGCAATTGCAACTAAGTACCAAATGAGTTCAAAGGATGTACAA

5

10

15

20

25

30

35

40

45

50

55

564501 GCATATGTTATTGGTGAACATGGTGATAGTTCAGTAAGTATTATTTTCATC  
564551 AGCTAAAATTGCAGGACTATCACTAAAACATTTTTCTAAAAGCTAGTGATA  
564601 TTGAAAAAGAATTTGGTGAAATTGACCAATTTATCAGACGCAGAGCTTAT  
564651 GAAATTATTGAACGCAAAGGTGCTACTTTCTATGGAATTGGTGAAGCTAG  
564701 TGCTGATGTAGCTGAACAAATTTTGAAAGATACTAAAGAAGTTAGAGTAG  
564751 TGGCTCCTTTTACTTACTGGTCAGTATGGAGCGAAGGATATGATGTTTGGA  
564801 ACTCCTTGTTGCTACTTTCAAGAAAAGGTATTGAAAAGATCTTGAAATAGA  
564851 ACTTTCAAATACTGAAAAAGTTGCGCTTGAAAATTCAATTAAAGTTTTGA  
564901 AAGACAACATTAACTAGCAAAGCTTTAGTTTTGATAGAAAACATTAGCT  
564951 CATCTATAAAAAGAGTTTTCAAAAAATAACTCGTTACTTCTCTTAACAAG  
565001 CATACTAATTTCACTGAGATTTTTTAATCTTGTTTTGAGAAGTTTTTATTT  
565051 TTAATTCATTTTTGTGCTTATTTTCATCCTTCATAAAAACCTTAAATTGG  
565101 TTATTGAATTTAGTAATGAAATAACTAGGAGTTTGATATTCTTTTACTTT  
565151 TAATTCAAAATCAAGATCACGTTTTTCACAACCTTCATAAACTTTACTT  
565201 GAAATTTGAGAGTGTTAAGATACTATCTAGTAAGGTTTTTAATATTGCA  
565251 TCTTTAGTTGTTTCAAATGTATTAATAAAATGAGTGAAAAACATAATC  
565301 ATCTAACTTCACAAAAAAGTTAATAAACTTTTTTTAAACAACCTGGTTTT  
565351 TTAAAAGCGGTTTAATTACACTTTCAACATTCTTAAAGTTATGAAAATTA  
565401 AAGTTGTCTTCTTCAATTAAGCTTTAATCCGTTGAAAAACAAATCATAA  
565451 GTTAAGTTCTGTAGCAATACTTCTACCATCACTGTAGATTGATTGATACA  
565501 TGTGGTGTCTTGTTATCAAGAAGTTTCAATGAAAGGCAAGCATTTTTCT  
565551 TGAAAAACAATTTTATAAGTGCCCTGATTATCTACACATTCCATTCCATT  
565601 GATAATTGATTGATAATCAACTAATGAGTGACTGGTACCTGTAAAATAAG  
565651 CATCACGTAATAAATAATCCATTCTGTCTGTGTCAAGATCTGAAGAGATT  
565701 AGCTGTCTCATCCACCAGTTAATAGGTTGAATATTTTGATTTTCATCAAT  
565751 TAAAGCGCCAATCAGATTTGGATCTATCTTATTAGCTTTTAAGATAGAGA  
565801 CAATAGGTTCACTATTAACTAACATTGAAGTAACCTTTTCATGAATAAAA  
565851 AGTTGTTTTTTAAAATCAGGATTTTAGCAAAATAGATTTCAAAAGCATG  
565901 AGAATGAGGTCCATGACCAAGATCATGCAACAAACCAGCTACTAAAACAG  
565951 TTTGTTTTTTAATTTGATCAATATTTAAAAATGCAGAACTATTTAAGATC  
566001 CTTCTTATCAGTTCATAAACTCCTAAAGAATGGGCGTACCTAGTGTGAAC  
566051 TCCACTAGGATAAAAAATGGAAGTTAATTCCTAATTGTTTGATGTTTCTTA  
566101 ACCTTTGAAAAGCTTTTGATTGACCAATTTCATACATCCACTTTGTGTTT  
566151 TCATCAAAAATAATTTCTCCTAAATAGGATCTTTAAAAAAGGTTTGTTG  
566201 CATTAATAAATTGCTTAATTAAGTTTATTGCACTTTCTTTATCAAAAATT  
566251 TCAATAATATGTGCTAAATCAGGTCCATGCTCCTTATTTGTAAAAATTAA

566301 CCTTATTGGCATAAAAAGTTGTTTACCTTTTAAGTTAAACACTGCTCCTA  
566351 CTTTGTTAATAGTTGTTTAAATTTGCTCAGCTTTTCATTCTTCCAACCT  
566401 TGTAAAGATTTGGCAAGCTGTTCTAAAAAAGTTTGATGTTTTTAAACAA  
566451 AATATGACTTTTCTTAGCTAAGTTTCAACACCTATTTTAGTGGCAAAAG  
566501 ATTCTCTTATCAATTCGTTTATTTGAACACCATGGGTTATTTGATTTTTA  
566551 AAAAGTAAACTTATTTCCCTGTTTTTATCTTTTAAATAATCAACCTTAAC  
566601 ATCCAAGTAATTATCAATGAAATTGAAATAAGCATTATCAGTTAATTGTT  
566651 TAATGTAATTAGCATTGATTCATTGCAGCTTTTTAATATCAAAAAAAGCA  
566701 GGAGCACTAACAACTCTACTTAACTAAAGTTTTCAATTAAGTGTTCAA  
566751 ATTAAAAACTCCTGGTGTACTGTGGATGTCAACCTAAGAGTGCTAAGA  
566801 AATTTAATAATGCTTCAGGTAGATAGCCTTGTTGTTTAACTGCTCAATA  
566851 AACTGAGTAGTTTtCTCATCACGTTTAGAAAAGTTTTTGCCTTTTCATC  
566901 AACAAATACTGAAAGATGACCAAAGCGGGAATTCTTTTAAACCTAATG  
566951 CTTGATATATAGCAAGTTGGTATGCAGTGTTAGAGATGTGCTCAGCTCCC  
567001 CTTAAACATCAGTAATTTCCATATCATAATCATCAATAACAACTGCAA  
567051 GTTATAAGTAGCAACACCATTAGCTTTAAGAATAACTATATCTGTTAACG  
567101 CACTGCCGGGAATAGTAATTTGTCCCTAACCAGATCATTTCAACTATAT  
567151 TCAGCTTCATTGTTTATTTTTAAGCGGATAGTAAAAGGATCATTTTTTTC  
567201 TAAGTGATTAGTAATTTCTTGGAATGTAAATTACGACAATGACCTAAGT  
567251 ATTTAGGGGTTTTGTGGTTATTAATGGCTTGTTTTCTATCTGACTCTAAT  
567301 TTTTCTTTGCTACAGAAGCAACGATATGCCAGATTTTTTTCAATTAAATC  
567351 AAATGCTAGTTTTTTATAAACTGCTAGTTTTTGTGATTGCAGATATGGAC  
567401 CATAATTGCCAGGGTTATAAACCGATTCTCTGCAATGACTCCAAGCCAA  
567451 CGCAAGTTATCAAATTGTGAATTAATTCCTTCTTTTATGTTTCTTTTCAGT  
567501 ATCAGTATCTTCTATCCTGATAATAAACTCACCATTAAAGTGCTTGGCTA  
567551 GTAAAAAGTTAAAGATTGCTGTTCTTGTACCACCAACATGCAGATATCCT  
567601 GTTGGGGATGGTGCATAACGTGTTCTAATTTTTTCCATTACAAATGTTTT  
567651 GGTAAAGATTAAAGAGTTGACAAGGACTCAACTCTTGCGCTCTAATGCTA  
567701 GTCTTTAAATTTTGCTTTTGAATAATGTTAAGTAAATAATCAACTGCAA  
567751 AAAATGCTTTAAGTTATTAATTAACATCTTCCTTCTTTGATTGAAACATT  
567801 GCTTTAAAAACAGACCAAACCTTAAAGTCATAACTAACCGATTTATTTTTt  
567851 TCTAATAATATTAAGGTTGAATCCACCTTAGGTTTAGGTTTAAAGCATG  
567901 CCTATCAATTTTAAAACTGTTGTAATAGTCAAATAGTATTGACAAAAAG  
567951 CACCAAAGGCACTATAATCACTAGAATTAACCTTTGCCAGAAGCCGATTA  
568001 GCAAACCTCTTTTGTGTCATTAAAACAAAGCTTCGAAGCTTTGATTCTAA  
568051 AAACCTATTGATTATTGGAGATGTAATGCTATATGGGATATTACCACACA



568101 ATAATGGACTTAAATTTTCAAAAAAACTATTAAAGTCCTTTTTGAGAATA  
568151 TCGCCTTTAACTAGTTGGTCTTCAGTTAATATCTTTtCAACTAGAAGATA  
568201 TTCAATTAAGCGTTTATCAATTTCTATCCCCTTGTAAGGTATTTTGAGTT  
568251 TTAACAAATAATTTGTTAACGCTCCTTTACCAACACCTATTTCAACAATT  
568301 GCTTGTGGATTTAAATTTTAAACAAAAGCAAAAATTCTTTTAATGACGCT  
568351 TAAATTAACCGTAAAATTTTGACCTAATTTACGTGAAGGAAAAAACTAT  
568401 TCACGCTCTAAAATCAAATCTAATTTGGAATAATTTTGCTTTCTTTTTTC  
568451 CCTTCTTTTGACAATGAAAACATGGGTAAATAAGATTGTAATAAGTAA  
568501 ACAAAGCATTTAAAAACCAATAAACACCAACTCCAGCAGCACTAAATGCA  
568551 GTAATAGCAGCAAACACAAAGTAAAAAATTAATTGCATCTTTTAGTTTT  
568601 GTTGAGTTGTTCAATACTTTTTTGAGAATGGGCTTTCGCATTCTCATTAC  
568651 GCTTACTTGCCCACTTGAGGAAGTTTTTGAGAGAGAAATTGGACTGGT  
568701 AAAACAATCACTAAAAAGATGATGAAAGGTCAACCAGTTGTAGTGAAATT  
568751 AGAGAAAATTTCTGTTAAAGGTACTTTTGAAAGATCCCAAAAGTTAAATA  
568801 AGATGATTGCTTTAATTGGTCTTAAAGTAGTAACAATCCTATAAAATAATT  
568851 AAAAAGATAGGTAAAGTTACAAAACTTGAACAAAAGCAGCAGATGATTT  
568901 AATGTTGTGTTTTTTTATAAAGTGACATTATCTCTAACTGTCTGTTCTTT  
568951 TACTTTGTAAATCTATTGCCCCCTTTATATTTAGCGTTAATTTCTGCTAAT  
569001 TTACCTTGCACTTCATTCATCTTTTCAAGTGCTAAAGTAGAGTTAAGGT  
569051 AATCACAATAGTTATCAAGCGAACTAATAGTAAAAGTACTATTAATGAAA  
569101 GAATCATGTTAAACCCAAGTTCACCCCGCTACCTAGTGGAAGCTCTGGTT  
569151 GCATACATAATTGGTAAAACTATTTGCGCTGCAGGCCAGACAAATCATCC  
569201 ATAAAAAGGGCCATATGCTAAGGTGTAATCACTAAAGGTGAAATAAGGGC  
569251 CAAAGTTATTTGAAATCAAATCATACCTATAATCACCAGTAGTACCAAAT  
569301 TTATAACCTATCTCAAGTCCTGAACCTAAGACTTGATTAGTACCTGTTCA  
569351 GGGTTGTGCTAAGGTTTGAGTACAGCCCCAAAGCCCAACAATAGTTAAAA  
569401 AAATAAAGATAAAAAACCTTAATAACCTTTATGAAAATAGCTGAAAACTTT  
569451 TTGAAGTTTTTTTTCAGTTGTTTTTTTTCATTAACAACTGCTGCTGATCAAAA  
569501 AGGATTAAAGGTGGTTTTTATCTCTTTATTTGTTTGCGCTAGTTTGATAG  
569551 GCATCTACTTCTTTTATCCGCTTTAATAGTTGCAAAAAAGTTTTTGTTT  
569601 TTCTTTAAATGTTAATTCAATAAAGCCTTTGTTGACAATAACTAAAATAT  
569651 CTCAAGGTTCTAAATTATTACTAATTTGTTGAAAGATACTACGGATCTGA  
569701 CGCTTAATTAGGTTACGTTGTACTGCTAGCTTATATTTAGTTTTTGCAAT  
569751 TGATATTGCAACCTTCAAGTAGAATGATTATTCTTAATAAAATAAGCGT  
569801 TAATAAAGGTACCAAAGAACCTGGTTTTACTTTGAAGAATGGTTGTAAAA  
569851 ACCTTGCGTTCTCTTAAGCTGTGACTCTTTTTAACGCTCACTGGAAACCG

569901 TGAGTTGAGCACGATTTTAAACGTCTTTGCCTTAAACTTTACGTCCT  
569951 TGTGCAGTTGCCATCCTAGCCATAAAACCATGGGTTTTAGCACGCTTTAA  
570001 TTTGCTTGGTTGGTATGTTTCGTTTCATGAAACAATTAATCAGGTGATTAT  
570051 AACTAAACTAAGGGTCTGACTAATTGGTTAGATACTATTTTACCATCTGA  
570101 AATTTTAATGATTCTATTAGCTATCCTTGTTAGGCTTACATCATGGGTAA  
570151 CCATTAGGATGGTTTGCTTATATGTTTTGTTAATTGTTTGAATAAATTA  
570201 ATGATATTTTCCGCAGAATTACTATCAAGTGCACCAGTAGGTTTCATCACA  
570251 AAGTAATAGTTTAGGTTCTTTAATAATAGCACGGGCGATGGCCACTCTTT  
570301 GTTTTGGCCACCTGACATCTCATAAGGAAATTTATACAAGATTTCTTTA  
570351 ATATCTAATTTTTCAGCCAACCTCTTCTATATCAAGTCGTCTTTGATATTT  
570401 GGGAATTAAGTTTTGTGAAATGGCAATATTATCATAAGCACTTAACAATT  
570451 CAATCAGATTATAACGCTGATAGACATAACCAAGGTATTCTTTTCGATAA  
570501 GTTAAAGTTGTTCACTAGTACATTTTCTAATGGACAGTTTGCTACGAT  
570551 ACAACTCCCTAACGAGATAGAATCATAACCACCTATCAGGTTTAAAGGG  
570601 TTGTTTTACCTGATCCTGAAGAACCTAAAATGATTACTATTTACCATAA  
570651 GCTATCTGTAAAGAAACATCTGAAAGGATAGAAATCTCTTGCTTTGAATC  
570701 ATCATTATGAACATTTTTTACATCTTATTGATGGTAATAACAATCCCT  
570751 TAGCTTGTTGAGCAAAAGGAGGGATATATAAGGTATTGGCTTTTTGCTTT  
570801 TTATTAGCTTTCTTTTGGAGCTTTAGCTCAGCTTTTTTAATGTTATTTAA  
570851 AACTTTTTTATTCTTCTTAGGAGGTTTAGATTTACTCTTTTGAAATAAT  
570901 CATCGAAATTGGCACTAAAAGAAGGACTTTTAACGTTATCTAAGATATCA  
570951 ATACATTCATTTCAAACAGTTTTATTGCCTTTTTTCATTAACATAAACCC  
571001 TTCCTTCAGTTCAGCTGAGCGTAACTTAATTCAAAGTAAGAACCAATTA  
571051 CAAAGATAGTAACACCAAATAATACTATCCCTACCATGTATGGCAAGAAC  
571101 TCAAATACATTAGTTAAAAAGACTTGTGCAACATTGAAAAACAACCGCTTG  
571151 GATACCAATTAAACACCAGCTAAACTCCAATAGAAATTAGTAATGCTA  
571201 AAACAAATGCAGGGATAAAGAAGGTAAGTAACTAATTAAATTTTGACA  
571251 TCTCTATAGCCAATAGCCTTAAGTGAAATAAAGATTCTTTTCATCTCTTC  
571301 TAACATTGAGATACCAAGTACAACAAGTAATGAAAATGAAAGGAATAA  
571351 TAGTTCCTAAAAGAAACGCATCTACTTGATTACAGTGTTAAACAAAAC  
571401 TCAGCATTATTTCTAATGATCTGAGCACTAGTTCAGCTGCATCAATATT  
571451 GAGTACAGGAGCAATAATGTTATTACCAAAAATACTACTTGCAATTTGGG  
571501 AAAGTAAATTAACACTATTTCACTCTGTTTTGTATTTATTAAGTAGTTCT  
571551 TTACGAAGCGATTATTAATAATTTAGGATCAGTAGGTAGTATGGATGTAA  
571601 TTGTGCTAACTTATTAATAATTTAGGATCAGTAGGTAGTATGGATGTAA  
571651 TAACCTTTATCAAGTTTATTCTTACTAAATTTTGGAATTTATTACCAAAG

571701 TCAGTGAAATTACCCCAAACACCAATTATCGAGTTTAATACTAATGCCTT  
571751 ATTTAATAAAGAAGGTTTAAATTCTTTGGAAAATACACCATTAAAAGGAA  
571801 CATAACCGTTTGGTTTTACATAATCAATTCATATTCATCACTACTTTGA  
571851 GATTGGCCATTTGTCTTTTAAATAACATCTCTAATAATACCTCTGCCCTG  
571901 ATTACCACTTAGTTTTAATAAGTTATTAGCAATGTGTTGGTTAATATAAA  
571951 GTTCTTGTCAAAAGCATCAGTAGAAACACCAACAACCTTTAAATGCTACT  
572001 GTTGAATTATTTAAGGGTGCTTTTAGAAAATTTTCAGAGTATCTTGTGGC  
572051 AGTATTTTTCGGTTTTATATAAACATAATCACCAATATTAATGTTGTAG  
572101 CATATTGAAAACCAGCATTAACAATTACATTCATTTCTGATCAGAACTA  
572151 ATTAAATTTCTTAAAGAGTTACCACTACCATCTATCAGATTAACAAAACCT  
572201 TGATTCAGGGTTAATCCCTGTTAAAGTGTATGGTGAATTCTCATCAAGAT  
572251 TATCTTCTTGAAAACCAAATGGGCCTTCAACATAAGTGTAGGTTTCTTCT  
572301 ATGGCAGGGTCAACAGGAACAATCCCAAAATTTAACTTAGAATCTTGT  
572351 TGCAAGTTCAAAATCCCATAACTTTCAACATAAACTAAGAAAGCTAT  
572401 CATTAAATTTAACCCACCAGGATTAAATACATCAATTGTAGTTAGTACC  
572451 CTACTAGCATCTAACTGAATTTGATTAGTTCTAGGGTTTCTAATTAAAAA  
572501 CCCATTAGCATTTAAGTTATTGAAAAAGTCATCAGTTAATACTGAAATTA  
572551 AAAACTGATCACTAGATGCTGAAAGTAACTGAGTAATCTGTTTAGGAATT  
572601 GATTTTTCAACAATTTCCCAAGGGTTAATGTTAGAACCGCCAACCTAAT  
572651 AGGAAAGTCAATAATCCATTTTGATAGAGAGGCATGCCTAAAGAAATTCT  
572701 CATCAGTGTTTAACTGTTGAGCACCACCATAACTAGGCAAAAGTAAGTtG  
572751 CCCAATTCAAGCTCAGTTCCATCTGCTGCTTTTATTGGTTGATCCTGGCG  
572801 GTTTTTAAGTTTTAAATTAATTTGTTTATAAGGGTGCTCATTTTGAGAAT  
572851 TTGCTTGAACACTTTTCGTTATACAAGGTTTTAATACCATTATTATTATCA  
572901 GTAAC TCCAAAGTGTGAATAGGGTTGAATTGCATACCATCCAGATTGCTC  
572951 TGTTGGTGTTTGTAAATTCAACTTATAGTTAAAGTTTCTATTTAAGGAAG  
573001 TGCTTGTTTGTGCTGCACTAAATTTTTGGGGAATAGTACCTGCAATCCCA  
573051 ATTAATAAAAGTGCAACTGAACTCAATCCTACATAGGTAAATAAaACGTGA  
573101 AAAACGTGAAACGATTAATGAAACCCTAAACTTGGTCAAGGGTGACATTG  
573151 TATGACTTTTATGTTTTAAAAGATGAAGAAGAACTGAAAACCTGGTCTCA  
573201 TTGCCTTGATCAATTAAGACATTAACAGGTTTACTAAACAACCTGTTTAAA  
573251 GGCAATTCAACTAATAAAATTCAAAAACAAAAAGGTTATAAAGAAAGAAC  
573301 CAAAAACGATAACCAGTTAAAGCTATTTTCAGGTAAAGCAATAAACCAA  
573351 TACCTATTTATGATTCCTTTACTTGTCCTTCTAGAAGAAAGGCAAATAA  
573401 AACTCCTAAAAAACTAGAAACAATTGCAACAATACCAGCAAACACACTCA  
573451 TTCCAACAATAAATTTAGTTGTTGAAAATCCCCCTGCTCTGATAATAGAA

573501 AACTCAGTTTGATTCTTTTTAATAAATGACTTAATTTAAAGAATAATTAA  
573551 ATAAAGAGCAAGAATAATCAAAAATATAGCAATAACAGTACTTACTATTG  
573601 CCAATAGCTTTGCACTAAATCAGGAAAATAGTTTCTTGCTGTTGTCAGA  
573651 TAATTAACTTAGAAATATCTTTAACATTAAATGCTAAATCACTTCTAGG  
573701 AACATCTAGATATCCCTCTAATCTATTAGCAATAAACTGCACTGGGTCTT  
573751 GGTCAGTGTGCTGTTTTAAATCTGTTGACTTAAAGCATAATAATTTTCT  
573801 TGGTTAGCTGCTGGTACAGCAAACAGAATACTTCTGTAAGCTTGATCATT  
573851 AACAAAGATTAACGCTTCATCTTGGGTATTAGGCAACGGAGATTGTAAAG  
573901 ATAACACTGGGTAACCACTTTCTACTGATTACCTTATACCTAAAATTGCA  
573951 AATGTTAGTCCGTTAATACTAAATTTATAACGATCAGGTAGATCATTTAA  
574001 CCAGTTAGGGAAATGTTTGGTGTGCAATGCAGTTTTTCAAGCATATT  
574051 CCCCTTCCTGGGGAAGAATTTCTTTATTGTGTCTAAACAACCATTGTTGA  
574101 GAAACAACCGCTCCGTGTGCTTCAGGGGTTTGCACAACTAAATTTTGTG  
574151 ATCAGTAGGTAATATTAATGGATTGACCCCATTTTTAACAGTAATAGGGA  
574201 TCTCAAGCATTTGGCGATTTGTCTCTATTAATTCATTAGGATCTTGAAAA  
574251 GCAGGAGTAAATAACTTAAAGTGCAAGATAATTATTAGCTGCTTTTCG  
574301 TTTATCTTCTTCTTAAGATTATTAAATCCATTGGCATCTAAATTAGTTC  
574351 ATGTTTTTAAAGCATCTAAAGCAGTAGTTGGGATATTAGTAGCTTCTGGT  
574401 AATTGGGCTTGAGCAATAATATTTGCTAACTTTGGATAAATGGGAAATTT  
574451 AGTAGATTTTGGACTTAAAGCTTGGGTATTTTTTAACTAGCAGTCATTC  
574501 CACCACTACTGGTGCTTGGTTTTAAATTCATAATCAATTTTTTGTAATAAT  
574551 CCATTATTAGCATCTTGACCACCATAAATGTGTCTAAAGGGTTTGATTC  
574601 ATTTTGCTCAGGTTTAAATAACCAAGATTTAAGATCAACGCCATCAATTA  
574651 AAGAAAGATCGTTGTATCTCTGTTTCATCTTTGTTGGAACTAAAAAACTT  
574701 GCTGACTCTGCTGAACTAACATTGTTAGCTATTGCGATATTTTGCTTTGA  
574751 ATAATCAATGTTATTGAAAGCAGTGGCTTTTAAAAAATGATCACGGTACT  
574801 TTTCTAAAAGATCAACTGTTTTTTTAAACAAGATCCTCTTGAAAGATACTA  
574851 CGTCATTGATCAAGTACTGCTGCATAAACTGCATCAAGGGTTTTTTCAGG  
574901 AGTGTATTGGACTGGTGAATTTTATTGTATGCAGTTTGAACATTTGAAA  
574951 AGTTAGGATCAGCTATTCCATTACTTGCTTGACTGTTTGAATTTGAACT  
575001 AATTGGAGATTGTTGCTTGAAGGTTGAAAAGAAAGATTATTATTTCTTAC  
575051 CATCATTCATTCTGAGTTTTAAAGATTGTGTCTTTATCACTATCACTAA  
575101 AACCTGGTAAGGAATTGAGAATTGTATCTTTCTCAGATTCAACTTTCTTT  
575151 TTAAGTCAATCTTTATTAATTTTTAGTTCAAATTTCTTAAGTTGCTTAAG  
575201 TTTATTTTCAAGATCTCAATCTCCAAAAGAGGAATTATTGGCTATAGTTT  
575251 TAGCATTAGTTTCTAACCCTTTAACTGTTTATTATCTAGCTTATTTAAT

575301 TTAGAAATATCTAAATTAAAAGTTAATGTAAAACTTTGATTATCTTTACT  
575351 TTCTTTTTGGGTTTGAAATTCCTCAACAATTTCTTTAAAAGGATTGACAT  
575401 CTTTCCAAAATTGAGAACCAGGATCGATTTCTAAATCAATTGGGATGTTT  
575451 GCATAAAGATTGGGAAATCAGTTAGCAGCTTCATTACCACCTGTAAATAG  
575501 ATAGTTAGCAGATATATCAGTATTATCTGCTTTGGTCTCATCACTCTTAA  
575551 ACCAAACTTTATCTTTGTTATTGGTTTTATAAAGTGAATTAACAGTACTG  
575601 TCTTTTTGTGGATCATGTGTTGTTGTGCTTTTGTGTAATTTTTACTTG  
575651 TGTTCTGTGCTTTTTCTTTATCACCAGGAAAACGCGCAATGCCAGCAC  
575701 GCAATGAGATAGTTTCTTTAATTAAACCATCAGCAAAATAACCTAGAAGG  
575751 TTACCACTAGCATCATAAATAAGGTTTTGAGGGTCTGATATTATGTGTCT  
575801 ATTTGTAATGGAATCACTAATATCACTACCATTAAAAGAATCAGTATTAT  
575851 TAAAAGAACTGCTAACCCCTTTATAAATCTTTTTTTCAGCAATATTGGCT  
575901 TCTCCATATGCTTTTAAAATACCTCTTTTCTTGCTAAAAAGAGTTTATC  
575951 TTTTTCATTAAACATCGCCTTTGCGGGGAATGGTTTTGTTTGGTTATCAC  
576001 CACTACCATTACTTTGTCCTGAATCACTTCCAAAATCATTTTCTTGATAA  
576051 GGAAAAAGATAGTTAATTTTTTATCATCTATCTTTATTTTGGAAAAATA  
576101 ACCACTATCATTAGTTAAACTGGCTATATAAACAGGATTAGCTTCCTTTA  
576151 AAATAGCAGGAGCTACTATATCAGAAGAGTTAGTTTTAGATACTAATGTA  
576201 GTGTAGGTACTAACTAAGTTGTTACTTAACTGAACAATAGATGTTTCAAG  
576251 GAAAAATAATGCTAAATAAAACAAAGATAATTCCAAATAATAAAAAGAAGA  
576301 ACTTTTTAAGCGATTAAATATCTGTTAAAAAAGAAAACATCTCAATT  
576351 AAACCTCAGTTAATTGTTCGATGGTTTTTGGATTCTGATTAAATAATCA  
576401 ACGATTATCTTGCCATCATGGATTTTAATTACCCGTTTAGCTAATTCCAC  
576451 TATCTTTTCGTTGTGGGTAACCTATTACTATAGTAGTACCTTTGTCACGAT  
576501 TATATTCCACAAAAAATTGCAATATTTTTTTGGAAATATCAATATTAACCT  
576551 GCTCCAGTAGGTTTCATCACCAAACAAAATTTTAGGTTCTTTAATTAAAGC  
576601 CCGAGCAATAGCAACACGTTGTTGTTGTCCACCAGAGAGTTTATGAACTT  
576651 TCTTATGTCTATGTTCTTTTAATTCCAAGCGTTCTAATAATTCTTCAAGA  
576701 TTATTATTAAACCTTTTTTTTAATGGTAGAGCAAGCTTAATATTATCATC  
576751 AACGTCAAGATCACGCAATAAACCATATTGTTGAAAAATATAACCAACGT  
576801 TTTTATTTCTTAACGCGGTTAGTTTTGCATCACTACAACATATGGTGTTA  
576851 GTTCCACAAACAAAACCTATCGCCGCTAGTTGGTCGATCTAATGCGGAAAT  
576901 TAAAGAAAGTAAGCTGGTTTTTACCCTACCAGATTTACCAAGAATAACAA  
576951 CAAATTCTCCTGGAAGAATTTTTAAATTAATGTGGTTACAAATAAGTTGg  
577001 TGTTAATGCCATTTGTAACAGCTTTACAAACTTCTTTGAAGTAAATATCA  
577051 TACTTTTTAGCTTCAAATGAATTAAGTGATTTTCTTTTGGGGTGCTTTTT

5

10

15

20

25

30

35

40

45

50

55

577101 ATTTAACTTTTTAATTAATTTAGATGCTTTTTTACTAACAGCAAAATCTG  
577151 ATGATTTTAAAGTAAATATCAAACCTTTTGTCTCTTTTGTTTTAAACC  
577201 ATAAACAATCATTAAAGTCATCTAAAAAATACCCTGAGAACACTATTAGA  
577251 AAATTTTAATTTTGCTAAATTACTAATGATGTAATTACATCCCGTAATGA  
577301 ACTGTCATTTTCAATCATTTTAGCAACTCTTTTAACTGCCATTAATACAC  
577351 TTGAATGACTTCTCTTAAATATTTTGCCAATTTGTTGAAATTGCATGTTG  
577401 TACTTTTGACGCAAAAGGTAATTACACACATCACGAACACGGACAAGTTC  
577451 TGCTTTACGATTTTCTGAAAGTACACTGTCCATAGGAACATTAAATCTAC  
577501 GGCAAACGTTCTCTATTAATAAATAAGGATCAAAGCTCTTTTATGAAAC  
577551 TTCTCAAATTCCTCAAAAAGAATTTCTTTTAAATTTTCAGTATTTATTAA  
577601 ATTTTGTGTTTGAAGTTTGTAGCAAAAAATAATAACTTTGTTGCAATTCAT  
577651 TTAAAGCACGCACATCGTTACCTGAAATTTGTGCTGCATCATGTCTTGCC  
577701 TCATTAGTTATTTGGATGTTAGGATCTTTTTCTTTTAAATTTAACAGTAAG  
577751 TATTTTCAAAAGTGAAGACAAATTATGCTTTTCTATCTTTAGTAATAATC  
577801 CTGATTTTAAAGCGAGAAATCATTCTTGATCAATATCAATTAGTTCATCA  
577851 GGAGCCTTATCAGAAACTAAAACAATTTGTTTTTTATTAGAACTAGGTT  
577901 ATTA AAAATATTGAAAAGAATTTCTAAGGTTTTTCTTTTCTGCCAATA  
577951 TTTGAGTGTCATCTATTAAACTAAATCTAAATTTTCATAATTTTTTTTT  
578001 AGTTTTTCTATACCTTTATCCCTTTGATAAAAAGCATCAACAACTTCTTG  
578051 GGCAAAATCACTTGAAACAACATACTTTACTCTGGCATTGGAATAATTAC  
578101 GAAATTTTTCATTTCTTATTGCTTGTAGTAGGTGAGTTTACCAAGACCG  
578151 GTTCTCCGTAAATAAAAAGCGGTGAAAATTCGTTATCTTGAGTTTCAGC  
578201 TAATCTAACGCCTGCTTCATAAGCTCTTTTATTTCTTCATAATTACAA  
578251 AGTTTTGAAAAGTATAGTTTTTACTCAATCCAGAATTTTGATAAAGAGTA  
578301 TCACGACTATTTTCTTCTAATTTTGCTAAGTTAAAAAAGAAATCTTGCTC  
578351 ATTAACAAAATTAACACTTTTAATTCCTTCATACAACTTTTCAGCTAAAT  
578401 GAATAATTTTCAAGATTATCATTTAAGGAATTACGAGCAAATTCATTTTCT  
578451 AAAAGAATTAAAAGAACATTATTTTAAATACGAAACGATTAATGTCCTT  
578501 AATGTATTTATCATGAAAACCTATTGTTTTTTCATAATGCTTTTTTAATA  
578551 GAGATTTTAAAGGCATTAAATGTTCCATTATTCTTCTATAACATTGTCAA  
578601 GAATGATAGTTAAAATTCTCGAAATTGGGATATTAAGTCTTTGGAGTAA  
578651 TTTCTAACTTTTGTCTACTCTTTGACTTGTATAGAAGTGTACACCTGT  
578701 ATCTAGTTTTTCTTGCGTTCAACAGGAATAATCCTGGTATTTTTGTTT  
578751 TAGGTTGGGGAGGAATAGGCTGTGGTTGTGTGAATTGTTGTTGAAAATTT  
578801 TGATTTTTTGTCTGTAAGAAACCATTATTATGATATTGAAAATTTGTTC  
578851 CTCTTGAAAATATCTCTCTTTTTTTGGTTTTCCAGAAAATTTGATGAAA

578901 AAGATTTTCCTTCATTTCAATTTTCAAGATTATTTTCATTTTGTTGATTT  
578951 ATTTGCTCAGGCTGTTGAAATGAATTATTTTTTGATCAAAAAGATTTTGG  
579001 AAAGGTTTTTTCAAAGCAGATAAAGGTCCAAAATCAAATGAAGATGAAT  
579051 CTTTGTCAAAGATGTTTCTTCTCTTTTTGACAAATTTTGTTTTTGATTA  
579101 AACTTATTTTTATTTTGGGGTGTTACTTTTTCTTTTATGGAAAACAAATC  
579151 TTCTTCTAAAAGACTTTGTTCTGGGTCATCATCTTGTGCTAAATCAAAGA  
579201 AAAAACGTTTCTTTTTGTTATTAATGGACATTGTAATTTGCTAAATTTAG  
579251 GATTTCTTTTGTTATTTCTAAATACTCATTTAGATATTTTTTACTTGGTG  
579301 ATGATACTAATGATATTGGCAATTTTTCATACCTACAGCTGCTGATGAT  
579351 TTTGATGTCAGAGAAACAAAATTTTTAGAAAAAGCTACATTATTTTTTTT  
579401 AGCTTTTGTTTTAGCTAAATCTATTACTTCATTATGAAGACGAGTACGAA  
579451 CGTTAACTTTTGTAGGAACATAAATAGTTTTAAGATTGTATTTTTTTCC  
579501 TTAAATGTATCTATTGTTTCAACTATTCTCATCAAACCTAGCATCGAATA  
579551 TTGATCTGGTTCAAAGGGAATAACTATGACATCTGATAAACTCATTGCAG  
579601 TAGAACTAAAGTTGCCATATTTGGTGGTGTATCTAATAAAACAAATTCA  
579651 TATCTTTTGTCTAGTTGCTTAACTATTTCTGCTATATCTGAGGCCTTATA  
579701 TTTTTTACGTGATATGTCTATATCAGCAAAATTAAGTTCAAATTACAAG  
579751 GAAGAATATCAAGTCCCTCATATACAGATAGCAAGCAATCATCTATTTCA  
579801 ATGAAATTATTTGAACCACTGAATTTTGGAACCTTCAACAAAATGTCAAT  
579851 TAACGTGTTATTCAATCTTTCAGGGTTTTGTCCAAATGATGCAGAAACAT  
579901 TCCCCTGCCCCGTCAAGATCAAGAATGACTTTTCGCCTTTCTGGACAAAGT  
579951 TTAACCAATGATCCTGCAACATTAGTTGCCATTGTAGTTTTTAATACGCC  
580001 GCCTTTATTATTTACAAAAGAAATGATCATATATTTAAATGATTATAATA  
580051 TTTCTTTAATACTAAAAAATAC

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications recited herein are hereby incorporated by reference.

TABLE 3

Whole Genome Sequencing Strategy	
Stage	Description
Random small insert and large insert library construction	Randomly shear genomic DNA on the order of 2 kb and 15-20 kb, respectively
Library plating	Maximize random selection of small insert and large insert clones for template production
High-throughput DNA sequencing	Sequence xxx,xxx templates from both ends (>99% genome coverage)
Assembly (TIGR Assembler, GRASTA)	Assembly of sequence fragments into contigs
Gap closure	
a. Physical gaps	Order all contigs into a circular genome and provide templates for closure of all physical gaps
b. Sequence gaps	Complete the genome by primer walking
Editing	Visual inspection and resolution of all sequence ambiguities when possible, including frameshifts
Annotation	Identification and description of all ORF's, putative identification, role assignments

TABLE 4

Computer simulation of random sequencing experiments where L = 580,000 and w = 400.				
Clones sequenced (n)	Percent of genome unsequenced	Base pairs unsequenced	Number of double strand gaps	Average gap length (bp)
1000	50.18	291014	501	580
2000	25.18	146016	503	289
4000	6.34	36759	253	145
6000	1.60	9254	97	96
7250	0.67	3886	48	80
8000	0.40	2330	32	72
10000	0.10	586	10	59